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"**ASSESS OF GENETIC DIVERSITY OF *PISTACIA* SPP. IN WILD POPULATIONS AND FIELD GENE BANKS FROM CENTRAL AND WEST ASIA**".

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ASSESS OF GENETIC DIVERSITY OF *PISTACIA* SPP. IN WILD POPULATIONS AND FIELD GENE BANKS FROM CENTRAL AND WEST ASIA

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Dedication

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To my brothers **Adel** and **Emad**,

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1.1. Background information on the *Pistacia*

1.1.1. *Pistacia* taxonomy

The genus *Pistacia* was defined by Linneas in 1737 and includes deciduous trees except *P. lentiscus* and most of *Pistacia* species trees are dioecious. Zohary (1952) recognized 11 *Pistacia* species based on morphological characters, and placed them in four sections. Hence, the genus *Pistacia* is classified as follows according to some published taxonomic studies (Zohary, 1952; Alyafi, 1979; USDA-NRCS, 2006)

Super-division:	Spermatophyta
Division:	Magnoliophyta
Class:	Dicotyledoneae
Subclass:	Rosidae
Order:	Sapindales
Family:	*Anacardiaceae* (70 Genus 850 Species)
Genus:	*Pistacia* L.

The eleven species of *Pistacia* are divided into four sections due to leaf characters and fruit morphology as following (Zohary, 1952):

1. **Section Lentiscella Zohary**: (*P. mexicana* HBK and *P. texana* Swingle);
2. **Section Lentiscus Zohary**: (*P. lentiscus* L. and *P. weinmannifolia* Poisson);
3. **Section Butmela Zohary**: (*P. atlantica* Desf. including *P. mutica* Fischer & C.A. Meyer);
4. **Section Terebinthus Zohary**: (*P. terebinthus* L., *P. palaestina* Boiss., *P. khinjuk* Stocks, *P. vera* L. and *P. chinensis* Burge).

Yaltirik (1967) classified *Pistacia* species in Turkey and added a new species, called *P. eurycarpa* that grows in Bitlis, Mardin and Hakkari provinces. Al-Yafi (1978) divided *P. atlantica* into subspecies according to their leaf morphology. Kokwaro and Gillett (1980) described a new *Pistacia* species in East Africa, *P. aethiopica* Kokwaro. The worldwide genetic diversity in *Pistacia vera* is considered to be very narrow. Maggs (1973) reported that a global total of only about 100 pistachio cultivars has been described and in inadequate matter.

1.1.2. Botanical description

The main diagnostic traits used to distinguish between the various species are mainly leaf characteristics and nut morphology. The following botanical descriptions are used for some of *Pistacia* trees (Zohary, 1996):

- *P. vera* L. is a deciduous tree, up to 8-10 m high, with one or several main trunks and with dense spreading crowns and large. The shining leaves 12 cm long usually have 3, 5 or 7 large leathery leaflets. The fruits are relatively big 1-3.5 cm long, smaller in wild forms and larger in the cultivated varieties. They are also very variable in shape with a relatively thick, bony shell that frequently splits longitudinally at maturity.
- *P. atlantica* Desf. is relatively large tree, up to 20 m tall, with flattened and winged leaf rachis. 3-5 Leaflets 2.5-7 cm long. Drupes are 6-8 mm long with bony shell.
- *P. khinjuk* Stocks is a small deciduous tree 3-7 m high, with relatively long leaves, having 1-3 up to 4 pairs of 3-10 cm long leaflets. Fruits are 4-6 mm in diameter.
- *P. terebinthus* L. is a small, deciduous tree 2-6 m tall. Leaves are 10-20 cm long with unwinged rachis, and usually with 4-6 pairs of 3-5 cm long leaflets. The terminal leaflet is well developed, and it is similar in size to the lateral ones. Fruits are 6-7 mm long, 5-6 mm broad.
- *P. palaestina* Boiss. is very similar morphologically to *P. terebinthus* but the terminal leaflet is reduced or even absent in *P. palaestina.*
- *P. lentiscus* L. is an evergreen shrub with leathery leaves and winged leaf rachis. The leaves bear 2-3 pairs of 1.5-3.0 cm long leaflets. The fruits are about 3-4 mm across, red when young and turn black at maturity.

1.1.3. Origin and distribution

The *Pistacia* L. is mainly a subtropical genus. Eight species are endemic to the old word; two occur in the southern United States of America and Mexico. Zohary (1996) reported that geographically, the largest concentration of *Pistacia* species is found in West Asia (six species) and in the Mediterranean basin (four species).

P. vera is native to Western Asia, where it can still be found wildly, and Asia Minor, from Syria to the Caucasus and Afghanistan. Pistachio cultivation has spread to the Mediterranean region, which has become its second most important center of diversity, after the central Asia Vavilovian center of origin (Vavilov, 1960). Archaeological evidence

discovered in Turkey indicates the nuts were being used for food as early as 7,000 B.C. (Vavilov, 1926; CRFG, 1997). The pistachio was introduced in Italy from Syria early in the first century A.D. Subsequently its cultivation spread to other Mediterranean countries. In Spain was first introduced from Asia by the Romans; the crop was developed during the Middle Ages and later disappeared for unknown reasons, perhaps due to the fact that unbearing male trees were removed, preventing the production of the nuts. It was reintroduced in Spain in the early 1980s (Batlle *et al*., 1996). Charles Mason introduced the tree to the USA in 1854 distributing seeds for experimental plantings in California, Texas. In early 1900's the U.S. Dept. of Agriculture assembled a collection of *Pistacia* species and pistachio nut varieties at the Plant Introduction Station in Chico, California. The major growing areas in Near East are Iran, Turkey, Syria, and to a lesser extent India, Greece and Pakistan (Barone & Caruso, 1996).

P. atlantica is one of the most widely distributed wild species. It is spread almost continuously over the whole Near and Middle East area including northern and western Pakistan, Afghanistan, Iran, north Iraq, south Turkey, Syria, Lebanon, Jordan and Palestine. Outside this rather continuous range, *P. atlantica* builds massive stands in the Maghreb countries extending even to the Canary Islands. Isolated stands of *P. atlantica* also occur in north Turkey. The range of *P. khinjuk* distribution coincides to a large extent with the area of *P. atlantica* in southwest Asia. *P. terebinthus* is a Mediterranean element native to the western and central parts of the Mediterranean basin, while *P. palaestina* is an eastern Mediterranean element, closely related to *P. terebinthus*, replacing the latter in the eastern part of the Mediterranean basin (south Turkey, Syria, Lebanon, Israel and Jordan). *P. lentiscus*, a circum-Mediterranean species, extends to Madeira Island, and reappearing in East Africa from Somalia to Kenya and Uganda (Zohary, 1996).

1.1.4. Importance of genus *Pistacia*

The importance of *Pistacia* is not limited to nut product alone, the tree's great tolerance to drought and their ability to thrive in poor soil conditions make them particularly suitable for forestry programs on marginal lands, where can present a source of additional income to local farmers (Padulosi *et al.*, 1998).

The *Pistacia* genus is underutilized in the Mediterranean region. Ethnobotanical reports point out that this genus has many biotechnological, medicinal and horticultural potentialities which have not been explored yet (Golan-Goldhirsh & Kostiukovsky, 1998). Research efforts have mainly focused on Pistachio (*P. vera* L.) because of its economic

importance, while the other species have been overlooked to a large extent. Some of the other species, e.g. *P. atlantica*, *P. terebinthus* and *P. khinjuk*, are already very useful in pistachio cultivation since they provide vigorous and resistant stock material for cultivar grafting. All are also attractive for the future breeding work in this crop (Browicz, 1988).

Pistachio is one of the most promising nut trees in the central and west Asia and North Africa region due to its high nutritional and medicinal value. It is a major crop, which contributes to the economy and nutrition of many poor communities in the region and the wild species such as *P. atlantica*, *P. palaestina*, *P. Khinjuk*, and *P. terebinthus* constitute an important source of genetic diversity for the pistachio crop (Ezyaguirre *et al.*, 1999).

Currently, pistachio cultivation is spreading all over the subtropical countries. These cultivations are concentrated in Middle East, USA and Europe viz. Greece, Italy and Spain. The total world pistachios cultivation area is about 425,000 hectares, which produces more than 500,000 Mt. The leading countries of pistachio production (Figure 1) are, in the order, Iran, USA, Syria, Turkey and China (FAO, 2006).

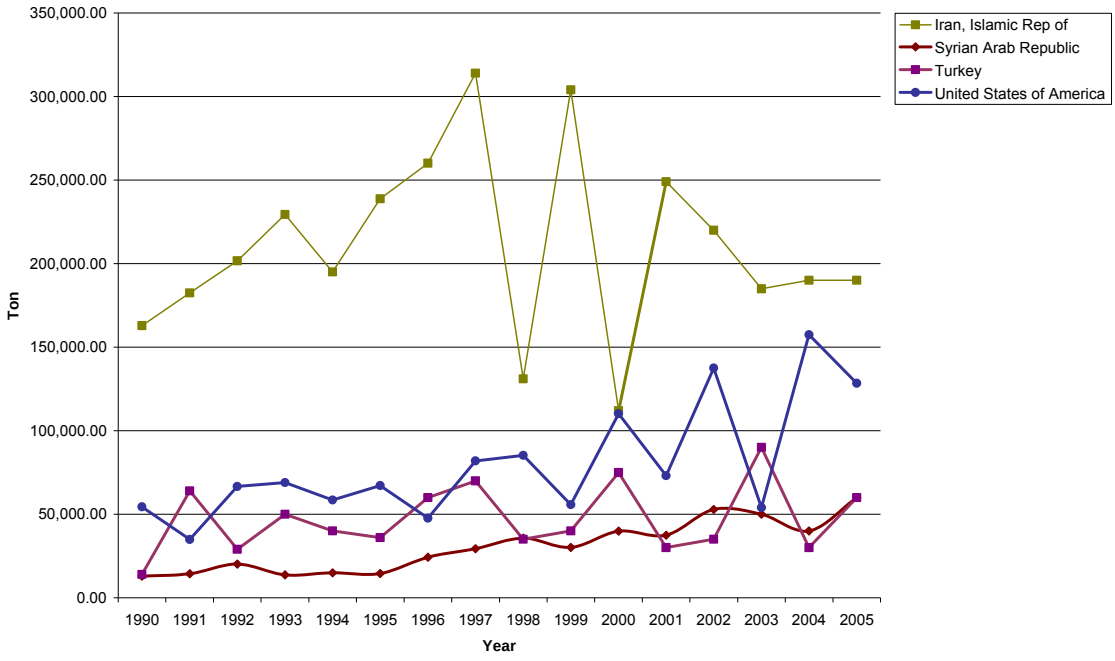


Figure 1. The leading countries in pistachio production from 1990 to 2005 (FAO, 2006).

1.1.5. View of alimentary, medicinal and industrial value

Pistachios, like all nuts, are an important part of a nutritious diet. Pistachio nuts, consumed raw, roasted and salted, have a high nutritional value. 100g of the nuts contains 54g fat, 21g protein, 12.7g water content, 7g carbohydrates, 2g fibers and 3.39g ashes. The nuts

also contain valuable minerals such as 77mg iron, 138mg calcium, 525mg phosphorus, 1027mg Potassium (Duke, 1989; USDA Nutrient Data Laboratory, 2002).

Pistachios are also valued for their therapeutic properties and the nuts could be a folk remedy for scirrhus of the liver and anodyne. Pistachio is a folk remedy for abdominal ailments, abscess, amenorrhea, chest ailments, dysentery, bruises and circulation problems (Duke, 1989). The seed is said to be sedative and tonic (Chopra *et al.*, 1986; Al-Qabani, 1994).

The resin obtained from the *P. lentiscus*, *P. terebinthus* and *P. atlantica* could be employed as an expectorant (Yaltirik, 1967; Chiej, 1984; Chevallier, 1996). The resin is antiseptic, analgesic, antitussive, carminative, diuretic, vulnerary, expectorant, cytostatic, odontalgic, antispasmodic, sedative and stimulant (Uphof, 1959; Grieve, 1984; Duke & Ayensu, 1985). It is used, mixed with other substances as a temporary filling for carious teeth. It could be also used in the internal treatment of children's diarrhea and it is applied, externally, to boils, ulcers, ringworm and muscular stiffness. It is taken in the internal treatment of chronic bronchial infections, streptococcal, urinary and renal infections, hemorrhage, gallstones, tapeworm and rheumatism. It is used to external treatment of arthritis, gout, sciatica, scabies and lice (Bown, 1995).

On the other hand, the resin can be dried and used as a powder, or distilled for oil and essence (Bown, 1995). It is used in high-grade varnishes, as a fixative in perfumes, toothpastes, glue, embalming, etc (Hill, 1952; Huxley, 1992). It is used to seal the edges of microscope mounts and is also chewed to preserve the teeth and gums. An oil obtained from the seed is used for lighting, soap making etc (Bean, 1981). The ancient Egyptians used it to paint the mummy tombs. The leaves contain up to 19% tannin, they are often used as an adulterant of sumac, *Rhus coriaria* (Rottsieper, 1946). A gum is obtained from the *P. atlantica* tree. It is used medicinally (Yaltirik, 1967). Tannin is obtained from galls that develop on the tree as a result of a fungus. It is used to make an ink and a dye (Usher, 1971). The leaves contain 22.2% tannin (Rottsieper, 1946). The wood is suitable for turnery epically to produce Arabic coffee mortar (Hadj Ibrahim *et al.*, 1998; Hanetl, 2001). The turpentine galls contains up to 60% tannin. In the orient countries, such as China, used the tannin to dye silk clothes and vine. In vinegar and salt picked fruits are eaten. The seed are used in pastries (Hanetl, 2001).

1.2. The status of pistachio genetic resources

The genetic resources are the total genetic diversity of a cultivated species and its wild relatives (Ford-Lloyd, 2001). The wild relatives (*P. atlantica*, *P. khinjuk*, *P. terebinthus*, *P. palaestina* and *P. lentiscus*) together with local varieties of *P. vera* form the total *Pistacia* genetic resources. The pistachio crop depends on a very narrow genetic base with a consequent risk for the sustainability of this economy. Moreover, the acknowledgement of the *Pistacia* species' genetic diversity is jeopardy because little attention has been given to the conservation and evaluation of its resources (Tous & Fergunson, 1996). Indeed, traditional cultivars are still being replaced by a few improved types in those areas of greatest diversity and the destruction of natural habitats contributes to the loss of wild species. Meanwhile, research effort is being directed mainly towards crop breeding (Parfitt, 1995).

The strategy that was developed by Underutilized Mediterranean Species (UMS) Project of IPGRI, for promoting *Pistacia* genetic resources, consists of step-by-step approach. The first important action implemented, in order to allow any further work in this area, was the development of two standardized international descriptor lists, one for *Pistacia vera* L. and one for all other *Pistacia* species (IPGRI, 1997; 1998). Other specific tasks, set by the project for the medium-term period, consist of biometric and molecular evaluation of pistachio cultivars along with the characterization of their growing environments (Padulosi *et al.*, 1998). Within this cooperative research programme, on the conservation and utilization of *P. vera* genetic resources, special attention was given to the identification of germplasm and the evaluation of genetic diversity. Many of the male and female accessions, originating in Mediterranean and Central Asian countries and collected in Italy, Greece, Morocco, Spain, and Turkey, were examined for a common set of qualitative and quantitative morphological descriptors previously confirmed to be highly discriminatory (Caruso *et al.*, 1998). In the following paragraphs are summarized statuses of pistachio genetic resources.

1.2.1. Mediterranean basin

Pistachio could be considered as a traditional cultivation in Syria, which is an important area for a natural distribution of wild *Pistacia*, s.a. *P. atlantica*, *P. palaestina*, *P. khinjuk* and *P. lentiscus* (Khalife, 1958; Chandler, 1965; Maggs, 1973). Syrian government has signed the convention in 1995 and established a unit for the bio-diversity at the Ministry of

Environment being the focal point for the convention. A national study for the bio-diversity was prepared in 2000. In the frame of CBD Syria established some protected areas in Syria receive very good attention from the scientific community. Nevertheless, their legislation and administration are still at an early stages and would need further development. Some areas were protected for *in situ* conservation of the populations living there, this is the case for Jabal Al Bala'as (12000 ha) in Hama and Jabal Abdul-Aziz (84050 ha) in Deir el-Zour which are addressed for conserving the *Pistacia atlantica* Stand. Jabal Abou Rajman, desert Mountain, is also suggested to be a protected area for *Pistacia atlantica* (Barkoudah *et al.*, 2000).

Hadj-Hassan (1988) reported the presence of historical pistachio fields, hosting very old trees of *P. vera* (oldest specimens are over thousand years old), in the Ain Al-Tainah village, Kalamoun District, about 60 km north of Damascus. These trees are still in production. This old pistachio variety needs to be safeguarded in order to prevent act of vandalism, which are causing the complete loss of this local variety. In Syria there are several pistachio collections or field gene banks for Syrian varieties:

1. Field gene bank established in the 1984, in the faculty of agriculture of Aleppo University which contains 10 female and 10 male varieties, planted in an area 4X4 m under irrigation (Hadj Hassan, 2003);
2. Field gene bank in the Arab Center for the Studies of Arid Zones and Dry Lands (ACSAD) Izraa, Dara'a (Hadj Ibrahim, 1998);
3. Private Field gene bank contains most of the Syrian pistachio varieties (Table 1) were introduced into to be conserved in 2003 (Ibrahim Basha *et al.*, 2003).
4. Two pistachio collections belonging to Syrian ministry of agriculture and agrarian reform in Aleppo and Hama (Hadj Hassan, 2003).

In Lebanon, *P. palaestina*, *P. lentiscus*, *P. atlantica, P. vera* and the hybrid *P. palaestina* X *P. lentiscus* were found. *P. palaestina* can be considered to be the main species in this country, while the distribution of the remaining species was limited to few locations. The habitats harboring these species, however, have been found to be highly threatened by urban expansion (Talhouk *et al.*, 1998).

Table 1. Germplasm collection of Syrian female varieties grafted on *P. vera*.

	Variety	No. of trees		Variety	No. of trees
1	Ashoury	200	14	Bayd Al Tair	10
2	Red Oleimy	10	15	Ain Al Arab	10
3	Baidy	10	16	Sen Al Feel	10
4	Red Jalab	10	17	Wardany	10
5	Nab Al Dajaml	25	18	White Oleimy	10
6	Marawhy	10	19	Zaroory	5
7	Boundouky	10	20	Abu Rieha	10
8	White Ashoury	10	21	Lesan Al Tair	5
9	Entaby1	15	22	Al Grahy	10
10	Entaby2	15	23	Botmy	5
11	Lazwardy	10	24	White Turkey	10
12	Batoury	10	25	Ain Al Tinaha	5
13	Ajamy	10			

Anatolia is one of the richest source of *Pistacia* genetic diversity in the world. In Turkey, it is estimated that the number of wild *Pistacia* trees is around 66 million. Few millions of these trees have been top-worked in different parts of the country, but the majorities are still standing untouched (Kaska *et al.,* 1996). In Turkey, there are eight main domestic varieties, viz. Uzun, Kirmizi, Halebi, Siirt, Beyazben, Sultani, Değirmi and Keten Gömleği and five foreign varieties, viz. Ohadi, Bilgen, Vahidi, Sefidi and Momtaz. The germplasm of Turkish and international varieties is being maintained in Gaziantep in the field collection of the Pistachio Research Institute. The same varieties are also preserved in Ceylanpinar Experimental State Farm. In order to safeguard the genetic identity of each variety and to best contribute to their preservation, global and regional field collections should be established to this regard with the aim of preserving all varieties and possible ecotypes (Tekin & Akkök, 1995).

In Greece, four *Pistacia* species are recorded as occurring naturally, and two other species are cultivated in orchards. Some additional species and a number of spontaneous or cultivated hybrids also exit (Rouskas, 1996). A major constraint for carrying out proper conservation of *Pistacia* germplasm in Greece is the lake of adequate financial support (Rouskas, 1996). A number of research institutes, including universities, have tried to contribute to the preservation of this valuable indigenous germplasm by establish several germplasm collections. This is the case of the University of Athens, the Agriculture

Research Station ARS in Rhodos, and the pomology Institute in Naoussa. The collections, created at the ARS of Vardates, are also the most recent (Rouskas, 1996).

The Italian pistachio germplasm would represent about 10% of the whole world diversity of this crop. In Sicily, where more than 95% of the Italian pistachio industry is located, only some 10 female cultivars, most of them as relic trees, are now grown, together with even fewer unnamed male selections. Bianca or Napoletana is particularly the only used cultivar while the others represent only 3% of the cultivated area, mostly in abandoned settlements. Some other relic varieties, such as Natalora, Rappa di Sessa, Minnulina and Agostina, may have been lost already since they can no longer be found in the orchards. Nevertheless, a considerable variation can still be found, especially in pistachio male germplasm, which makes it worth describing and preserving also for future breeding purpose (Barone & Caruso, 1996). The situation is similar in other traditional growing areas such as Syria, Turkey and Greece (Barone *et al.*, 1996; Rouskas, 1996).

The Spanish *Pistacia* germplasm bank is held at IRTA Mas Bové in Reus (Tarragona), currently the gene bank holds gemplasm material belonging to six species: *P. vera, P. atlantica, P. integrrima, P. khinjuk, P. palaestina*, and *P. terebenthus*. The *P. vera* collection comprises 46 female and 29 male cultivars from most important producing countries. There are also over 2000 seedlings of *P. vera* from the breeding programme under evaluation (Vargas *et al.*, 1993). The material has been documented and part of it has been isoenzymatically characterized (Rovira *et al.*, 1994; Vargas *et al.*, 1994). IRTA's wild and cultivated *Pistacia* gene bank (Table 2) is probably the largest in the Mediterranean Region and it has been used to provide *P. vera* cultivars and wild species to a large number of institutions of several countries (graft wood or seed material). The are also two smaller pistachio living collections in Spain, namely the SIA's in Zaragoza and CMA's in Ciudad Real (Batlle *et al.*, 1996).

Table 2. *Pistacia* species held at IRTA Mas Bové gene bank.

Species	No. of trees	Origin
P. atlantica	65	USA and Syria
P. integerrima	35	USA
P. khinjuk	33	Turkey
P. palaestina	32	Greece, Syria and USA
P. terebinthus	54	Greece and Spain
P. vera cultivars	75	13 different countries
P. vera seedling	>2,000	IRTA breeding programme

The pistachio of the Atlas is, among those species, the most in danger of genetic erosion in North Africa. The area of distribution is very large; however, its presence has become rarer due mainly to human pressure, pasture and firewood. Collecting are among

the most destructive factors; herds of animals and timber cuts continuously reduce the size of existing populations and particularly of those isolated old trees growing in depressions and talwegs. It has to be mentioned that efforts are being made by North African countries for safeguarding the species. Unfortunately, these are of a limited nature and no continuity (Khaldi & Khouja, 1996).

In Tunisia, which has the largest concentration of pistachio orchards in North Africa, there were no selected female varieties before the introduction of the cultivar Mateur. The two other local varieties from this country are Sfax and El Guettar. At present the most commonly cultivated variety in Tunisia is Mateur, which resembles the Syrian variety Achoury (Jacquy, 1973). This variety includes three main genotypes: male precocious 25A, male late 40A and female 11D (Ghorbel & Kchouk, 1996; Mlika, 1998). Tunisian pistachio cultivation is seriously threatened by genetic erosion as a result of increased monoculture (Ghorbel & Kchouk, 1998). At the national scale, the first established pistachio germplasm collection occupied 3 ha and included 680 lines. It was designed to host local pistachio varieties (female and male trees) and rootstocks (*Pistacia vera* and other species) for vegetation and fruit bearing comparative studies. Unfortunately, this collection was depleted and all varieties are presently found in private parcels (Ghorbel & Kchouk, 1996).

A Mediterranean *Pistacia* germplasm collection is being established at the Jacob Blaustein Institute for desert Research in 1996. The collection consists of live seedling collection and seed collection. The broad objective of this germplasm collection is to evaluate the accession in the collection at macroscopic, molecular and biotechnological levels. In some Mediterranean countries the increasing need, due to land aridization, to protect soil against erosion makes such drought-resistant plants most useful. Thus the collection and selection of native *Pistacia* genetic resources is necessary for their use both as rootstock and planting to prevent soil erosion (Golan-Goldhirsh & Kostiukovsky, 1998).

1.2.2. Central Asia and Iran

In the central Asian only one species of *Pistacia* can be commonly found viz. *Pistacia vera* L. the ancestor of pistachio. These regions are natural centers of diversity for the species and offer great potentials for exploitation of the cultigens through dry horticultural systems. The regions of *P. vera* are characterized by a variety and complexity of reliefs hillsides are often crossed by ravines. At present, in Central Asia, *P. vera* is underexploited, on average less than 5 kg/ha. Indeed, *P. vera* stand in Central Asia are

characterized by a greater diversity, but the destruction of the ecosystems will affected the conservation of the valuable genetic diversity, which is so important for crop improvement programs (Kayimov *et al.*, 1998).

In 1935, Vavilov wrote "We only started to study the forms of wild pistachio, but at present we already have found a greater variety of forms, including large fruit-size type, similar to the best California pistachios". Pistachio “the Green Gold” is one of the most important agricultural products of Iran. In the Kerman Province, the genetic diversity of pistachio is very high if compared with other regions. More than 70 pistachio cultivars are being grown in the Kerman Province alone, each variety having its distinct traits (Esmail-Pour, 1988a).

Currently, the Rafsanjan Pistachio Research Institute in Iran has 3 collections of male and female pistachio varieties along with some accessions of *Pistacia* species. The female pistachio collection is the largest and includes 45 varieties from Kerman, Gliazvin and Semnan Provinces. These germplasm collections were established in 1982. Each variety is represented by 18 trees. One of the most important national projects conducted by the Rafsanjan Institute is the identification, collection, conservation and regeneration of pistachio genetic resources. This project involves 8 Provinces and its main goal is the identification of new varieties, the prevention of their genetic erosion, their collection and the conservation of all varieties in 3 sites (located in Kerman, Ghazvin and Semnan Provinces). This project includes also the evaluation of each variety to assess their performance in various conditions (Esmail-Pour, 1988b).

1.3. Importance of variability and its conservation

The Convention on Biological Diversity, Article 2 defines biodiversity as: «the variability among living organisms from all sources including, inter alia, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part» (CBD, 1992).

There are several methods to measure biodiversity. It is usually plotted as taxonomic richness of a geographic area, with some reference to a temporal scale. Whittaker (1972) described three common metrics used to measure species-level biodiversity, encompassing attention to species richness or species evenness viz. (Species richness - the most primitive of the indices available, Simpson index and Shannon index). Moreover there are three other indices, which are used by ecologists viz. (Alpha diversity, Beta diversity Gamma diversity).

Plant biodiversity represents the primary source for food, feed, shelter, medicines and many other products and means that make life on Earth possible and enjoyable (WCMC, 1992; UNEP, 1995). The diversity of plant life is an essential underpinning of most of our terrestrial ecosystems. Humans and most other animals are dependent on plants, directly or indirectly, as a source of energy through their ability to convert the sun's energy through photosynthesis in chemicals which could be conserved and used. Worldwide tens of thousands of higher plants species, and several hundred lower plants, are currently used by humans for a wide range of purposes, i.e. as food, fuel, fiber, oil, herbs, spices, industrial crops, forage and fodder for domesticated animals. In the tropics alone, it has been estimated that 25,000-30,000 species are in use (Heywood, 1992) and most of them have been used in traditional medicines. Another important role of plant life is the provision of ecosystem services the protection of watersheds, stabilization of slopes, improvement of soils, moderation of climate and the provision of a habitat for much of our wild fauna. The plants that we already use as crops are still dependent upon the broad of genetic base that exist in their wild relatives. The plant biodiversity could be also used in breeding programs to improve or better protected crops (Maxted *et al.*, 1997a).

While it is now generally accepted that the conservation of all biodiversity is imperative, especially through the preservation and sustainable use of natural habitats, this task is unlikely to be achieved and there are realistic scientific, economic and sociological reasons for giving tough priority to actions for the conservation of the major centers of plant diversity throughout the world, especially as this will very often also lead to the conservation of much animal and micro-organism diversity as well. Of course, the different strategy of conservation to be used strongly depends on the nature of the material and on the objectives and scope of the conservation activity (Frankel, 1970). There are two basic approaches to germplasm conservation, namely *in situ* and *ex situ* conservation.

In-situ conservation means on-site conservation. As definition, it is the process of protecting an endangered plant species in its natural habitat, either by protecting or cleaning up the habitat itself. While *ex-situ* conservation means literally, off-site conservation, which is the process of protecting an endangered species of plant by removing it from an unsafe or threatened habitat and placing it or part of it under the care of humans. The model of genetic conservation could be summarized as follows in accord with Maxted *et al*., (1997b):

1. Selection of target data;
2. Project commission;

3. Eco-geographic survey / preliminary survey mission;
4. Conservation objectives;
5. Field exploration;
6. Conservation strategies
   a) ***Ex situ*** (Sampling, transfer and storage):
      - **Seed storage**: seed storage is the preservation of seeds under controlled environmental conditions, which will prolong the viability of the seeds for long periods. The International Board of Plant Genetic Resources (IBPGR) Advisory Committee, which is changed into International Plant Genetic Resources Institute (IPGRI) in 1991 and in 2006 it is known as Bioversity International, on Seed Storage has recommended storage conditions:
        - **For base collections** (store accessions for long-term storage. They are not used as a routine source for distribution of germplasm but as a security against loss), seeds of between 3 - 7% moisture content should be stored in sealed containers. Sub-zero temperatures are acceptable, but –18°C or less is preferred.
        - **For active collections** (store accessions from which seed samples are drawn for distribution, regeneration and evaluation of plant characteristics, seeds are stored for shorter periods "medium-term") sealed storage of seeds dried to 7% moisture content or less is recommended at temperatures of less than 15°C (Hanson, 1985).
      - ***In vitro*** **- slow growth conservation:** Slow growth methods, employing the use of additives or growth retardants in media or reduced storage temperature or oxygen tension (Taylor, 1996), provide a medium term storage option for conservation and can allow subculture intervals to be extended significantly.
      - **Cryopreservation**: For long-term *in vitro* storage, cryopreservation, storage at ultra low temperatures, using liquid nitrogen (-196°C) is employed. At this temperature, all cellular division and metabolic processes are suspended with minimal impact on genetic stability. Theoretically, plant material can thus be stored without alteration or modification for an unlimited period of time (Withers & Engels, 1990; Maxted *et al.,* 1997b). Cryopreservation protocols are now available for cell suspensions, callus, apices, zygotic and somatic embryos of several hundred species of temperate and tropical origin (Engelmann, 1997).

- **Pollen storage**: Pollen storage is considered an emerging technology for genetic conservation (Harrington, 1970; Roberts, 1975; Zhang *et al.*, 1993; Towill & Walters, 2000). Cryopreservation storage of pollen has been used to assist with hybridization of species with asynchronous flowering. Consequently, this method can help in enhancing utilization of available genetic resources. Pollen can be easily collected and cryopreserved in large quantities in a relatively small space.
- **Field gene banks**: Although the field gene banks hazard is to being damaged by natural calamities, infection, neglect or abuse, it is still necessary for many important varieties such as horticultural and forestry species which are either difficult or impossible to conserve as seeds (i.e. no seeds are formed or if formed, they are recalcitrant) or reproduce vegetatively (Ramanatha Rao & Riley, 1995; Ramanatha Rao *et al.*, 1996).
- **DNA storage**: DNA banks provide a new option for an assemblage of plant germplasm (Peacock, 1989; Adams *et al.*, 1994). Samples of genomics DNA are made with isolated directly for plant tissue. Major disadvantage of DNA banks is that the total DNA samples are essentially non-renewable. Therefore, DNA banking did not offer a conserving solution for plant genetic resources, but only for particular gene sequences.
- **Botanical garden**: This is the most ancient and widely known conservation strategy. Moreover, they conduct or facilitate botanical research, especially in plant taxonomy (Frankel *et al.*, 1998). Worldwide, 1500 Botanical gardens (11% private) maintain living collections of plants. Most of the botanical gardens (915) are situated in Europe the former Soviet union and USA (Scarascia-Mugnozza & Perrino, 2002)

b) ***In situ*** (Designation, management, and monitoring):

- **Biosphere reserves/protected areas**: Conservation of wild species crop relatives in genetic reserves involves the location, designation, management and monitoring of genetic diversity in a particular, natural location (Maxted *et al.*, 1997a). However, it must be remembered that genetic reserves are often not very accessible for use. Additionally, if the monitoring and management may not be optimal due to difficult conditions under which these need to be performed.

- **On-farm conservation**: *In situ* conservation of agro-biodiversity or on-farm conservation involves the maintenance of traditional crop cultivars (landraces) or farming systems by farmers within traditional agricultural systems (Hodgkin *et al.*, 1993).
- **Home gardens**: Home garden conservation is very similar to on-farm conservation; however, the scale is smaller. In most rural situations, home gardens tend to contain a wide spectrum of species, such as vegetables, fruits, medicinal plants and spices, than on-farm plots.

7. Conservation products (seed, live and dried plants, in vitro explants, DNA, pollen, data);
8. Characterized /evaluation;
9. Plant genetic resources utilization: (breeding / biotechnology);
10. Utilization products (breeding new varieties and crop, pharmaceuticals, pure and applied research, on-farm diversity, recreation).

1.4. Centers of diversity

In 1882, De Candolle published his book ‘origine des plantes cultivees’, which can be considered as the first significant contribution to understanding the agriculture origins. On other hand, in the book "Centers of origin of cultivated plants" Vavilov (1926) focused on the diversity of crop plants and enunciate the theory on centers of diversity, which he interpreted as centers of origin for many crops. Subsequently, the center of origin of crops was considered only the ones which contains not only a wide variation of forms for the crop, but also the presence of its wild relatives. Vavilov proposed eight primary and some secondary centers (Figure 2) on the based of analyses from hundred of thousands of collection expeditions conducted from 1923 to 1933. The eight Vavilovian Centers are:

1. **Chinese Center:** The largest independent center, which has 136 endemic plants which are a few known to us as important crops;
2. **Indian Center:** This area has two sub-centers:
    a. Main Center (Hindustan): contains 117 endemic plants;
    b. Indo-Malayan Center: contains fifty-five plants;
3. **Central Asian Center:** contains forty-three plants including pistachio;
4. **Asia Minor Center:** contains eighty-three species including nine species of wheat were located in this region;

5. **Mediterranean Center:** contains eighty-four plants including olive and many cultivated vegetables and forages;
6. **Abyssinian Center:** contains 38 species;
7. **South Mexican and Central American Center;**
8. **South American Center:** contains 62 species. Three sub-centers are found:
    a. Peruvian, Ecuadorian, Bolivian Center;
    b. Chilean Center;
    c. Brazilian-Paraguayan Center.

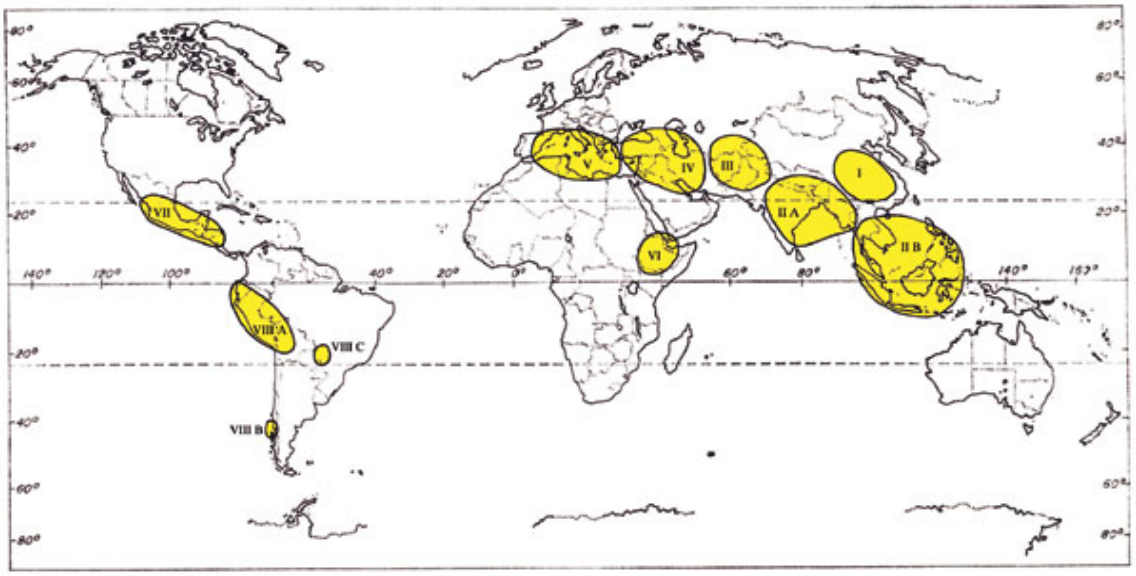


Figure 2. The eight primary with the secondary Vavilovian centers of origin for crop plants (After Vavilov, 1960).

1.5. Ecogeographic survey

An ecogeographic study is the process of obtaining, collating and analyzing different kinds of existing data pertaining to a taxon within a defined region (Maxted *et al.*, 1995). Such a study is generally seen as an essential first step in the development of a comprehensive strategy for the conservation and use of plant genetic resources. The concept of ecogeographic studies was originally developed almost entirely in the context of conservation of wild plant gene pools. For example, an early IBPGR publication on the subject was specifically concerned about crop relatives (IBPGR, 1985). IBPGR (1985) described ecogeographic surveying as the determination of distribution of particular species in particular regions and ecosystems; patterns of infra-specific diversity; and relations between survival and frequency of variants and associated ecological conditions.

Maxted *et al.* (1995) and Maxted and Kell (1998) state that an ecogeographic survey consists of three phases, each made up of a number of distinct, though interlinked, steps:

Phase 1: Design the project

- Commission the project
- Identify taxon expertise
- Select target taxon taxonomy
- Delimit and characterize the target region
- Identify taxon collections

Phase 2: Collect and analyze data

- Inventory conserved germplasm
- Collate data from taxon collections
- Survey other sources of information
- Analyze the data

Phase 3: Generate ecogeographic products

- Ecogeographic database, conspectus and report
- Identify conservation priorities

Specific examples of ecogeographic studies and surveys applications on crop and wild species germplasm include: rice *Oryza sativa* L. (Yawen *et al.*, 2003) *Trifolium* species (Bennett & Bullitta, 2003) and the forage species *Vicia* (Maxted, 1995; Bennet & Maxted, 1997; Maxted & Kell, 1998). Detailed ecogeographic study was made for annual legume species in Syria. This study showed the importance of annual rainfall and how this affected the populations genetic erosion (Ehrman & Cocks, 1990). Dulloo *et al.* (1999) made herbarium based ecogeographic survey supplemented by detailed field surveys of wild *Coffea* species in the Mascarene Islands to enable an assessment of the IUCN conservation status of native *Coffea* species.

Ecogeographic survey was carried out in Syria to lead a better definition of pistachio cultivating zones across the country (Ibrahim Basha *et al.*, 2003). At the same time, these expeditions yielded 114 representative phenotypes from 37 ecologically different sites localized by using GPS. The latitude ranged between N 32° 38.989' (Dara'a) and N 36° 53.352' (Ain Al-Arab, Aleppo), the longitude ranged between E 36° 05.755' (Dara'a) and 40° 37.664' (Al-Malkeiha, Al-Hasaka), while the altitude ranges between 321m asl (Al-Raqqa) and 1200 m asl (Ain Al-Tainah, Damascus). A map with the distribution of pistachio were developed using GIS data. Pistachio is cultivated in 2nd, 3rd

and 4th climatic zones where the rainfall ranges between 190- 350 mm/year (average of 40 years data). The soil of most studied sites was light loamy with pH ranged from moderate to alkaline, poor in organic matter (< 2%), and not salty (Ibrahim Basha *et al.*, 2003). Pomegranate is another important horticulture crop in Syria, therefore also an ecogeographic survey were developed to identify the conditions of this valuable crop. The data from this survey indicated that the majority of the production is concentrated in the first settlement zone characterized by annual rainfall over 350 mm. Generally, the sour varieties prevail in the northeast semi-arid regions: Jarablos, Manbej, Al-Bab whereas the sweet as well as semi-sour types in the internal and coastal regions site: Arbin, Hafa, Darkoush, Basuta (Yossef *et al.*, 2003).

1.6. Diversity studies

Variation can be assessed at the phenotypic and/or genotypic levels. The assessment of phenotypic variation focuses on morphological traits that define the shape and appearance of a set of individuals. These morphological traits should be Mendelian characters i.e. they should be heritable and not, or very little, affected by the environment. The assessment of genotypic variation is done at the DNA level by molecule markers (De Vicente & Fulton, 2003).

1.6.2. Morphometric diversity

Traditionally, diversity within and between populations was studied by assessing differences in the morphology, such as morphometric traits which are observable characters of the individual and are the result of genetic differences in loci distributed throughout the genome (Kermali, 1994). These measures have the advantage of being readily available, do not require sophisticated equipment and are the most direct measure of phenotype, thus they are available for immediate use. However, morphological determinations need to be taken by an expert in the species, they could be subject to changes due to environmental factors and may vary at different developmental stages; moreover, their number is limited (De Vicente & Fulton, 2003). The International Plant Genetic Resources Institute (IPGRI) has published descriptor lists, which provide detailed information about how to collect phenotypic data for the characterization of a wide range of agricultural crops in different languages (IPGRI, 1996; 1998).

The detection of regional and local patterns of phenotypic variation offers an effective method of stratifying and sampling variation in germplasm collection (Peeters *et*

al., 1990) and assist in the formulation of conservation priorities (Maxted *et al.,* 1995). The results of these works can specifically be used in the planning of future collection missions (Bennett & Maxted, 1997), creating core collections (Tohme *et al.*, 1995) and identifying possible sources of parental material for breeding programs. Furthermore, the assessment of phenotypic variation is also useful for studying phylogeny and habitat adaptations of species and varieties (Hedenäs & Kooijman, 1996).

Since in the characterization, evaluation and classification of plant genetic resources are usually used a large number of accessions and several characters of agronomic and physiological importance, multivariate analyses, which are able to deal with many variables, are very useful (Peeters & Martinelli, 1989). The value of multivariate methods for handling morphological variation in germplasm collections have been demonstrated in many crop plants. The information generated can be useful for identifying groups of accessions that have desirable characters for crossing, for planning efficient germplasm collecting expeditions, for establishing core collections, for revealing the patterns of variation in germplasm collections and for investigating some aspects of crop evolution (Camussi *et al*., 1985; Cowen & Frey, 1987; Peeters & Martinelli, 1989; Brown, 1991; Perry & Mcintosh, 1991; Souza & Sorrels, 1991). The principal component and cluster analyses have been utilized for the evaluation of germplasm banks (Mardia *et al.* 1979; Cruz & Regazzi 1994).

1.6.2.1. Morphometric diversity in Pistachio

The first monographic study of the genus *Pistacia* was made by Engler (1883) who described eight species and a few varieties. After Engler, several additional species have been described by various authors, and so far the most complete taxonomic study was done by Zohary (1952, 1972). In his monography, the genus is sub-divided into four sections as reported in paragraph 1.1.1. The main diagnostic traits used to distinguish between the various species are mainly leaf characteristics and nut morphology (Yaltirik, 1967; Al-Yafi, 1978, Kokwaro & Gillett, 1980). Lin *et al.* (1984) compared leaf morphology, photosynthesis and leaf conductance of nine *Pistacia* species. El-Oqlah (1996) described Jordanian *Pistacia* species morphologically, anatomically and palynologically.

Al-Husny (1972) published some general information on the characteristics of Syrian female varieties. While Nahlawi *et al.* (1985) published results of a comparative study involving 5 varieties, namely Ashoury, Batoury, Oleimy, Bundouky and Ain Al-Tainah, being conducted under relatively dry environmental conditions, in Houran, South

Syria. Hadj-Hassan (1998) studied some of main Syrian female varieties in Aleppo during the period of 1978-1979. The 11 varieties characterized were: Ashoury, Red Oleimy, White Oleimy, White Jalab, Red Jalab, Nab Al Dajaml, Marawhy, Lazwardy, Boundouky, Batoury and Ajamy. The characters studied regarding the growth of fruit shoots, inflorescence and flowering date and the factors affecting the fruit production. Overall look to the total cultivation, the Ashoury variety ranks in the first order with 85% of total cultivation, followed Red Oleimy (5%) and Batoury (5%) and remaining varieties (5% as whole). In Turkey the survey and the morphological characterization regarded the common three wild *Pistacia* species, *P. terebinthus* L., *P. atlantica* Desf. and *P. eurycarpa* Yalt, (Kafkas *et al*., 2002). Ibrahim Basha *et al.* (2003) characterized about 25 Syrian female varieties using IPGRI descriptor list. These varieties represent almost all the Syrian varieties some of these varieties are well none while other were identified for the first time.

1.6.3. Biochemical methods

To overcome the limitations of morphological traits, other markers have been developed at both the protein level (phenotype) and the DNA level (genotype). Protein markers are usually named biochemical markers. Protein markers (seed storage proteins and isozymes) are detected through electrophoresis. The analysis of polymorphisms by protein markers has some of the advantages as using morphological ones. However, protein markers are also limited by being influenced by the environment and changes in different developmental stages. Even so, isozymes are a robust complement to the simple morphometric analysis of variation (De Vicente & Fulton, 2003).

Enzymes are a particular type of protein that act as catalysts. Each enzyme is highly specific with regard to the type of chemical reaction that it catalyzes and to the substances (called substrates) on which it acts. According to how enzymes are coded, they could be divided into (i) Allozymes: enzymes coded by different alleles at one gene locus and (ii) Isozymes: enzymes coded by alleles at more than one gene locus. Polymorphisms are generated by changes in the amino acids that may result in changes in the primary structure of the enzyme. One of the most widely used procedures for revealing variation in enzymes and other proteins is electrophoresis, a technique that came into widespread use in the late 1960s (Griffiths *et al*., 1966; Harris, 1966; Lewontin & Hubby, 1966).

Isozyme analysis is, in principle, a robust and reproducible method. In addition, isozymes are codominant markers and are suitable for estimating all population genetics parameters and for genetic mapping. About 90 isozyme systems have been used in plants,

with isozyme loci being mapped in many cases. The major limitation of isozyme analysis is the low number of markers. Consequently, the percentage of genome coverage is inadequate for a thorough study of genetic diversity. Another disadvantage of isozyme analysis lies in the markers being based on phenotype. As such, they may be influenced by environmental factors, with differences in expression confounding the results interpretation. Since differential expression of the genes may occur at different developmental stages, or in different tissues, the same type of material must be used for all experiments (De Vicente & Fulton, 2003).

1.6.4. Use of molecular techniques in genetic diversity studies

DNA polymorphisms can be detected in nuclear and organelles DNA, which is found in mitochondria and chloroplasts. Molecular markers concern the DNA molecule itself and, as such, are considered to be objective measures of variation. They are not subject to environmental influences; tests can be carried out at any time during plant development; and, they have the potential of existing in unlimited numbers, covering the entire genome. A good marker is (De Vicente & Fulton, 2003; De Vienne, 2003):

- Polymorphic: it is variable among individuals;
- Reproducible: in any laboratory experiment, whether within experimental events in the same laboratory or between different laboratories performing identically;
- Codominant: a heterozygous hybrid presents simultaneously the combined genotype of the two homozygous parents;
- Evenly distributed throughout the genome: the more distributed and dense genome coverage is, the better the assessment of polymorphism;
- Discriminating: that is able to detect differences between closely related individuals;
- Insensitive to environmental influences: the inference of a marker's genotype should be independent of the environment in which the individual lives or its developmental stage;
- Neutral: the allelic substitutions at the marker locus do not have phenotypic or selective effects;
- Inexpensive: easy, fast and cheap in detecting across numerous individuals.

Due to the rapid developments, in the field of molecular genetics, a variety of different techniques have emerged to analyze genetic variation during the last few decades (Whitkus *et al.* 1994; Karp *et al.* 1996, 1997a,b; Parker *et al.* 1998; Schlötterer 2004). These techniques may differ with respect to important features, such as genomic abundance, level of polymorphism detected, locus specificity, reproducibility, technical requirements and financial investment. No marker is superior to all others for a wide range of applications (Spooner *et al.*, 2005).

1.7. Molecular marker techniques

A whole range of different techniques can be used to detect polymorphisms at the DNA level. These Marker techniques could be divided into three broad categories with respect to basic strategy (Karp & Edwards, 1997):

I. Non-PCR based approaches**;**

II. PCR Arbitrary priming;

III. Targeted-PCR and sequencing.

These techniques are very fruitful tools in diversity assessment on the level of DNA sequences which became important method in studding plant genetics (Gebhardt *et al.*, 1991).

1.7.1. Non-PCR based techniques

1.7.1.1 Restriction Fragment Length Polymorphism (RFLP)

RFLP analysis was one of the first molecular techniques used for enabled the detection of polymorphisms at the sequence level. The principle behind the technology rests on the possibility of comparing band profiles generated after restriction enzyme digestion in DNA molecules of different individuals. These differences in fragment lengths can be seen after gel electrophoresis, blotting the fragments to a filter and hybridizing probes and visualization (Karp & Edwards, 1995).

RFLP analysis was used extensively in the construction of genetic maps and has been successfully applied to genetic diversity assessments, particularly in cultivated plants such as rice and maize (Ahn & Tanksley, 1993; Dubreuil & Charcosset, 1999), wheat (Enjalbert, 1999) and *Brassica* (Lagercrantz & Lydiate, 1996), but also in populations and wild accessions e.g. Scots pine (Sinclair *et al.*, 1999), wild rice (Sun *et al.,* 2001). RFLP technique was used to characterizing 79 types of peach cultivated in Yugoslavia (Gaћic *et*

al., 2001). As a technique for diversity studies, there are three important advantages which should be considered (Karp & Edwards, 1997):

- RFLPs are highly reproducible between laboratories and the diversity profiles generated can be reliably transferred.
- RFLPs are co-dominant markers, enabling heterozygotes to be distinguished from homozygotes.
- No sequence-specific information is required and the approach can be applied immediately for diversity screening in any system.

There are serious limitations in RFLP technique such as it needs large amount of DNA, can not be automated, needs a suitable probe library, and consumes time and costly.

1.7.2. PCR arbitrary priming

With the advent of PCR, a number of techniques became available for the screening of genetic diversity. These require no prior sequence-specific information and can, therefore, be applied directly to any organism. Three main techniques fall within the category of PCR-based markers using arbitrary primers: RAPD, DAF and AP-PCR. MAAP is the acronym proposed by Caetano-Anollés *et al.* (1992) to encompass all of these closely related techniques. The techniques are based on the use of a single 'arbitrary' primer, which may be purchased from commercial companies, in a PCR reaction on genomic DNA and result in the amplification of several discrete DNA products.

1.7.2.1. Randomly Amplified Polymorphic DNA (RAPD)

The most commonly used is RAPD analysis in which the primers are usually 10-mer or 20mers and in which the amplification products are separated on agarose gels in the presence of ethidium bromide and visualized under ultraviolet light (Williams *et al.*, 1990). Polymorphisms are detected as the presence or absence of bands and result from sequence differences in one or both of the primer binding sites.

RAPD techniques played an important role in characterizing the plant genetic resources around the world (Lee *et al.*, 2001). For instance, 52 genotypes of peach were characterized and genetically assessed by RAPD; the results showed a very high genetic relation between the studied types (Quarta *et al.*, 2001). This technique helped also in genetic relatedness assessment for varieties of citrus (Cabrita *et al.*, 2001), date palm (Javouhey *et al.*, 2000), banana (Howel *et al.*, 1994), Moroccan olives (Khadari & Bervillé, 2001), broccoli and cauliflower (Hu & Quiros, 1991). The company Keygene N.

V., (Wageningen, the Netherlands) has developed a method which is universally applicable, which reveals very high levels of polymorphism and which is highly reproducible. This procedure, termed Amplified Fragment Length Polymorphism (AFLP) (Zabeau & Vos, 1993).

1.7.2.2. Amplified Fragment Length Polymorphism (AFLP)

Vos *et al.* (1995) described the AFLP technique as being based on the detection of restriction fragments by PCR amplification and argued that the reliability of the RFLP technique is combined with the power of the PCR technique. Other recommendations include those of Powell *et al.* (1996a) who suggested that AFLP provides high levels of resolution to allow delineation of complex genetic structures, whilst Winfield *et al.* (1998) saw AFLPs as reliable and informative multilocus probes.

AFLPs are DNA fragments (80–500 bp) obtained from digestion with restriction enzymes, followed by ligation of oligonucleotide adapters to the digestion products and selective amplification by the PCR. This technique is essentially involves both RFLPs and PCR, in that the first step is restriction digestion of the genomic DNA but this is then followed by selective rounds of PCR amplifications of the restricted fragments that are then separated by polyacrylamide gel electrophoresis AFLPs are dominant markers. This technique can be analyzed on automatic sequencers (Winfield *et al.*, 1998) using fluorescent labeled primers and, therefore, high throughput can be achieved. There are synonyms sometimes used to refer to AFLP such as Selective Fragment Length Amplification (SFLA) and Selective Restriction Fragment Amplification (SRFA) (Spooner *et al.*, 2005, Weising *et al*., 2005).

The strengths of AFLPs lie in their high genomic abundance, considerable reproducibility, the generation of many informative bands per reaction, their wide range of applications, and the fact that no sequence data for primer construction are required. AFLP is a widely valued technology for gene mapping studies (Vos *et al.*, 1995). The key feature of AFLP is its capacity for the simultaneous screening of many different DNA regions distributed randomly throughout the genome (Mueller & Wolfenbarger, 1999). Disadvantages of AFLP include the need for purified, high molecular weight DNA, the dominance of alleles, and the possible non-homology (Spooner *et al.*, 2005).

AFLP has proven to be extremely proficient in revealing diversity studies for several crops such as pea (Lu *et al.*, 1996), grapes (Sensi *et al.*, 1996), wild beans (Tohme *et al.*, 1996), common bean (Xu *et al.*, 2000), sugarcane (Besse *et al.*, 1998), intergeneric

and interspecific relationships in *Araceae* (Loh *et al.*, 2000), *Phaseolus lunatus* and related wild species (Caicedo *et al.*, 1999), *Vigna minima* (Yoon *et al.*, 2000), *Oryza sp.* (Federici *et al*., 2001) and characterization of germplasm genetic diversity in cultivated and wild cherry trees (Tavaud *et al.*, 2001). Russell *et al.* (1999) investigated the genetic variation of *Calycophyllum spruceanum* (Rubiaceae), a fast growing pioneer tree of the Amazon Basin. AFLPs were successful utilized to construct integration linkage map for some crops such as sugar beet (Schondelmaier *et al.*, 1996), durum wheat (Nachit *et al*., 2001), sorghum (Boivin *et al.*, 1999), oat (Jin *et al.*, 2000), tomato (Haanstra *et al.,* 1999), *Curcumis melo* L. (Wang *et al.*, 1997), rice (Zhu *et al.*, 1998) and *Zea* (Xu *et al.*, 1999).

AFLP markers have also been used at the level of the individual, for paternity analyses and gene-flow investigations, *e.g.* Krauss & Peakall (1998) analysed paternity in natural populations of *Persoonia mollis* (Proteaceae), a long-lived fire-sensitive shrub from southern Australia. Several studies have used AFLP markers in phylogenetic analyses. Heun *et al.* (1997) used a phylogenetic analysis of the allele frequency at different AFLP loci to suggest that *Triticum monococcum* subsp. *boeticum* (*Poaceae*) was the likely progenitor of cultivated einkorn wheat varieties. Others, including Aggarwal *et al.* (1999) who investigated the phylogenetic relationships among *Oryza* species using AFLPs and Kardolus *et al.* (1998), who applied AFLPs to *Solanum* taxonomy, concluded that AFLP was an efficient and reliable technique for evolutionary studies. Other researchers use AFLPs to create dendrograms, and suggest evolutionary hypotheses, or correlate AFLP pattern similarity with phylogenetic closeness (Mace *et al.*, 1999). There are only few studies (*e.g.* Russell *et al.*, 1999; Muluvi *et al.*, 1999) that used AFLP to investigate the systematic of taxonomically complex or unknown groups, *i.e. Eucalyptus*, *Carex*, *Solanum brevicaule* Sens. Other studies have more specific goals such as the investigations into introgression and hybridization, *e.g.* Rieseberg *et al.* (1999) looked at introgression between cultivated sunflowers and a sympatric wild sunflower *Helianthus petiolaris* (Asteraceae), and Beismann *et al.* (1997) looked at the distribution of two *Salix* species and their hybrid. AFLP is a very helpful method for enrich the genetic maps for each population with specific traits and the most efficient way to generate a large number of markers that are linked to target genes. For istance, Thomas *et al.* (1995) investigated the markers associated with the resistance genes for scab disease *Cladosporium fulvum* in Tomato; Hartl *et al.* (1999) studied the markers closely linked to the powdery mildew

resistance genes; and Bradshaw *et al.* (1998) identified markers associated with quantitative resistance to *Globodera pallida* (Stone) in tetraploid potato.

1.7.2.3. Inter Simple Sequence Repeats (ISSR)

ISSRs are DNA fragments of about 100–3000 bp located between adjacent, oppositely oriented microsatellite regions. The technique is based on PCR amplification of intermicrosatellite sequences. ISSRs are amplified by PCR using, as primers (16-18 bp), an oligonucleotide sequence typical of the microsatellite repeats (see section 1.7.3.) ending with few selective nucleotides which anchors the primers into the adjacent non-repeat regions. About 10–60 fragments from multiple loci are generated simultaneously, separated by gel electrophoresis and scored as presence or absence of fragments of particular size. The ISSR primers are used to detect the variation in a given DNA sample include one of these highly variable microsatellite sequences and arbitrary pair of bases at the 3'end (Zietkiewicz *et al.*, 1994; Godwin *et al.*, 1997).

The main advantage of ISSRs are: (i) no sequence data for primer construction are needed, (ii) the analytical procedures include PCR, hence only low quantities of template DNA are required (5–50 ng per reaction), (iii) are randomly distributed throughout the genome, and (iv) the variation within unique regions of the genome may be found at several loci. Furthermore, it is very useful marker for DNA profiling, especially for closely related species. Since ISSR is a multilocus technique, disadvantages include the possible non-homology of similar sized fragments, and ISSR is dominant marker. Moreover, ISSR, like RAPD, can have reproducibility problems (Spooner *et al.*, 2005).

ISSR analysis can be applied in studies involving genetic identity, parentage, clone and strain identification, and taxonomic studies of closely related species. In addition, ISSRs are considered useful in gene mapping studies (Zietkiewicz *et al*., 1994; Godwin *et al*., 1997; Joshi *et al*., 2000).

Pasqualone *et al.* (2001) successfully used ISSR technique for identification genotyping of variants in Italian olives. Large numbers of ISSR markers were used in fingerprinting Tunisian cultivars of *Ficus carica* L., and in the understanding of the genetic relationships among these accessions (Salhi-Hannachi *et al.*, 2004). Tikunov *et al.* (2003) found that ISSR is a powerful tool also to enrich the knowledge in the genome organization of *Lycopersicon* spp. ISSR markers were used in tomato for identification of genotypes, detection of interspecific hybrids, and development of gene markers. ISSR markers provide highly effective plant fingerprinting in several species such as citrus (Fang *et al.*, 1998), potato (Prevost & Wilkinson, 1999), sweet potato (Huang & Sun, 2000), rice

(Joshi *et al.*, 2000), wild and cultivated mulberry (Vijayan *et al.*, 2006) and chickpea (Sudupak, 2004).

Sankar & Moore (2001) reported that the incorporation of ISSR markers into the genetic linkage map demonstrates that ISSR markers are suitable for genetic mapping in *Citrus*. Several studies were conducted including ISSRs into genetic linkage map such as chickpea (Winter *et al*., 2000), Japanese larch (Arcade *et al*., 2000), coconut (Herrán *et al.*, 2000), *Fragaria* (Cekic *et al.*, 2001) and watermelon (Levi *et al.*, 2002). Furthermore, ISSRs were extremely useful for tagging agronomical important traits such as seed size in wheat (Ammiraju *et al.*, 2001), salinity tolerance in rice (Kaushik *et al.*, 2003), hardness in bread wheat (Galande *et al.*, 2001) and disease resistance to fusarium wilt in chickpea (Ratnaparkhe *et al.*, 1998; Winter *et al*., 2000).

1.7.3. Targeted-PCR and sequencing

1.7.3.1. Microsatellites, Simple Sequence Repeats (SSRs)

Microsatellites, also called Simple Sequence Repeats (SSRs) and, occasionally, Sequence-Tagged Microsatellite Sites (STMS) or Simple Sequence Repeat Polymorphisms (SSRPs) (Hearne *et al.*, 1992; Morgante & Olivieri, 1993; Queller *et al.*, 1993; Jarne & Lagoda, 1996), represent short tandem repeats (1–10 base pairs). If nucleotide sequences in the flanking regions of the microsatellite are known, specific primers (generally 20–25 bp) can be designed to amplify the microsatellite by PCR. Microsatellites and their flanking sequences can be identified by constructing a small-insert genomic library. This type of repeated DNA is common in eukaryotes, the number of repeated units varying widely among organisms (Holton, 2001; Spooner *et al.*, 2005, Weising *et al*., 2005).

These polymorphisms are identified by constructing PCR primers homologous to the DNA sequences flanking the microsatellite region. PCR product size variation is caused by differences in the number of microsatellite repeat units. SSR polymorphisms can be visualized by agarose or polyacrylamide gel electrophoresis. Microsatellite alleles can be detected, using various methods: ethidium bromide, silver staining, radioisotopes or fluorescence. Since microsatellite analysis is, in principle, a single-locus technique, multiple microsatellites may be multiplexed during PCR or gel electrophoresis if the size ranges of the alleles of different loci do not overlap (Dean *et al.*, 1999; Ghislain *et al.*, 2004).

The advantages of microsatellites include their codominance, high genomic abundance in eukaryotes and random distribution throughout the genome, with preferential

association in low-copy regions (Morgante *et al.*, 2002). Because the technique is PCR-based, only low quantities (10–100 ng per reaction) and not necessarily high quality DNA are required. Due to the use of long PCR primers, the reproducibility of microsatellites is high. This decreases significantly the analytical costs. Furthermore, the screening of microsatellite variation can be automated, if the use of automatic sequencers is an option. One of the main microsatellite disadvantages is their high development costs if adequate primer sequences for the species of interest are unavailable, making them difficult to apply to unstudied groups. Although microsatellites are in principle codominant markers, mutations in the primer annealing sites may result in the occurrence of null alleles (no amplification of the intended PCR product), which may lead to errors in genotype scoring. The potential presence of null alleles increases with the use of microsatellite primers generated from germplasm unrelated to the analysed species. A very common observation in microsatellite analysis is the appearance of stutter bands which are artifacts products that occur by DNA slippage during PCR amplification. These can complicate the interpretation of the band profiles because size determination of the fragments is more difficult and heterozygotes may be confused with homozygotes. However, the interpretation may be clarified by including appropriate reference genotypes of known band sizes in the experiment (Ribaut *et al.*, 2002; De Vicente & Fulton, 2003; Spooner *et al.*, 2005).

Simple sequence repeats (SSRs) have become important molecular markers for a broad range of applications, such as genome mapping and characterization, phenotype mapping, marker assisted selection of crop plants and a range of molecular ecology and diversity studies (Robinson *et al.*, 2004). Microsatellites are also considered ideal markers in gene mapping studies (Hearne *et al*., 1992; Morgante & Olivieri, 1993; Queller *et al.*, 1993; Jarne & Lagoda, 1996). The development of SSRs in plants is accelerating, and SSR loci are now being incorporated into established genetic maps of all the major cereals (Liu *et al.*, 1996; Korzun *et al.*, 1997; Smith *et al.*, 1997; Stephenson *et al.*, 1998). Also a rice RFLP map constructed by using IR64/Azucena DHs has been saturated with more than 500 SSR markers (Chen *et al.*, 1997; Temnykh *et al.*, 2000; 2001).

In general, Microsatellites show a high level of polymorphism. As a consequence, they are very informative markers that can be used for many population genetics studies, ranging from the individual level (e.g. clone and strain identification) to that of closely related species. SSRs have been shown to provide a powerful methodology for discrimination between genotypes (Yang *et al.*, 1994; Russell *et al.*, 1997). For example, closely related tomato cultivars presented genetic variation at the interspecific level as

detected by microsatellites (Vosman *et al.*, 1992; Rus-Kortekaas *et al.*, 1994; Arens *et al.*, 1995; Smulders *et al.*, 1997). Many studies have been undertaken to examine the level of polymorphism of SSR markers in a large number of barley varieties and *Hordeum* species (Holton, 2001; Chabane *et al*., 2005). A study by Olufowote *et al.* (1997) showed that a selection of six SSR markers was sufficient to discriminate between 71 related lines of rice. The development and application of the tea tree microsatellites is described fully by Rossetto *et al.* (1999a, b). An enriched DNA library of simple sequence repeats (SSRs) was produced based on the method of Edwards *et al.* (1996). SSRs could easily differentiate between olive varieties (Cipriani *et al.*, 2002), Sorghum (Dean *et al.*, 1999) and *Brassica nigra* genebank accessions (Westman & Kresovich, 1999).

1.8. Use of molecular markers in *Pistacia* researches

To give an idea about the utilization of molecular marker techniques for discrimination between *Pistacia* species and pistachio's variety identification, some results of previous studies could be summarized as follows:

- Relationships among *Pistacia* species have been based on morphology characterization as well as geographical distribution. The results of the phylogenetic relationships study for 10 *Pistacia* species by using RFLP divided the genus into two major groups. *P. vera* was determined to be the most ancient of the 10 species studied. *P. integerrima* and *P. chinensis* were shown to be distinct species (Parfitt & Badenes, 1998).
- Fingerprinting analysis was conducted using RAPDs extracted from the leaves of 24 accessions (8 male and 16 female cultivars) gathered in a collection located in Sicily. This technique was unable to clearly separate the accessions into two groups (Caruso *et al.*, 1998). Similar case was found when Hormaza *et al.* (1994) studied female varieties cultivated in Mediterranean and the Iranian- Caspian pools.
- RAPDs were used to study the taxonomic relationships and genetic variation of wild *Pistacia* germplasm in Turkey. The four *Pistacia* species (*P. vera*, *P. atlantica*, *P. terebinthus* and *P. eurycarpa*) are clearly separated each other. *P. terebinthus* appears to be the most diverged species, and the closest pair of species was found to be *P. atlantica* and *P. eurycarpa* (Kafkas & Perl-Treves, 2001a). Also RAPDs were used to determine the genetic variability in Turkmen populations of *Pistacia vera* (Barazani *et al.*, 2003).

- Several markers (RAPDs) were used for sex determination of wild *Pistacia* species (*P. atlantica, P. terebinthus,* and *P. eurycarpa*), but the results showed that in each of the putative sex related bands, the correlation with sex is only partial, and some individuals have the marker-phenotype of the opposite sex (Kafkas *et al*., 2001). On the other hand Hormaza *et al*. confirmed that the OPO08 RAPD marker could be used to screen the gender of pistachio plants long before they reach reproductive maturity.
- AFLPs were used as a powerful tool for identification of Syrian pistachio varieties (Ibrahim Basha *et al.*, 2003). The AFLP technique was also found to be effective for characterizing wild *P. vera* material, which was genetically the closest to cultivated pistachio when it was used to characterize the Afghan pistachio accessions (Kafkas *et al.*, 2006).
- Some studies were used both AFLP and RAPD markers in order to study the genetic relationships among species and cultivars of *Pistacia*. In Greece, the study was conducted to detect the relationships of native and introduced *Pistacia* species. The phenotypes were comparable with minor clustering differences between the two techniques (Katsiotis *et al.*, 2003). Also Genetic relationships among Mediterranean *Pistacia* species were evaluated by RAPD and AFLP markers and similar results were obtained (Golan-Goldhirsh *et al.*, 2004).
- Microsatellite markers have been developed from pistachio *P. vera*; 14 pairs of primers were amplified cleanly and generate an easily interpretable PCR product. The SSR markers distinguished most of the tested cultivars from USA, Turkey, Iran and Syria (Ahmad *et al.*, 2003).

1.9. Research objectives

The main object of present thesis could be summarized in the following points:

1. Assess the distribution of *Pistacia* diversity in Syria and Central Asia;
2. Characterize *Pistacia* species using agro-morphological descriptors;
3. Assess the extent of genetic diversity in *Pistacia* in both natural and cultivated populations, using molecular techniques (i.e. AFLP, ISSR and SSR);
4. Develop complementary conservation strategies to strengthen the sustainable use of pistachio natural forests and cultivations in Central and West Asia.

2. Chapter Two: Materials and Methods

The surveys of *Pistacia* genetic resources were carried out in Syria, Uzbekistan, Tajikistan and partial in Sicily (Italy). The laboratorial analyses were done in several laboratories: I) Molecular Laboratory in Department of Agrobiology and Agrochemistry, Tuscia University – Italy. II) Biotechnology and Molecular Laboratories, International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo - Syria. This study had taken place, including the thesis writing, during years 2004-2006.

2.1. Plant materials

This study was focused on *Pistacia* genetic resources including 6 species: *P. vera*, *P. atlantica, P. palaestina, P. terebinthus, P. lentiscus* and *P. khinjuk.* Total plant materials comprised 324 phenotypes (Table 4). Fifty-four different sites were surveyed in 4 countries including natural population and field gene banks: Syria (38 sites), Turkey (2 sites), Italy (8 sites) Tajikistan (5sites) and one gene bank site in Uzbekistan which contains accessions of wild *P. vera* introduced from several countries in Central Asia . These plant materials were utilized for both (i) morphological characterization and (ii) molecular assessment.

Table 3. Number of studied samples from each speices according to countries visited.

Syrian Samples	**No.**	**Turkish Samples**	**No.**	**Central Asia Samples**	**No.**	**Italian Samples**	**No.**
P. atlantica	80	*P. atlantica*	7	wild *P. vera* (Kyrgyzstan)	2	*P. vera*	12
P. palaestina	60	*P. terebinthus*	4	wild *P. vera* (Azerbaijan)	6	*P. lentiscus*	2
P. vera	59	*P. lentiscus*	5	wild *P. vera* (Uzbekistan)	2	*P. terebinthus*	2
P. lentiscus	15	*P. vera*	4	wild *P. vera* (Iran)	1		
P. terebinthus	5			wild *P. vera* (Tajikistan)	53		
P. khinjuk	5						
Total	224		20		64		16

2.2. Ecogeographic survey

The ecogeographic survey, on the *Pistacia* species, was carried out in Syria and in Tajikistan. Extensive fieldwork was undertaken in native forest areas likely to contain native *Pistacia* species, and field gene banks for the cultivated pistachio. These areas were selected on the basis of the literature review especially the Syrian floras (Post, 1932; Khalife, 1958; Mouterde, 1966), national countries reports on biodiversity conservation (Barkoudah *et al*., 2000; Safarov, 2003) and pervious studies and reports done at Bioversity International, former IPGRI

In order to reach these sites consultations were obtained form experts in Agriculture and Agrarian Reform directorates in Syria and other experts form forestry research institutes in Tajikistan and Uzbekistan. In total 53 sites were selected to represent the broad distribution of the *Pistacia* populations in Syria and Tajikistan. In addition, Italy was included to have an idea about the *Pistacia* diversity in Sicily and one gene bank in Uzbekistan.

Latitude, longitude and elevation of the localities were determined by global position system (GPS) device in order to create maps of *Pistacia* distribution. Climatic data for each site were obtained from the meteorology directorate in Damascus, the countries national reports and climatology websites. Climatic data included annual rainfall, average monthly temperature, relative humidity and wind speed. On the other hand, climatic data layers with the mean minimum temperature of the coldest month (m), the mean maximum temperature of the warmest month (M), and the annual precipitation (P) were extracted from the DIVA-GIS climate data set for the whole world at different spatial resolutions available online from DIVA-GIS website (www.diva-gis.org). These data layers were used to calculate the pluviometric quotient (PMQ), which is an important measure for the aridity (Nahal, 1981). This was done according to the formula:

$$PMQ = \frac{2 \times 1000 \times P}{(M + m) \times (M - m)}$$

In the formula, the absolute temperatures should be used (temperature in degrees Celsius + 273.15). The distribution of the populations and their corresponding PMQ and m values were plotted to determine the actual bio-climatic range of the species. Also soil types for each locality were determined according to the digital soil map of the world FAO (1995) soil map. Mainly two software were used to complete soil maps drawing, which are DIVA-GIS V5.4.0.1 and ArcMAP V9.1.

The survey was carried out in the sites where the *Pistacia* species is found either cultivated or wild according to literatures as described below:

2.2.1. *P. vera*

P. vera is cultivated in Syria and has about 25 varieties which were distributed mainly in the northern of Syria (Aleppo and Idlib), and middle district Hama, Homs. In addition, some new Pistachio fields are established around other districts like Damascus, Dara'a and Sweida. Previous survey done before was taken in consideration (Ibrahim Basha *et al*., 2003). Therefore this study focuses just on the pistachios which are maintained in the field

gene-banks. On the other hand, this species wildly exists in Tajikistan (pure stand) in the forests and every little attention was given. The highest diversity location regarding Tajik scientist are Pjands and Kurgan-Tyube (south Dushanbe) and Dangare. Some Italian varieties were introduced to this study to assess their genetic variation.

2.2.2. *P. atlantica*

The distribution of *P. atlantica*, as wild species, in Syria is mainly located in Dara'a (Hourran from Al-Yarmok valley and south Basrah); Sweida (Itell village, the west side of Al-Arab mountain); Homs (Abo Roudjman mountain near Tadmour); Hama (Al-Balaas mountain); and Al-Hasakah (Abdul Aziz mountain). In this study was also included a site in South East Turkey, to be compared with the Syrian individuals.

2.2.3. *P. palaestina*

P palestina is mainly located in Syria at Aleppo (Afrien and Simon mountain); Idleb; Latakia (Costal mountains); Tartus (Banias); Hama (Mousiaf); Damascus (Qasun, Barada valley and Kalamon).

2.2.4. *P. terebinthus*

P. terebinthus does not exist in Syria except for very few stands near the Turkish border in Latakia (Kasab and Bier). Also one site in South East Turkey was included in this study, to be compared with the Syrian individuals.

2.2.5. *P. lentiscus*

The distribution of *P. lentiscus* in Syria is limited to the costal area of Latakia. Therefore, sites in South East Turkey and from Sicily in Italy where included in this study to be compared with the Syrian individuals.

2.2.6. *P. khinjuk*

P. khinjuk is located in Syria at the Northeastern part of Syria at Al-Hasakah (Abdul Aziz and Senjar Mountains (Sankary, 1987).

2.3. Morphological characterization

After sites definition, several expeditions were conducted during the years of study. The sites were visited during different phenology stages in order to characterize the spices in their nature habitats, especially those which are distributed in Syria, but due to time and financial constraints only one visit was carried out in Central Asia and in Italy. The morphology characters were recorded directly in the fields such as plant, leaf and nut

characters. In addition, leaf cuttings and nut samples were collected and preserved as a herbarium.

Morphological characterization was done according to IPGRI-descriptors for Pistachio - *Pistacia vera* L. (IPGRI, 1997) and IPGRI- descriptors for *Pistacia* spp. excluding *Pistacia vera* L. (IPGRI, 1998).

2.3.1. Plant descriptors

1. **Tree/Shrub vigor**: Low, Intermediate or High;
2. **Growth habit**: Tree with single trunk, Tree much branched form base, Shrub;
3. **Branching habit**: Sparse, Intermediate, Dense.

2.3.2. Leaf descriptors

Ten leaves were collected from different shoots of each phenotype. These samples were dried and preserved in a herbarium. The following aspects had been taken in consideration (Figure 3):

1. **Leaf Length;**
2. **Leaf width;**

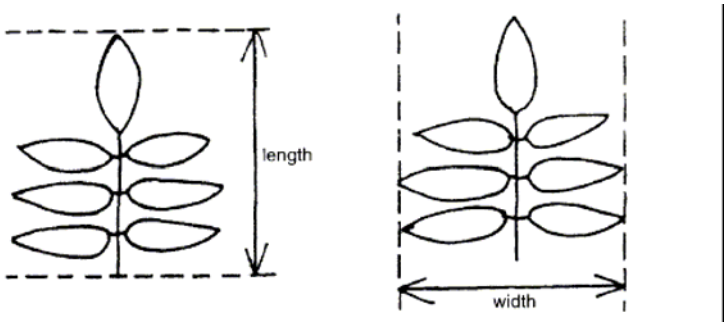


Figure 3. Leaf length and width.

3. **Leaf rachis wing:** Absent, Present in lead rachis only, Present in both leaf rachis and petiole (Figure 4);

Figure 4. Leaf rachis wing.

4. **Terminal leaflet:** absent, or present (Figure 5);

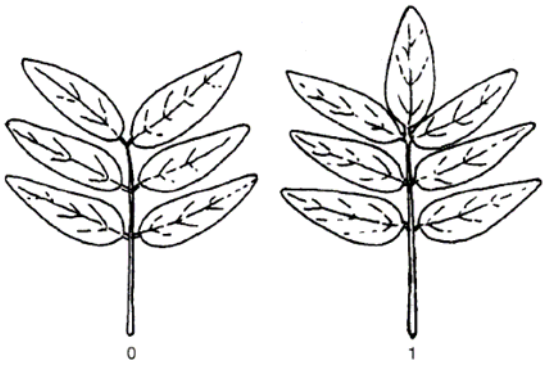


Figure 5. Terminal leaflet.

5. **Terminal leaflet size:** Smaller than lateral ones, as large as lateral ones, larger than lateral ones;
6. **Terminal leaflet length** (Figure 6)**;**
7. **Terminal leaflet width** (Figure 6) **;**

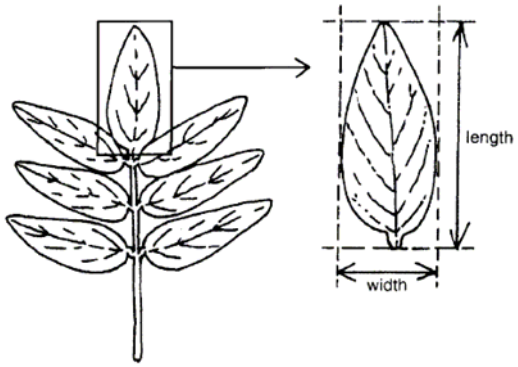


Figure 6. Terminal leaflet length and width.

8. **Terminal leaflet length/width ratio;**
9. **Number of pairs of leaflets;**
10. **Terminal leaflet shape:** 1-Lanceolate, 2- Ovate, 3- Ovate-oblong, 4- Oblong, 5- Elliptic, 6- Narrow elliptic, 7- Round ovate, 8- Roundish (Figure 7);

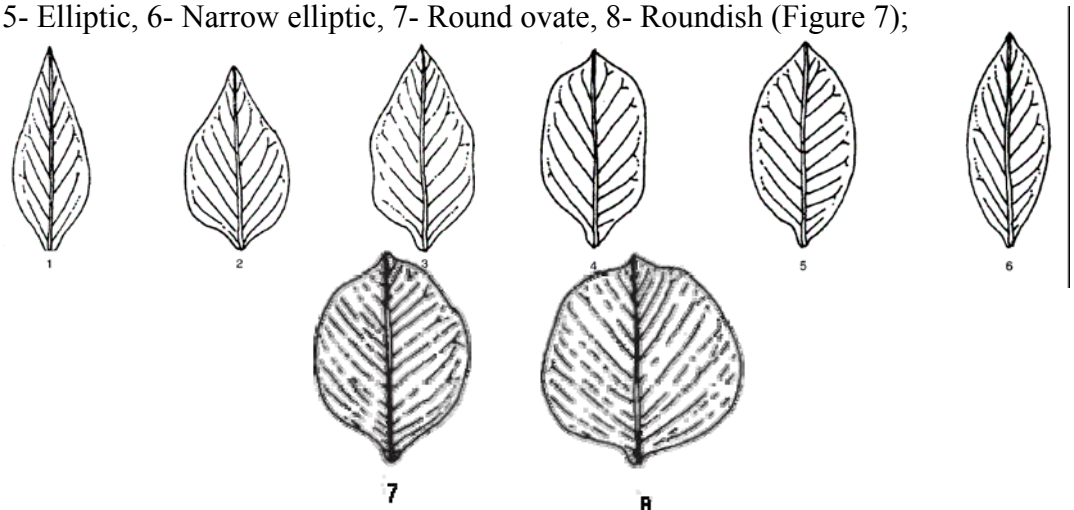


Figure 7. Terminal leaflet shape.

11. Terminal leaflet apex: 1- Mucronulate, 2- Acuminate, 3- Mucronate, 4- Caudate, 5- Cuspidate, 6- Acute, 7-Obtuse, 8- Retuse, 9- Emarginate (Figure 8);

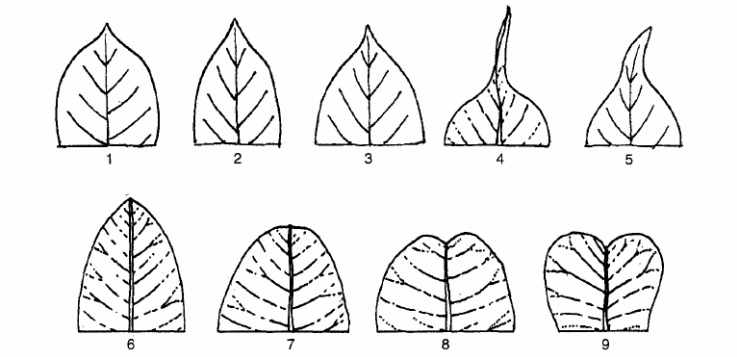


Figure 8. Terminal leaflet apex.

12. Leaf texture;

13. Petiole shape: Flattened, Rounded, Rounded straight adaxially.

2.2.3. Nut descriptors

1. **Nut length;**
2. **Nut width;**
3. **Nut thickness** (Figure 9)**;**

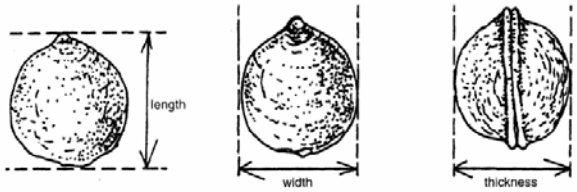


Figure 9. Nut dimenstions.

4. **Nut shape for wild relative:** 1- Globular, 2- Globular lenticular, 3- Obovoid globular, 4- Obovoid (Figure 10);

Figure 10. Nut shape.

5. **Nut shape for *P. vera*: 1**- Roundish, 2- Ovoid, 3- Elongate, 4- Narrowly Cordate, 5- Cordate (Figure 11);

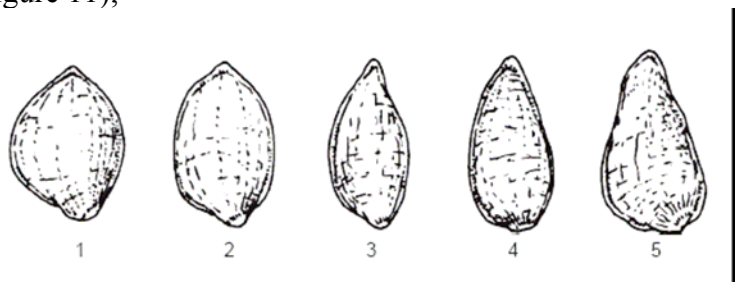


Figure 11. *P. vera* nut shape.

6. **Nut color after maturity:** Blue, Greenish blue, Dark green.

2.4. Molecular Markers

2.4.1. DNA extraction

Total genomic DNA was extracted from freeze-dried leaf-tissue by using Cetyl Trimethyl Ammonium Bromide (4X CTAB) mini-extraction protocol based on Sasanuma *et al.* (2002) with minor modifications. The extraction was done at the Genetic Resources Unit molecular laboratory of ICARDA (Syria):

1. 0.5 g of freeze-dried young leaves were ground to a fine powder in liquid nitrogen;
2. 50-100 mg of frozen leaf powder was placed in 2 ml Eppendorf tube and 1 ml of preheated extraction buffer (100 ml CTAB and 100 µl Mercaptoethanol);
3. The mixture was incubated for 1.5 hr at 65 °C then 5 minutes in ice;
4. 900 µl of Chloroform-Isoamyl Alcohol 24:1 was added and mixed by inversion for 15 min at room temperature;
5. The mixture was centrifuged for 5 minutes at 13000 rpm;
6. 750 µl of the top layer was transferred to new tube;
7. Steps 4-5-6 were repeated;
8. 83 µl of acetate mix (6:5 - Sodium acetate: Ammonium acetate) was added and mixed by hand for 2-3 min;
9. 500 µl ice-cold Isopropanol was added and mixed by inversion gently and put in freezer for about 2-3 days;
10. the tubs were Centrifuged at 5000 rpm for 10 minutes to see the pellet and the Isopropanol was poured off carefully;
11. 500 µl of washing buffer (100ml ethanol 70% + 100 µl of 10mM NH4Oac) was added to wash the pellet;
12. the tubes were Centrifuged at 4500 rpm for 5 minutes, and the ethanol Poured off carefully;
13. Steps 11-12 were repeated;
14. The DNA pellets were dried in a vacuum drier for 3 minute;
15. 80 µl of TE 1X (10 mM Tris –Hcl, 0.1 mM EDTA) + 1.5 µl RNAse (10mg/ml) was mixed and added in the tube containing DNA pellet;
16. The mixture was left overnight in shaker at 5°C.

2.4.2. DNA quantification

DNA quantification was done using spectrophotometer of UV absorption at wavelengths 260 and 280 nm. The A260 value provides a measure of concentration and pure DNA

solution has an A260:A280 ratio of 1.8 ± 1. In addition, the quality of DNA samples were checked by using electrophoresis technique by running the DNA samples on 1% agarose gel stained with ethidium bromide for 90 minutes at 80 volts (Figure 13). According to the DNA concentration, all DNA samples were diluted to 100 ng/µl.

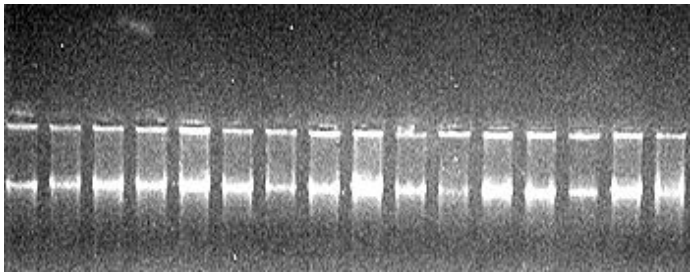


Figure 12. Agarose gel after half hour of DNA migration.

2.4.3. Amplified Fragment Length Polymorphism (AFLP)

The AFLP technique was done according to Vos *et al.* (1995) with minor modifications in Molecular laboratory of Department of Agrobiology and Agrochemistry, University of Tuscia – Viterbo, Italy.

2.4.3.1. DNA restriction digest

500 ng of DNA was double digested with *Eco*RI (10 U) and *Mse*I (5 U) enzymes. 8 µl 5X RL-Buffer (50mM Tris. HAc pH7.5, 50 mM MgAc, 250 mM Kac, 25mM DTT,250 ng/µl BSA) the total volume was completed up to 40µl with sterile and distilled water. This mixture was incubated for 3 hr in water bath at 37°C. The DNA restriction digest was tested using electrophoresis technique by running the samples on 1% agarose gel stained with ethidium bromide for 30 minutes at 80 volts (Figure 14).

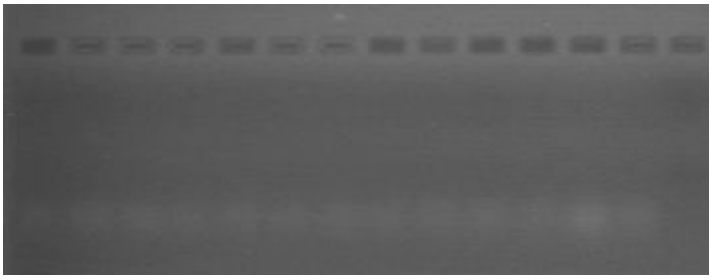


Figure 13. DNA absence after restriction digest and migration.

2.4.3.2. Adapter preparation

1. 8 µg of MseI adapter R and 7 µg of MseI adapter I were diluted in 30 µl of water to obtain 50 pmol/ µl MseI adapter R+I;
2. 8.5 µg of EcoRI adapter R and 9 µg of EcoRI adapter I were diluted in 300 µl of water to obtain 5 pmol/ µl EcoRI adapter R+I;
3. These two solutions were incubated for 5 min in water bath at 95°C then cooled to room temperature (21°C);

4. The two solutions were centrifuged for 10 min.

DNA ligation

For each 40 µl of DNA samples, the following materials were added:

- 1 µl MseI adapters (50 pmol);
- 1 µl EcoRI adapters (5 pmol);
- 1 µl ATP (10 mM);
- 0.5 µl of T4 ligase enzyme (1U);
- 4.45 µl of sterile and distilled water.

These mixtures were incubated for 4 hr in water bath at 37°C. The concentrations of the samples were reduced 5 times by adding TE.

DNA pre-amplification

The pre-amplification reaction amplified the genomic DNA with AFLP primers, each having one selective nucleotide. Each mixture contains the following materials:

- 1 µl Primer EcoRI 1base **A** (50ng/µl);
- 1 µl Primer MseI 1base **C** (50ng/µl);
- 1 µl of dNTPs (5mM);
- 1 U Taq DNA polymerase;
- 1 µl Buffer 10X (10 mM Tris-Cl, pH 8.3, 50 mM KCl);
- 9.9 sterile and distilled water;
- 5 µl previously prepared DNA.

The polymerase chain reaction was done by using Eppendorf Mastercycler Gradient with the following cycles:

1. Initial incubation at 72°C for 2 min;
2. Denaturation at 94°C for 0.5 min;
3. Annealing at 56°C for 1min;
4. Extension at 72°C for 1min;
5. Steps 2-3-4 were repeated 30 times;
6. Final extension at 72°C for 2 min;
7. Final incubation at 60°C for 30 min.

The PCR product was tested using electrophoresis technique by running the samples on 1% agarose gel stained with ethidium bromide for 90 minutes at 80 volts (Figure 15).

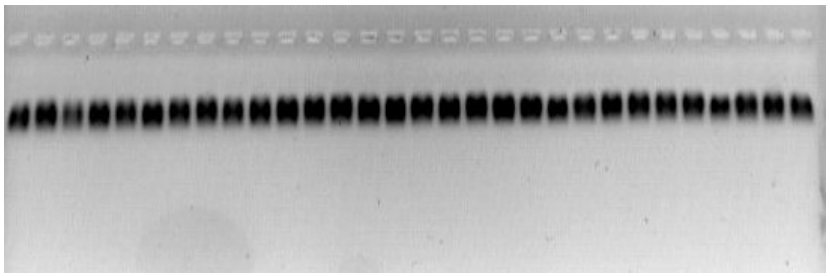


Figure 14. PCR product after pre- amplification and migration.

DNA selective amplification

The previous pre-selective PCR products were used as a template for the selective amplification with two AFLP primers, each having three selective nucleotides. The mixture was as following:

- 1 µl Primer EcoRI 3bases (50ng/µl) (Table 4) ;
- 1 µl Primer MseI 3bases (50ng/µl) (Table 4);
- 1 µl of dNTPs (5mM);
- 1 U Taq DNA polymerase;
- 1 µl Buffer 10X (100 mM Tris-Cl, pH 8.3, 500 mM KCl);
- 9.9 µl sterile and distilled water;
- 1µl previously pre-selective PCR product + 4 TE.

Table 4. The used primer combinations and its sequences to evaluate the genetic diversity (Ibrahim Basha *et al.*, 2003; Katsiotis *et al.*, 2003).

Primer	Sequences of primer	Primer	Sequences of primer
E- AAG	GACTGCGTACCAATTCAAG	M-CTA	CGATGAGTCCTGAGTAACTA
E- AAG	GACTGCGTACCAATTCAAG	M-CTC	CGATGAGTCCTGAGTAACTC
E- AGG	GACTGCGTACCAATTCAGG	M- CAA	CGATGAGTCCTGAGTAACAA
E- AGG	GACTGCGTACCAATTCAGG	M-CTC	CGATGAGTCCTGAGTAACTC

The polymerase chain reactions were done by Eppendorf Mastercycler Gradient with following cycles:

1. Initial denaturation at 94°C for 2 min;
2. Denaturation at 94°C for 0.5 min;
3. Annealing at 65 - 56°C for 0.5 min ;
4. Extension at 72°C for 2min;
5. Steps 2-3-4 were repeated 12 times and the annealing temperature was reduced each time by 0.7°C;
6. Denaturation at 94°C for 0.5 min;
7. Annealing at 56°C for 0.5min;

8. Extension at 72°C for 2min;
9. Steps 6-7-8 were repeated 20 times;
10. Final incubation at 60°C for 30 min.

The PCR product was tested using electrophoresis technique by running the samples on 1% agarose gel stained with ethidium bromide for 90 minutes at 80 volts (Figure 16).

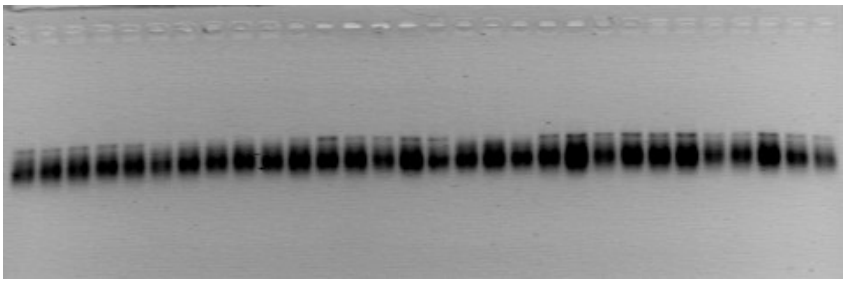


Figure 15. PCR product after selective amplification for one prime combination and migration.

The amplified products were separated on a denaturing 6% polyacrylamide sequencing gel. After electrophoresis, the gel was scanned with automated scanner connected to the computer and the images were acquired.

2.4.4. Inter Simple Sequence Repeats (ISSR)

The inter simple sequence repeats were applied according to Ratnaparkhe *et al.* (1998) with minor modifications each reaction contains a mixture as following:

- 1 µl DNA 100ng/ µl + 4 µl TE;
- 2 µl ISSR primer (12.5µM) (Table 5);
- 1 µl dNTPs (10mM);
- 1 U Taq DNA polymerase;
- 1 µl $MgCl_2$ (50mM);
- 2.5 µl PCR Buffer 10X (100 mM Tris-Cl, pH 8.3, 500 mM KCl);
- 13.3 µl sterile and distilled water.

Table 5. The used primer and its sequences and annealing temperature to evaluate the genetic diversity.

Primer	Sequences of primer	Annealing temperature°C
ISSR-826	ACACACACACACACACC	53.27 ≈ 53.3
ISSR-834	AGAGAGAGAGAGAGAGYT	45.37 ≈ 45.4
ISSR-841	AGAGAGAGAGAGAGAGYC	46
ISSR-847	CACACACACACACACARC	54.17 ≈ 54.2
ISSR-857	ACACACACACACACACYG	53.7 ≈ 53.7
ISSR-857C	ACACACACACACACACYGC	59.12 ≈ 59.1

The polymerase chain reaction was done by using Eppendorf Mastercycler Gradient with the following cycles:

1. Initial denaturation at 94°C for 7 min;
2. Denaturation at 94°C for 0.5 min;
3. Annealing at different temperatures for 0.5 min (Table 7);
4. Extension at 72°C for 2min;
5. Steps 2-3-4 were repeated 35 times;
6. Extension at 72°C for 10 min.

The amplified products were separated by on 1.5% agarose gel stained with ethidium bromide for 3 hr at 85 volts. After electrophoresis, the gel was pictured with digital camera connected to the computer and the images were acquired.

2.4.5. Microsatellites, Simple Sequence Repeats (SSRs)

Ten Simple Sequence Repeats primer pairs were tested as described by Ahmad *et al.* (2003). SSR designation, SSR motif, and annealing temperatures are presented in (Table 7). The forward primers were 5'–end–labeled either with the fluorescent tags 6-FAM (6-carboxyfluorescein), or HEX (4,7,2, 4',5',7'- hexachloro-6- carboxyfluorescein). Optimization of each reaction was carried out by trying a range of primers concentration, DNA concentration, and annealing temperature. PCR reactions were performed in a total volume of 12 µl containing 100 ng of DNA as follows:

- 2 µl DNA 50 ng/ µl;
- 3 µl SSR forward primer (30 pmol) (Table 6);
- 3 µl SSR reverse primer (30 pmol) (Table 6);
- 0.5µl dNTPs (10mM);
- 0.5 U Taq DNA polymerase;
- 0.5 µl $MgCl_2$ (50mM);

- 0.9 µl PCR Buffer 10X (100 mM Tris-Cl, pH 8.3, 500 mM KCl);
- 2 µl sterile and distilled water.

Table 6. The tested primers, their sequences and annealing temperature to evaluate the genetic diversity.

Primer	Sequences of primer	Tm°C	Primer	Sequences of primer	Tm°C
F PTMS-7	TGATGCTCTTGGTGTTGCTC	64.1	R PTMS-7	CCTGAGTAGCTCCAGTTCCG	63.8
F PTMS-33	TTCTGCTGGTCATGGGGC	67.5	R PTMS-33	TGCCATTTAACCCAAAGGAG	63.6
F PTMS-3	TGATGAACAAGTCCAAAAGGG	63.7	R PTMS-3	AAAACAGCACAGCATGCATC	63.8
F PTMS-10	CAGGATGCTTGTTGGTGATG	64.2	R PTMS-10	ACAGTGGATACAAACATGCTGC	63.8
F PTMS-31	CTGATCATGGGGCCTTTG	64.1	R PTMS-31	GGAAGCACACACATGCAAAC	64.2
F PTMS-9	TTGACCGTGGACTTGAAGC	63.9	R PTMS-9	AACCTCCTCTCTTCTCTTTGCC	63.8
F PTMS-40	CAGCTCTCACTGATCCGATTC	63.9	R PTMS-40	TTCGAAAGCCAGTCTCAGGT	63.9
F PTMS-41	AGAAGAGGGGAACAGGGAGA	64	R PTMS-41	CTGAGGACTGGGCAGAATGT	64.3
F PTMS-12	TCCGCTTCTCTGTGAGTGTG	64.4	R PTMS-12	CGATAGTTTCCTTCCCAGACC	63.5
F PTMS-14	GGGAAACACAAACATGCAAA	63.3	R PTMS-14	GGCCTCTGGAGAACATGGTA	64

The PCRs were performed according to each primer. For two of them were done according to their annealing temperature and in the other two steps down program was used as follows:

- PCR program for PTMS 10 and 33 primers.
  1. Denaturation at 94°C for 1min;
  2. Annealing at different temperatures for 1min (Table 7);
  3. Extension at 72°C for 2min;
  4. Steps 2-3-4 were repeated 35 times;
  5. Extension at 72°C for 1hr.
- PCR program for PTMS 7 and 3 primers.
  1. Initial denaturation at 94°C for 2 min;
  2. Denaturation at 94°C for 0.5 min;
  3. Annealing at 65 - 56°C for 0.5 min ;
  4. Extension at 72°C for 2min;
  5. Steps 2-3-4 were repeated 12 times and the annealing temperature was reduced each time 0.7°C;
  6. Denaturation at 94°C for 0.5 min;
  7. Annealing at 56°C for 0.5min;
  8. Extension at 72°C for 2min;
  9. Steps 6-7-8 were repeated 20 times;
  10. Final incubation at 60°C for 30 min.

The amplified products were resolved on 8% polyacrylamide sequencing gel. After electrophoresis, the gel was scanned with scanner connected to the computer and the images were acquired. Then for SSR allele sizing, ABI 377 DNA sequencer running Genescan and genotyper software was used.

2.5. Statistical analysis

Basic statistical parameters (mean, standard error, range, and coefficient of variation) for the morphological characters of the populations were calculated using SPSS 12 version for Windows statistical package and EXCEL 2003. Single classification ANOVA for unequal sample sizes was undertaken using procedures described by Sokal and Rohlf (1981).

According to the molecular marker data analyses, each of AFLP and ISSR gel were visually scored with the aid of digital pictures of the gels and adobe Photoshop computer software. AFLP possible bands were ranging in size from 150 -500bp, while ISSR between 400 – 1200bp. The bands were scored as present (1) and absent (0) binary matrix. Only the bands showing unambiguous polymorphism were considered in the statistical analysis. Frequencies for male and female individuals in each site were calculated in order to for the matrix for clustering analyses. In terms of SSR technique, the allele sizes detected by each primer combination were recorded and coded in a present (1) and absent (0) binary matrix by using a program developed by ICARDA statistic service department. Frequencies for male and female individuals in each site were calculated in order to for the matrix for clustering analyses.

The analyses of genetic similarity were carried out among and within species. To this aim the genetic similarity was calculated using Nei coefficient distance (Nei, 1972) by NTSYS-pc version 2.02i computer software (Rohlf, 2000) according to the following formula:

$$d_{ij} = -\ln\left[\frac{\sum_k \left|x_{ki}x_{kj}\right|}{\sqrt{\sum_k x_{ki}^2 x_j^2}}\right]$$

PHYLIP 3.66 software was used to carry out a boostrap of the data for 1000 times, which involves creating a new data set by sampling *N* characters randomly with replacement, so that the resulting data set has the same size as the original, but some characters have been left out and others are duplicated (Felsenstein, 1985). The genetic distances of each were calculated using Nei coefficient distance (Nei, 1972) for the 1000 binary code matrixes of

each technique. Then the dissimilarity matrices were subjected to cluster analysis by the un-weighted pair-group method with the arithmetic averages (UPGMA) cluster method for the 1000 dissimilarity matrixes. Then a consensus tree program was used to obtain the final distance tree out of 1000 and drawing the unrooted tree for clustering analyses. Also a principal component analysis was conducted based on correlation matrixes, using the DCENTER and EIGEN procedures in NTSYS (Rohlf, 1992).

The correlation between the three different techniques (AFLP, SSR and ISSR) genetic distance matrices, and the climatic data and quantitive morphological data of the leaves and nuts were calculated by the Mantel test of matrix correspondence (Mantel 1967; Smouse et al. 1986; Peakall et al. 1995) Statistical significance was determined by random permutation, with the number of permutations set to 1000 for each test.

3. Chapter three: Results

3.1. Ecogeographic survey

3.1.1. Geographic data

Fifty-four sites (population) were selected and surveyed to estimate the *Pistacia* species diversity. These sites were distributed over five countries Syria, Tajikistan, Uzbekistan, Turkey and Italy. Much attention was paid on Syria due to the existence of wild *Pistacia* species such as *P. atlantica, P. palaestina, P. khinjuk, P. lentiscus*, *P. terebinthus* and cultivated *P. vera*, therefore 38 sites were studied in Syria. Two sites from Turkey were selected to obtain some samples of *P. atlantica, P. lentiscus*, *P. terebinthus* and some Turkish cultivated varieties (Table 7).

The wild *P. vera* was studied in Central Asia 5 sites in Tajikistan and one site in Uzbekistan which represented *ex situ* filed gene bank of some accession gathered from all Central Asia countries such as Tajikistan, Uzbekistan, Azerbaijan, Kyrgyzstan and Iran. Eight sites were lately introduced in this study from Italy to estimate the genetic diversity of Italian pistachio varieties and the wildly existing *P. terebinthus* and *P. lentiscus* in Sicily Island (Table 7).

The studied sites in Syria were distributed between latitude 36°36.576' North (Izaz) in Aleppo and latitude 32°38.408' North (Al Kafer) in Sweida. The sites' longitudes were between 37°36.592' East (Ras Al Baset 1) in Latakia and 40°23.144' East (Abdul Aziz Mountain) in Al- Hasakah. The elevations of the sites ranged between 3 m a.s.l. (Ras Al Baset 2) in Latakia and 1588 m a.s.l. (Al Sarkha) in Damascus. The two Turkish sites were located in South East of this country in Adana, where *P. terebinthus* is wildly distributed (Figure 16).

Table 7. Latitude, longitude and elevation of the studied sites.

Country	Site No.	Site name	Latitude (N)		Longitude (E)		Elevation (m a.s.l.)	Species
Syria	1	Al Hamra	34°	19.217'	36°	38.283'	1307	*P. atlantica*
	2	Ain Al-Tina	33°	49.384'	36°	33.404'	1291	*P. atlantica*
	3	Al Sarkha	33°	53.635'	36°	35.794'	1588	*P. atlantica*
	4	Wadi Baradah	33°	36.655'	36°	9.209'	918	*P. palaestina*
	5	Salim	32°	46.827'	36°	34.305'	1015	*P. atlantica*
	6	Qanawat	32°	46.470'	36°	35.718'	1109	*P. atlantica*
	7	Al Kafer	32°	38.408'	36°	39.010'	1406	*P. atlantica*
	8	Izraa Gene bank	32°	51.024'	36°	14.155'	572	*P. vera*
	9	Maaria	32°	45.556'	35°	46.627'	237	*P. atlantica*
	10	Al Modawarah	32°	59.493'	36°	26.190'	724	*P. atlantica*
	11	Al Lajat	32°	57.879'	36°	23.239'	760	*P. atlantica*
	12	Palmyra Wadi	34°	52.227'	38°	18.860'	1240	*P. atlantica*
	13	Abo Roudjmain 1	34°	55.122'	38°	15.025'	1048	*P. atlantica*
	14	Rasm Al Abed	34°	55.493'	38°	14.464'	1006	*P. atlantica*
	15	Al Balaas 1	34°	57.066'	37°	36.592'	910	*P. atlantica*
	16	Al Balaas 2	34°	56.375'	37°	37.693'	953	*P. atlantica*, *P. khinjuk*
	17	Al Balaas 3	34°	55.801'	37°	38.564'	1005	*P. atlantica*
	18	Abdul Aziz 1	36°	24.929'	40°	23.144'	670	*P. atlantica*, *P. khinjuk*
	19	Abdul Aziz 2	36°	24.504'	40°	18.882'	770	*P. atlantica*
	20	Markab Ali	36°	25.755'	40°	18.097'	910	*P. atlantica*
	21	Al Mehwiye	36°	33.401'	35°	58.141'	132	*P. lentiscus*
	22	Al Moslemia Gene bank	36°	19.648'	37°	13.244'	422	*P. vera*
	23	Shahba Gene bank	36°	25.127'	37°	15.034'	447	*P. vera*
	24	Mantaf	35°	46.754'	36°	38.593'	627	*P. palaestina*
	25	Kafer Haya	35°	45.128'	36°	35.730'	774	*P. palaestina*
	26	Al Bara	35°	41.401'	36°	31.773'	681	*P. palaestina*
	27	Ain Al Gazal	35°	46.255'	36°	7.785'	430	*P. palaestina*
	28	Wadi Kandel	35°	41.979'	35°	53.688'	93	*P. palaestina*
	29	Ras Al Baset 1	35°	50.910'	35°	49.513'	5	*P. palaestina*
	30	Al Badrousia	35°	53.626'	35°	53.749'	80	*P. palaestina*
	31	Al Nabiaen	35°	54.707'	35°	58.320'	880	*P. palaestina*
	32	Frolok	35°	50.835'	36°	0.223'	580	*P. palaestina*
	33	Bhamra	35°	27.812'	36°	3.138'	265	*P. palaestina*
	34	Banias	35°	11.195'	35°	58.730'	176	*P. palaestina*
	35	Kadmous	35°	5.946'	36°	16.218'	1000	*P. palaestina*
	36	Derekish	34°	52.920'	36°	6.954'	275	*P. palaestina*
	37	Izaz	36°	36.576'	37°	5.418'	534	*P. palaestina*
	38	Ras Al Baset 2	35°	47.494'	35°	51.293'	3	*P. terebinthus*
Turkey	39	Adana 1	37°	1.909'	35°	21.825'	86	*P. terebinthus*
	40	Adana 2	37°	5.239'	35°	29.236'	183	*P. atlantica*, *P. lentiscus*
Uzbekistan	41	Galla Aral	40°	3.135'	67°	11.635'	742	*P. vera*
Tajikistan	42	Televiska	38°	18.620'	68°	39.795'	1446	*P. vera*
	43	Dangara 1	37°	59.917'	69°	9.434'	820	*P. vera*
	44	Dangara 2	37°	58.162'	69°	8.032'	1000	*P. vera*
	45	Korgan Tubye 1	37°	57.437'	68°	33.281'	740	*P. vera*
	46	Korgan Tubye 2	37°	54.605'	68°	34.583'	711	*P. vera*
Italy	47	Bronte 1	37°	42.780'	14°	50.340'	990	*P. vera*
	48	Bronte 2	37°	44.640'	14°	49.860'	755	*P. vera*
	49	Bronte 3	37°	48.000'	14°	49.140'	670	*P. vera*
	50	Bronte 4	37°	47.820'	14°	48.480'	594	*P. vera*
	51	Bronte 5	37°	46.980'	14°	48.720'	614	*P. vera*
	52	Bronte 6	37°	46.740'	14°	49.620'	783	*P. vera*, *P. terebinthus*
	53	Bronte 7	37°	45.180'	14°	48.960'	640	*P. terebinthus*
	54	Bronte 8	37°	42.900'	14°	48.180'	412	*P. lentiscus*

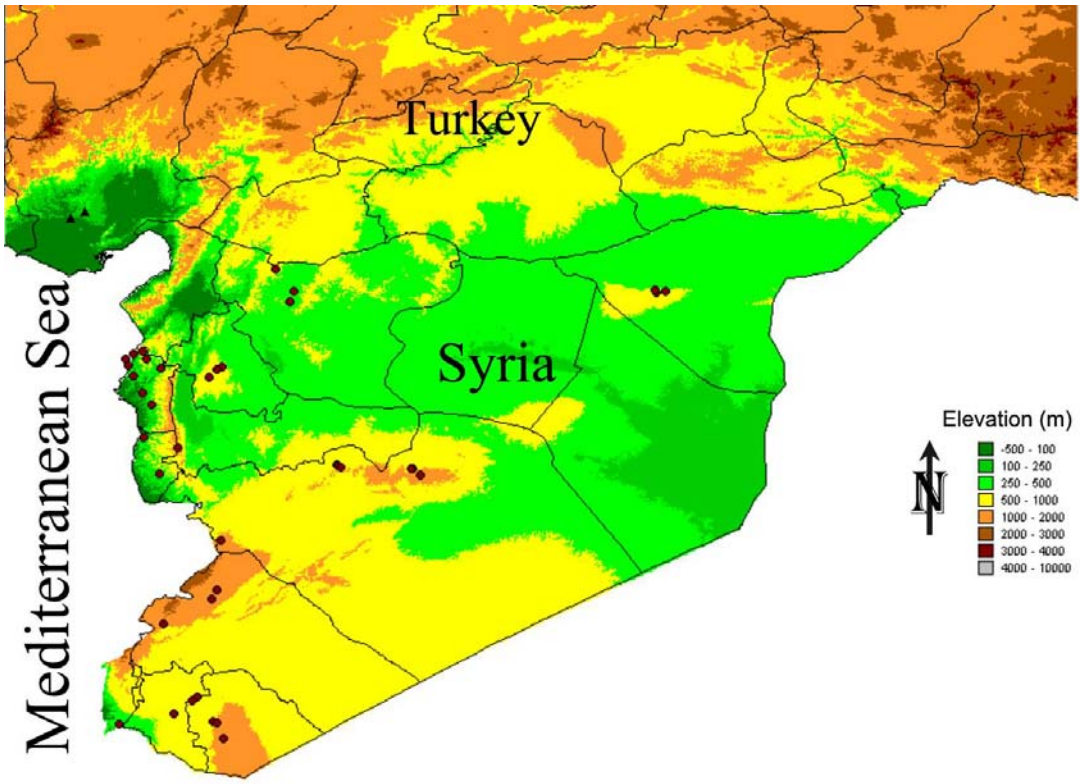


Figure 16. Collection sites of *Pistacia* spp. in Syria and Turkey.

In Tajikistan, the latitude of the selected sites were between 37°54.605' North in Televiska and 38°18.620' North in Dangara, while the longitude were between 68°39.795' East Televiska and 69°9.434' East in Dangara. The elevations of these sites ranged between 711 and 1446 m a.s.l. and the only species wildly distributed is *P. vera* (Figure 17).

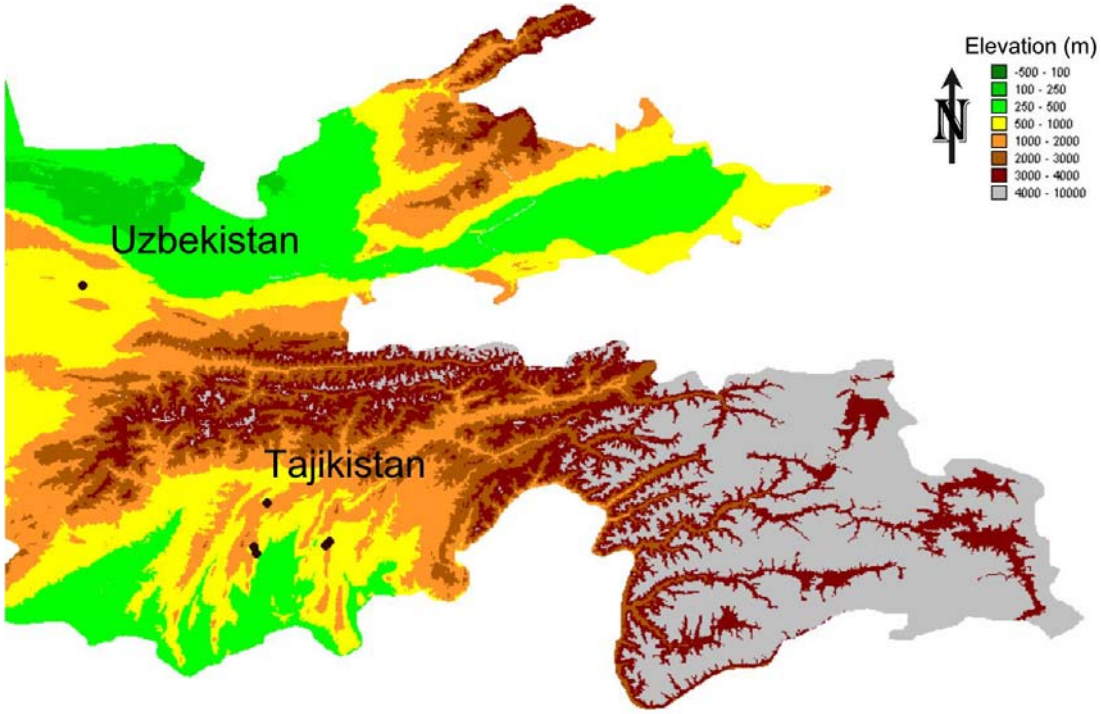


Figure 17. Collection sites of *Pistacia vera* in Tajikistan and Uzbekistan.

The pistachio cultivation in Italy is located in Sicily Island. The sites were selected in this Island near Bronte city, also *P. terebinthus* and *P. lentiscus* are wildly distributed. The latitude of selected sites were between 37°42.780' and 37°48.000' North and the longitudes ranged between 14°48.180' and 14°50.340' while the elevations were between 412 and 990 m a.s.l. (Figure 18).

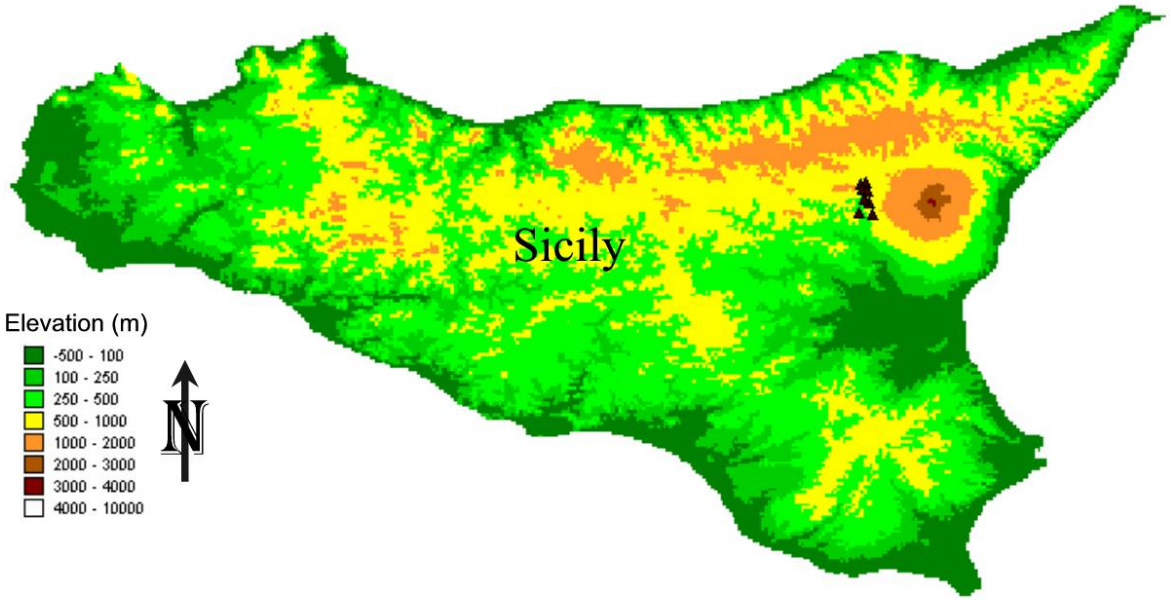


Figure 18. Collection sites of *Pistacia* in Sicily, Italy.

3.3.2. Soil characters

Table 9 shows the soil characters described according to FAO (1995) such as the name dominant soil, associated soils, dominant soils texture, slope class, soil features and general description. The studied sites were divided in 17 groups in accord with their soil characters:

1. Syria 10 groups (Figure 19);
2. Turkey one group (Figure 19);
3. Tajikistan 3 groups (Figure 20);
4. Uzbekistan one group (Figure 20);
5. Italy 2 groups (Figure 21).

Pistacia species were found in various soil types especially those shallow, moderately developed, or poorly developed of semi-deserts. The different *Pistacia* species were found in the following groups of soil (see Annex 1 for key to the FAO soil unit):

- ***P. vera:*** this species was found in several types of dominant soils such as Lithosols (I), Vertic Cambisols (Bv) , Chromic Luvisols (Lc), Calcic Xerosols (Xk), Eutric Cambisols (Be), Eutric Regosols (Re) with several types of associated soils sometimes

stony or petrocalcic. The slope ranged from gently undulating up to mountainous with slope percentage higher than 30%. The texture of these soils ranged between fine to medium, which can be described as very shallow soil, poorly developed soils of semi-deserts, rock debris, desert detritus, no significant profile development soils, moderately developed soils or non-acid soils with clay-enriched subsoil.

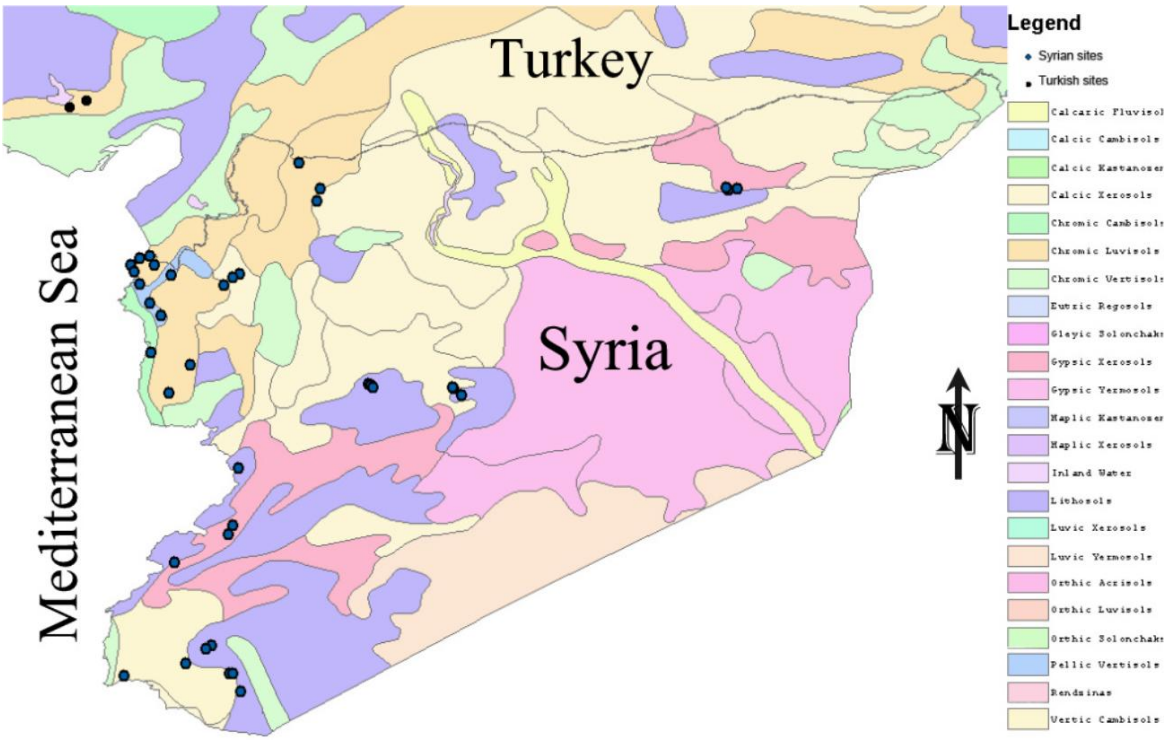


Figure 19. Dominant soil type of Syrian and Turkish sites.

- ***P. atlantica* and *P. khinjuk:*** these species were found in several types of dominant soils such as Lithosols (I), Vertic Cambisols (Bv), Calcic Xerosols (Xk), Gypsic Xerosols (Xy) with several types of associated soils sometimes stony. The slope ranged from gently undulating, up to mountainous with slope percentage more than 30%. *P. atlantica* and *P. khinjuk* grow in soils with texture ranging between fine to medium, which can be described as very shallow soil, poorly developed soils of semi-deserts, or moderately developed soils;
- ***P. palaestina* and *P. terebinthus*:** these species found in several types of dominant soils such as Eutric Cambisols (Be), Chromic Luvisols (Lc) and Eutric Regosols (Re) with several types of associated soils which were covering at least 20% of the area and sometimes was stony. The slope classes ranged from gently undulating, rolling to hilly, steeply dissected up to mountainous with a slope percentage higher than 30%. The texture of these soils ranged between fine to medium, which can be described as

moderately developed soils, non-acid soils with clay-enriched subsoil or no significant soil profile development;

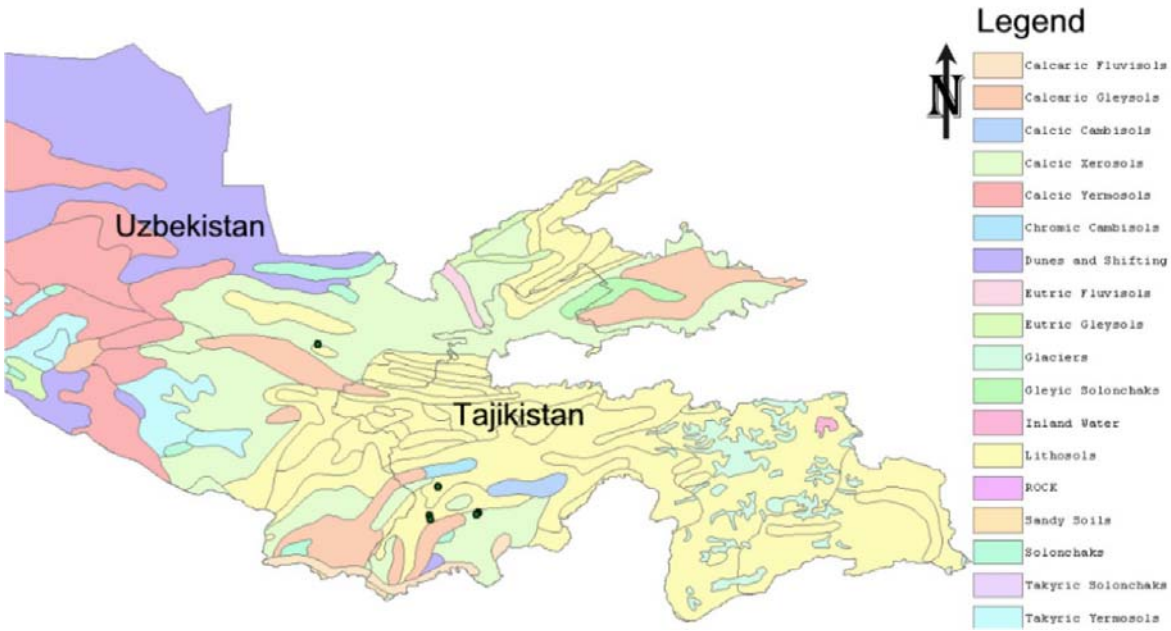


Figure 20. Dominant soil type of Central Asian sites.

- ***P. lentiscus*:** this species was found in several types of dominant soils such as Pellic Vertisols (Vp), Chromic Luvisols (Lc) and Eutric Regosols (Re) with several types of associated soils sometimes stony. The slope classes ranged from gently undulating up to mountainous with a degree higher than 30%. The texture ranged between fine to medium, which can be described as moderately developed soils, non-acid soils with clay-enriched subsoil or dark cracking clays with deficient drainage.

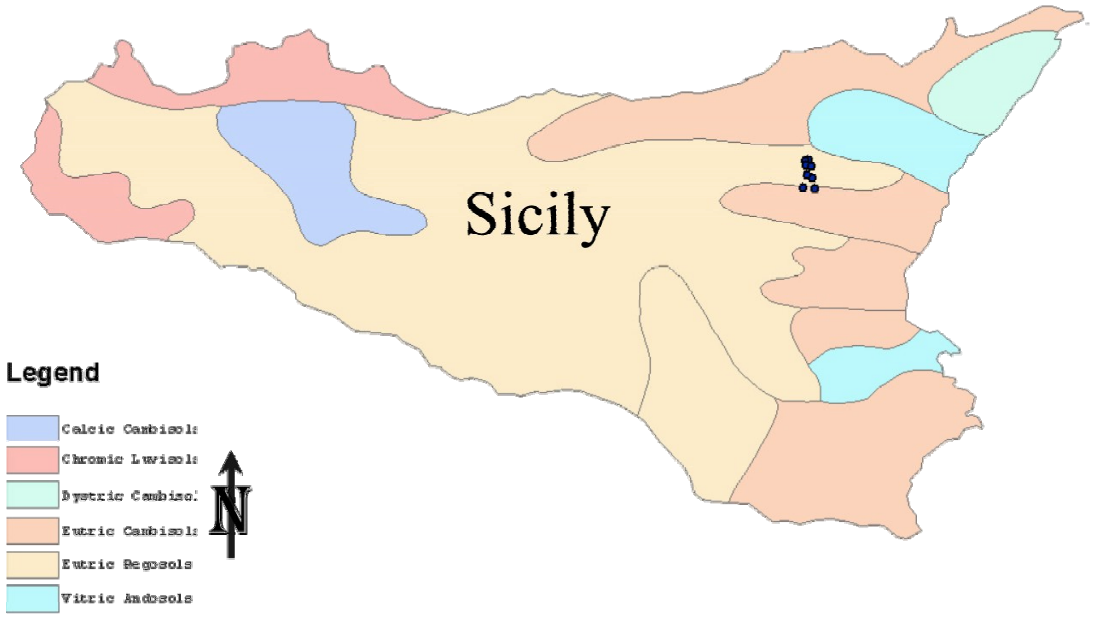


Figure 21. Dominant soil type of Italian sites.

Table 8. FAO description of the soil type and characterization for the studied sites.

Country	Sites' name	FAO Soil	Dominant soil	Associated soils	Dominant soils texture	Slope class	Soil features	Description
Syria	Banias	Be65-Ab	30% Eutric Cambisols (Be)	Calcic Cambisols Chromic Luvisols Eutric Regosols Eutric Fluvisols Vertisols	Medium	Level to gently undulating and rolling to hilly 0-30%	Stony	Moderately developed soils
	Salim Qanawat Izraa Gene bank Maaria	Bv15-3b	40% Vertic Cambisols (Bv)	Orthic Luvisols Chromic Ertisols Rendzinas Lithosols	Fine	Rolling to hilly 8-30%	Stony	Moderately developed soils
	Al Hamra Palmyra Wadi Al Balaas 1 - 2 -3	I-Xk-2c	50% Lithosols (I)	Calcic Xerosols	Medium	Steeply dissected to mountainous >30%	Stony	Very shallow soils
	Al Kafer Al Modawarah Al-Lagat	I-Yk-2ab	50% Lithosols (I)	Calcic Yermosols	Medium	Level to gently undulating and rolling to hilly <30%	Stony	Very shallow soils
	Al Bara Ain Al Gazal Ras Al Baset 1,2 Al Badrousia Al Nabiaen Frolok Kadmous Derekish	Lc63-3bc	50% Chromic Luvisols (Lc)	Calcic Cambisols Lithosols Calcaric Regosols	Fine	Rolling to hilly and steeply dissected to mountainous >8%	Stony	Non-acid soils with clay-enriched subsoil
	Al Shahba Gene bank Izaz	Lc69-3a	60% Chromic Luvisols (Lc)	Calcic Luvisols Lithosols	Fine	Level to gently undulating <8%	-	Non-acid soils with clay-enriched subsoil
	Al Mehwiye	Vp39-3b	50% Pellic Vertisols (Vp)	Vertic Cambisols Calcic Cambisols Calcaric Regosols	Fine	Rolling to hilly 8-30%	-	
	Abo Roudjmain 1	Xk26-2/3a	80% Calcic Xerosols (Xk)	Calcaric Regosols Chromic Vertisols	50% medium and 50% fine	Level to gently undulating <8%	-	Poorly developed soils of semi-deserts
	Al Moslemia Gene bank	Xk27-2ab	50% Calcic Xerosols (Xk)	Luvic Xerosols Lithosols Calcaric Regosols	Medium	Level to gently undulating and rolling to hilly <30%	Petrocalcic	Poorly developed soils of semi-deserts
	Ain Al-Tina Al-Sarkha Wadi Baradah Abdul Aziz 1 - 2 Markab Ali	Xy4-2/3a	50% Gypsic Xerosols (Xy)	Calcic Xerosols Lithosols Calcaric Regosols	50% medium and 50% fine	Level to gently undulating <8%	Stony	Poorly developed soils of semi-deserts
Turkey	Adana	Lc76-3b	60% Chromic Luvisols (Lc)	Chromic Cambisols Lithosols	Fine	Rolling to hilly 8-30%	-	Non-acid soils with clay-enriched subsoil
Tajikis-tan	Televiska	I-Bc-2c	50% Lithosols (I)	Chromic Cambisols	Medium	Steeply dissected to mountainous >30%	Rock debris or desert detritus	Very shallow soils
	Dangara 1- 2	Xk4-2b	100% Calcic Xerosols (Xk)	-	Medium	Rolling to hilly 8-30%	-	Poorly developed soils of semi-deserts
	Korgan Tubye 1-2	I-Xk-2c	50% Lithosols (I)	Calcic Xerosols	Medium	Steeply dissected to mountainous >30%	Stony	Very shallow soils
Uzbekis-tan	Galgral	Xk4-2ab	100% Calcic Xerosols (Xk)	-	Medium	Level to gently undulating and rolling to hilly <30%	-	Poorly developed soils of semi-deserts
Italy	Bronte 1 -8	Be130-2/3bc	50% Eutric Cambisols (Be)	Eutric Regosols Lithosols Orthic Luvisols	50% medium and 50% fine	Rolling to hilly and steeply dissected to mountainous >8%	Stony	Moderately developed soils
	Bronte 2 - 3 - 4 – 5-6-7	Re86-2/3b	50% Eutric Regosols (Re)	Eutric Cambisols Chromic Vertisols Eutric Fluvisols	50% medium and 50% fine	Rolling to hilly 8-30%	-	no significant soil profile development

3.3.3. Climate

Table 9 shows the fifty years mean climatic data for annual mean temperature, max temperature of warmest month, min temperature of coldest month, annual precipitation, precipitation of wettest month, precipitation of driest month and pluviometric quotient of each studied sites. The annual temperatures of Syrian sites range between 12 and 19.3ºC, while the minimum temperature of coldest month is -1.9ºC and the maximum temperature of warmest month is 39.3ºC. The annual precipitations of these sites ranged between 191 and 1280 mm, while the precipitation of wettest month is 286 mm till 0 mm in the driest month. In general, the precipitation season in Syria is limited from November to March. The Turkish sites, in Adana, have an annual mean temperature of about 19ºC and a precipitation of about 750 mm (Figure 22).

In Central Asia sites, the climate is colder and drier than Syria. The annual mean temperatures ranged between 12.3 and 14.2ºC, while the minimum temperature of coldest month is -4.5ºC and the maximum temperature of warmest month is 34.7ºC. The annual precipitations of these sites are between 33.8 and 58.6 mm, the precipitation of wettest month is 125 mm without any precipitation in the driest month (Figure 23).

Sicilian sites had a moderate costal climate. The annual mean temperatures ranged between 12.5 and 15.4ºC, the minimum temperature of coldest month is 2.4ºC and the maximum temperature of warmest month is 28.8ºC. The annual precipitations were relatively high ranging between 550 and 600mm. The precipitation of the wettest month was about 90mm and 9mm is in the driest month (Figure 24).

Table 9. The average climatic data for 50 years of the studied sites.

Country	Site name	Annual mean Temp. (°C)	Max Temp. of warmest month (°C)	Min Temp. of coldest month (°C)	Annual precipitation (mm)	Precipitation of wettest month (mm)	Precipitation of driest month (mm)	Pluviometric quotient PMQ	Studied Species
Syria	**Al Hamra**	12.4	29.2	-1.6	319	65	0	36.1	*P. atlantica*
	Ain Al-Tina	13.3	30.8	-1.0	201	41	0	21.9	*P. atlantica*
	Al Sarkha	12.0	28.8	-1.9	214	42	0	24.3	*P. atlantica*
	Wadi Baradah	13.8	30.6	0.0	470	107	0	53.2	*P. palaestina*
	Salim	16.1	32.0	2.2	280	60	0	32.4	*P. atlantica*
	Qanawat	14.8	30.3	0.5	313	67	0	36.4	*P. atlantica*
	Al Kafer	14.8	30.1	0.3	316	68	0	36.8	*P. atlantica*
	Izraa Gene bank	17.4	33.4	3.0	295	68	0	33.3	*P. vera*
	Maaria	19.3	33.9	6.2	417	102	0	51.3	*P. atlantica*
	Al Modawarah	16.7	33.6	2.1	231	51	0	25.2	*P. atlantica*
	Al Lajat	17.0	33.8	2.3	240	54	0	26.2	*P. atlantica*
	Palmyra Wadi	14.4	33.7	-1.9	218	35	0	21.2	*P. atlantica*
	Abo Roudjmain 1	15.9	35.4	-0.6	193	31	0	18.5	*P. atlantica*
	Rasm Al Abed	15.9	35.4	-0.5	191	31	0	18.3	*P. atlantica*
	Al Balaas 1	15.1	34.0	-0.8	216	38	0	21.4	*P. atlantica*
	Al Balaas 2	15.1	34.0	-0.8	216	38	0	21.4	*P. atlantica*, *P. khinjuk*
	Al Balaas 3	15.1	34.0	-0.8	216	38	0	21.4	*P. atlantica*
	Abdul Aziz 1	17.3	38.9	0.1	397	74	0	35.0	*P. atlantica*, *P. khinjuk*
	Abdul Aziz 2	17.3	38.9	0.0	396	74	0	34.8	*P. atlantica*
	Markab Ali	17.5	39.3	0.3	381	73	0	33.3	*P. atlantica*
	Al Mehwiye	18.8	32.0	6.5	887	206	2	119.0	*P. lentiscus*
	Al Moslemia Gene bank	16.8	35.6	0.8	350	68	0	34.5	*P. vera*
	Shahba Gene bank	17.0	35.9	0.9	360	70	0	35.3	*P. vera*
	Mantaf	16.2	33.5	1.3	529	108	0	56.5	*P. palaestina*
	Kafer Haya	16.2	33.5	1.3	529	108	0	56.5	*P. palaestina*
	Al Bara	16.0	32.9	1.4	644	134	1	70.4	*P. palaestina*
	Ain Al Gazal	17.5	32.4	4.2	1029	228	4	125.2	*P. palaestina*
	Wadi Kandel	18.7	31.1	6.6	955	226	3	133.5	*P. palaestina*
	Ras Al Baset 1	19.0	30.6	6.9	930	210	3	134.4	*P. palaestina*
	Al Badrousia	18.5	30.7	6.1	1014	229	4	141.4	*P. palaestina*
	Al Nabiaen	16.6	30.2	3.9	1280	286	7	167.7	*P. palaestina*
	Frolok	17.0	31.1	4.0	1181	261	6	149.9	*P. palaestina*
	Bhamra	18.2	32.5	5.4	1021	233	2	129.0	*P. palaestina*
	Banias	18.9	31.7	7.0	926	210	1	128.2	*P. palaestina*
	Kadmous	15.1	29.6	2.1	1138	237	1	143.2	*P. palaestina*
	Derekish	18.3	30.6	6.0	1139	242	1	158.9	*P. palaestina*
	Izaz	16.9	35.5	1.6	457	86	1	46.2	*P. palaestina*
	Ras Al Baset 2	18.4	30.9	6.0	1032	240	4	142.1	*P. terebinthus*
Turkey	**Adana 1**	19.4	34.8	4.8	695	141	6	79.1	*P. terebinthus*
	Adana 2	19.0	34.9	4.5	752	145	8	84.5	*P. atlantica*, *P. lentiscus*
Uzbekis-tan	**Galla Aral**	13.4	33.8	-4.0	368	65	0	33.8	*P. vera*
Tajikis-tan	**Televiska**	12.3	32.3	-4.5	619	125	0	58.6	*P. vera*
	Dangara 1	14.2	34.7	-3.1	523	109	0	47.9	*P. vera*
	Dangara 2	14.2	34.7	-3.1	523	109	0	47.9	*P. vera*
	Korgan Tubye 1	13.9	34.1	-3.2	474	101	0	44.0	*P. vera*
	Korgan Tubye 2	13.1	33.3	-4.1	495	104	0	46.0	*P. vera*
Italy	**Bronte 1**	12.5	25.9	2.4	591	90	12	87.5	*P. vera*
	Bronte 2	15.4	28.8	5.0	548	92	9	79.4	*P. vera*
	Bronte 3	14.0	27.4	3.9	566	89	11	83.4	*P. vera*
	Bronte 4	14.0	27.4	3.9	566	89	11	83.4	*P. vera*
	Bronte 5	14.0	27.4	3.9	566	89	11	83.4	*P. vera*
	Bronte 6	14.0	27.4	3.9	566	89	11	83.4	*P. vera*, *P. terebinthus*
	Bronte 7	14.0	27.4	3.9	566	89	11	83.4	*P. terebinthus*
	Bronte 8	15.4	28.8	5.0	548	92	9	79.4	*P. lentiscus*

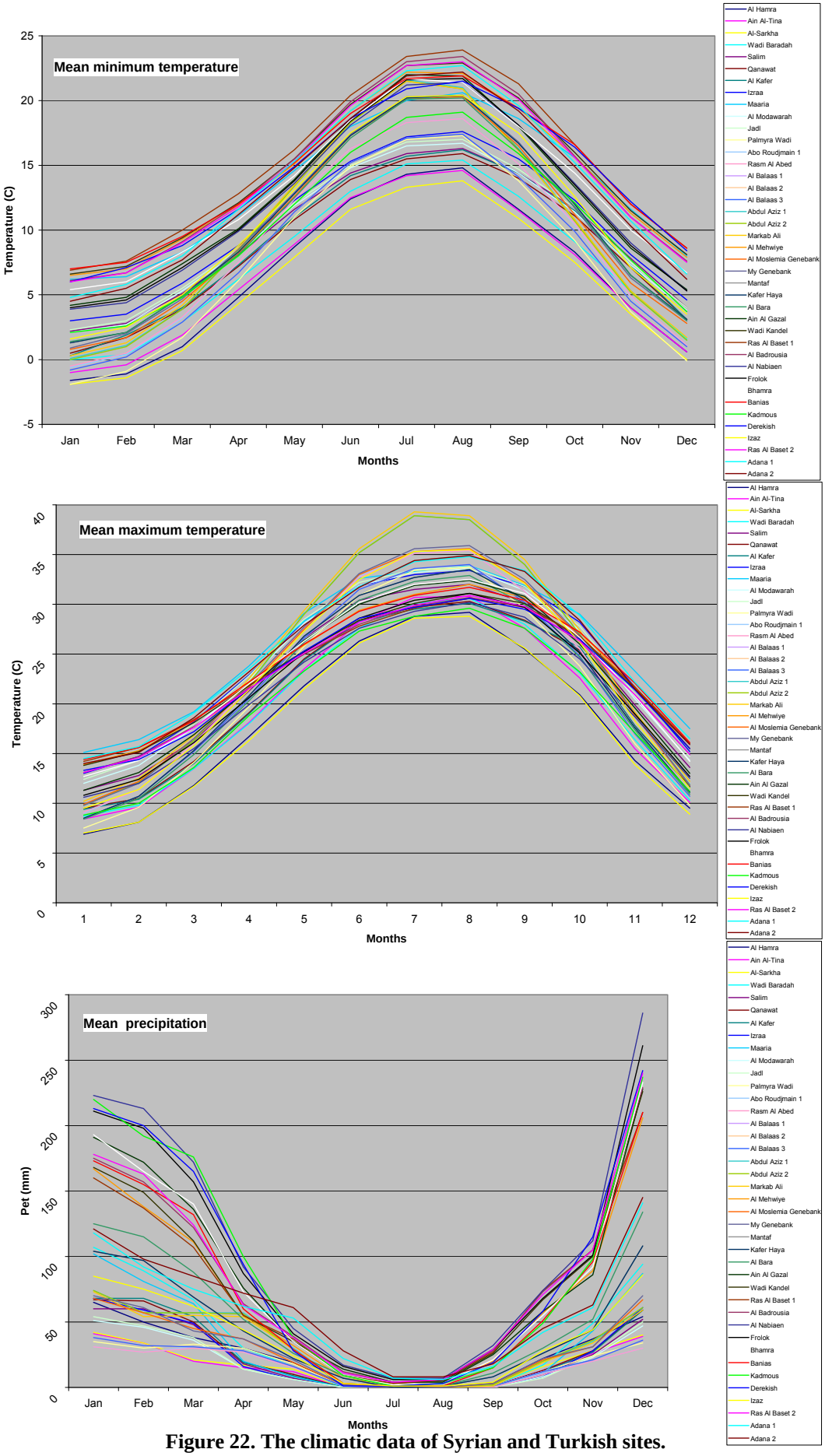


Figure 22. The climatic data of Syrian and Turkish sites.

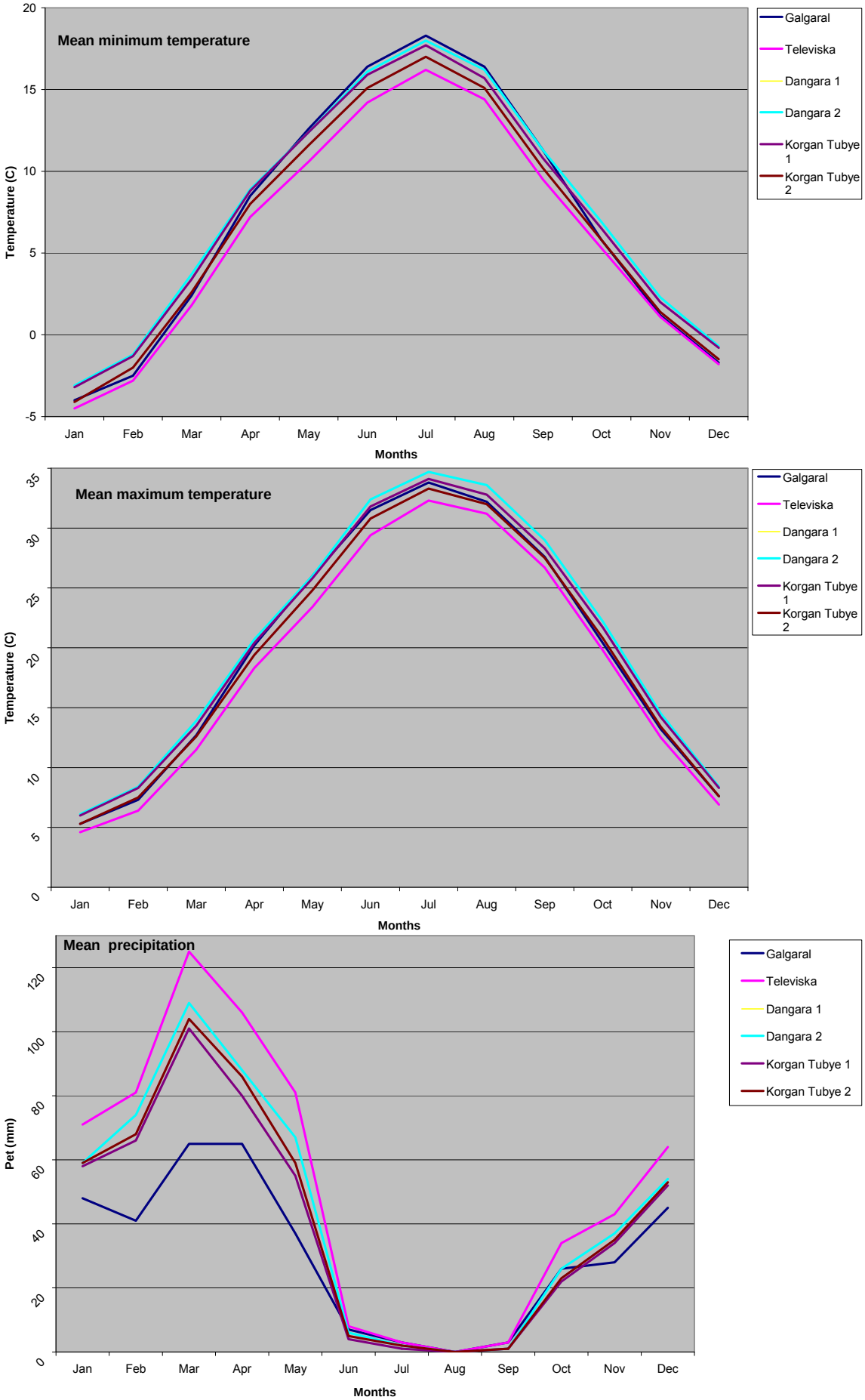
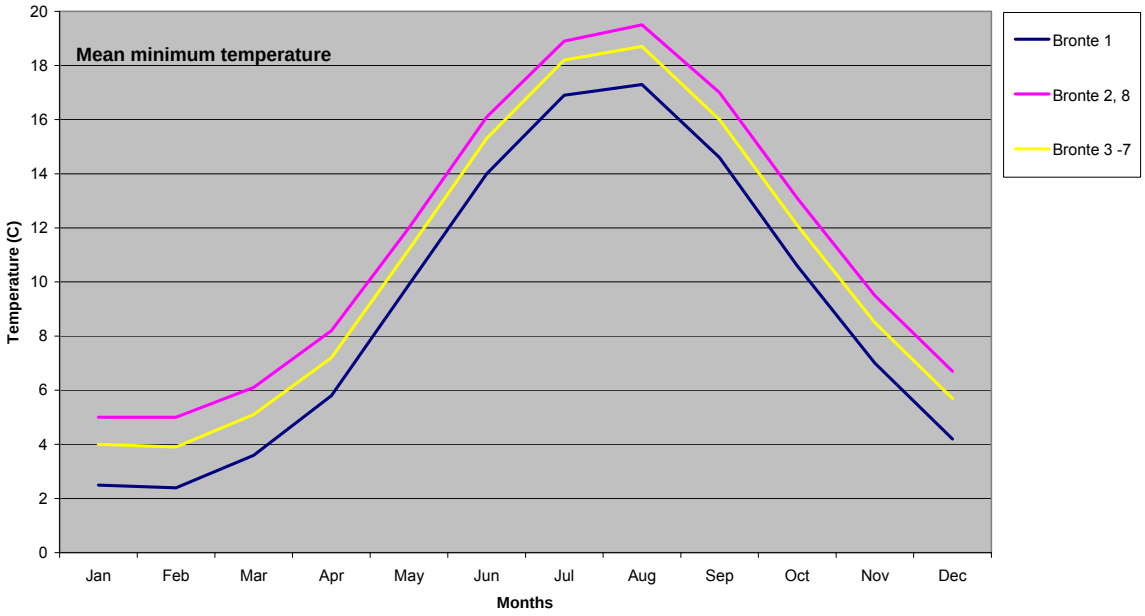
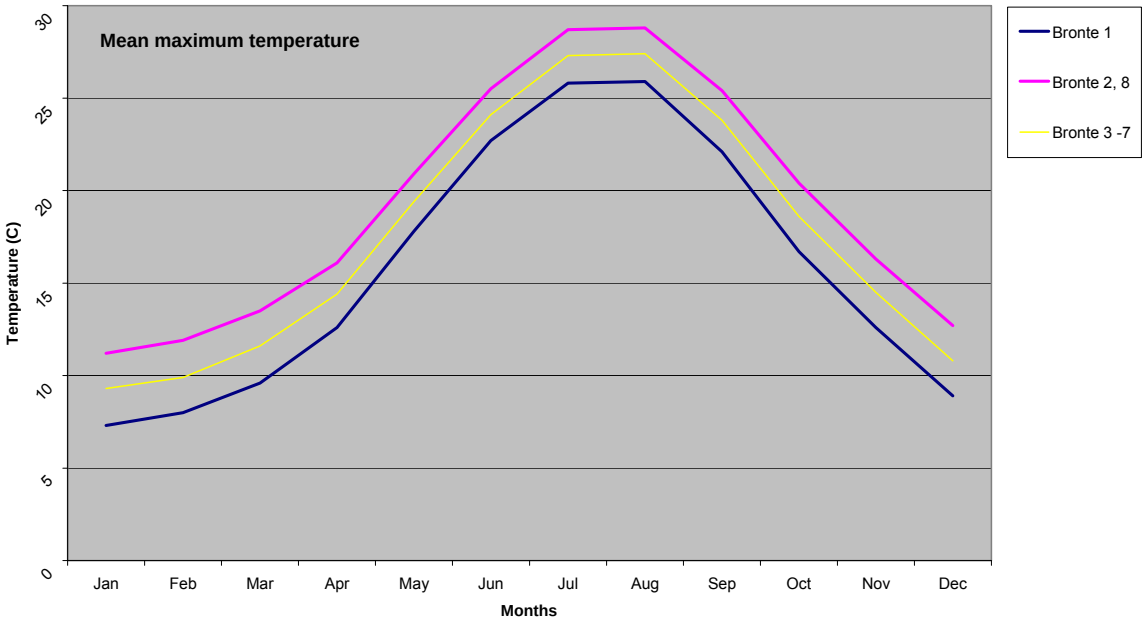


Figure 23. The climatic data of Central Asian sites.





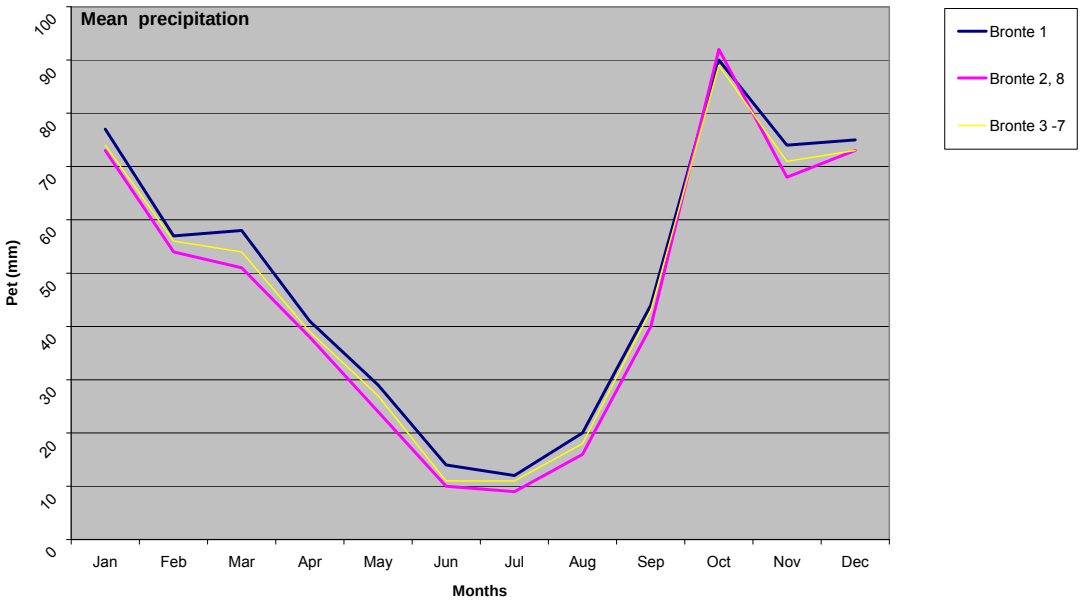


Figure 24. The climatic data of Italian sites.

The species can be found along a continuous range of mean minimum temperature. In addition, the pluviometric quotient PMQ shows the difference in aridity of the population sites (Table 9). According to the PMQ value, the populations in Syria can be divided into 5 groups in accord with the different aridity and temperature levels as follows (Figure 25):

I- **Arid zone:** this zone can be divided into two sub-zones according to the minimum temperature of the coldest months (m):

- **a. Arid Cold:** contains 6 sites (Rasm Al Abed, Abo Roudjmain 1, Al Balaas 1, Al Balaas 2, Al Balaas 3 and Ain Al-Tina). The PMQ value ranges between 18.3 and 21.9 and the average minimum temperature of the coldest months is m = -0.75ºC. The species in this zone are *P. atlantica* and *P. khinjuk*.
- **b. Arid Cool:** contains 4 sites (Al Modawarah, Al Lagat, Salim and Izraa Gene bank). PMQ value ranges between 25.2 and 33.3 and the average minimum temperature of the coldest months is -2.4ºC. The species in this zone are *P. atlantica* and *P. vera*.

II- **Semi-Arid zone:** this zone can be divided into three sub-zones according to the minimum temperature of the coldest months**:**

- **a. Semi-Arid Cold:** contains 3 sites (Al Hamra, Al Sarkha, Palmyra Wadi). PMQ value ranges between 21.2 and 36.1, and the average minimum temperature of the coldest months is -1.8ºC. The only species in this zone is *P. atlantica*;
- **b. Semi-Arid Cool:** contains 8 sites (Markab Ali, Al Moslemia Gene bank, Abdul Aziz 2, Abdul Aziz 1, Shahba Gene bank, Qanawat, Al Kafer and Izaz). PMQ value ranges between 33.3 and 46.2, and the average minimum temperature of the coldest months is 0.59ºC**.** The species in this zone are *P. atlantica*, *P. khinjuk, P. palaestina* and *P. vera*;
- **c. Semi-Arid Temperate:** contains only one site (Maaria) the PMQ value is 51.3 and the minimum temperature of the coldest months is 6.3ºC. *P. atlantica* is the species found there;

III- **Sub-Humid zone:** this zone can be divided into two sub-zones according to the minimum temperature of the coldest months:

- **a. Sub-Humid Cool:** contains 3 sites (Kafer Haya, Wadi Baradah, Al Bara). PMQ value ranges between 53.2 and 70.4 and the average minimum

temperature of the coldest months is 0.9ºC. The only species in this zone is *P. palaestina*;

b. **Sub-Humid Temperate:** contains 6 sites (Ain Al Gazal, Ras Al Baset 1, Banias, Wadi Kandel, Al Mehwiye and Bhamra). PMQ value ranges between 119 and 134.4, and the average minimum temperature of the coldest months is 6.24ºC. The species in this zone are *P. palaestina*, *P. terebinthus* and *P. lentiscus*;

IV- **Humid zone:** this zone can be divided into two sub-zones according to the minimum temperature of the coldest months:

a. **Humid cool:** contains only one site (Kadmous) the PMQ value is 143.2 and the minimum temperature of the coldest months is 2.1ºC. *P. palaestina* is the species found there**;**

b. **Humid Temperate:** contains 6 sites (Al Badrousia, Ras Al Baset 2, Frolok, Derekish and Al Nabiaen). PMQ value ranges between 141.4 and 167.7, and the average minimum temperature of the coldest months is 5.2ºC. *P. palaestina* and *P. terebinthus* are the species that found there**;**

The two Turkish sites are located in sub-humid temperate zone (PMQ= 79.08 - 84.47) with the average minimum temperature of the coldest months of 4.7ºC. The species in this zone are *P. terebinthus*, *P. lentiscus* and *P. vera* (Figure 25).

According to Tajikistan sites, which are located in sub-humid cold zone, the PMQ value ranges between 44.3 and 47.88 and the average minimum temperature of the coldest months is -3.38ºC. Only one site is located in humid cold zone (PMQ = 58.6) with the minimum temperature of the coldest months of -4.5ºC. The gene bank site of Uzbekistan is located in semi-arid cold zone (PMQ = 33.8) with the minimum temperature of the coldest months of -4ºC. The only species that is wildly distributed in these countries is *P. vera* (Figure 25).

The Italian sites are located into two zones sub-humid temperate (PMQ= 79.38-83.4) with the average minimum temperature of the coldest months of 4.2ºC. One site can be described as sub-humid temperate cool (PMQ= 87.54) and the minimum temperature of the coldest months of 2.4ºC (Figure 25).

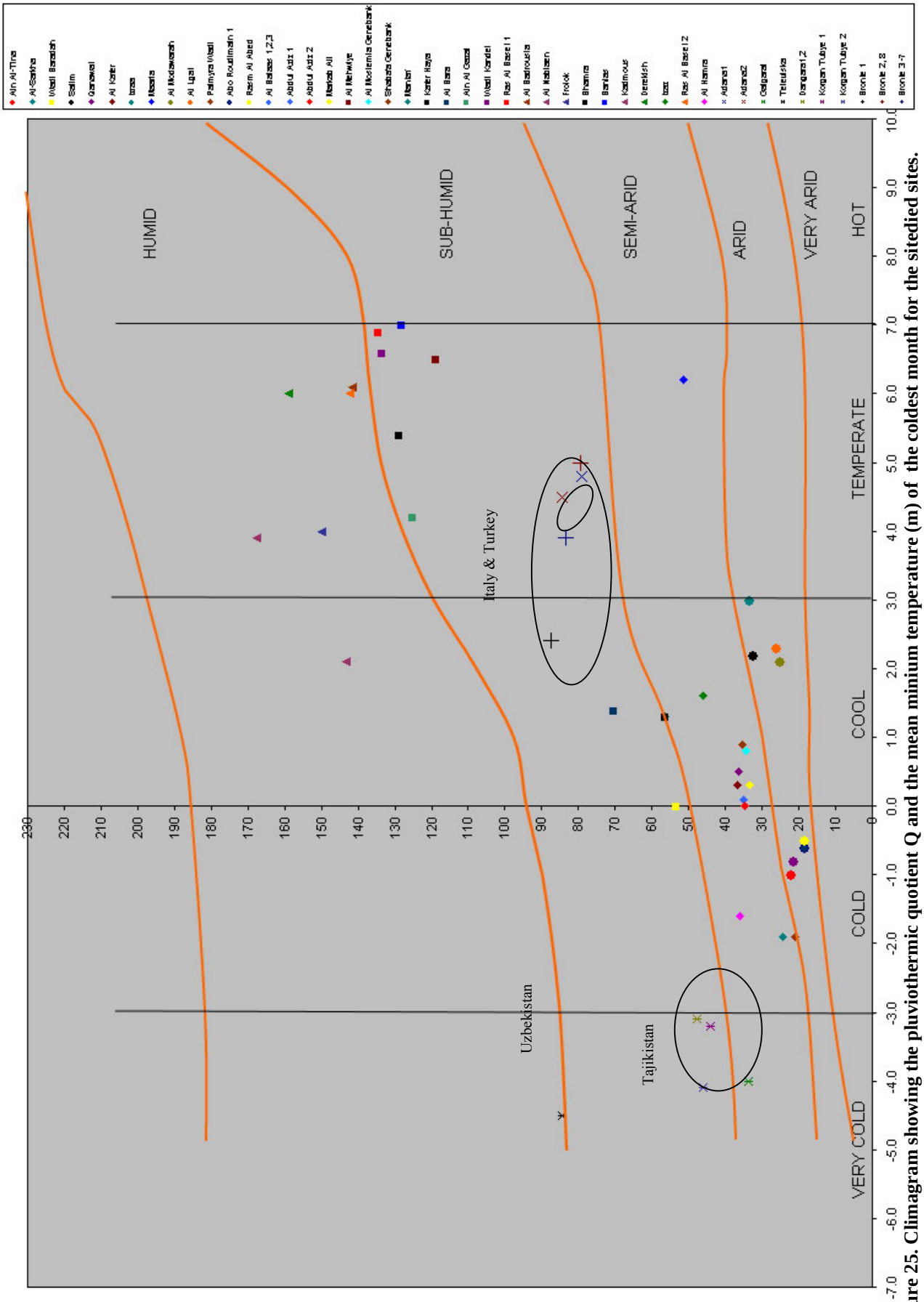


Figure 25. Climagram showing the pluviothermic quotient Q and the mean minium temperature (m) of the coldest month for the sitedied sites.

3.2. Morphological Characterization

Table 10 shows the studied species, their distribution in the sites and the number of individual selected for each species. The morphological characterization was recorded in each individual for all studied *Pistacia* species. The results is reported here for each population as its mean.

Table 10. Distribution sites of the studied *Pistacia* species and no. of individuals.

Species	No.	Distribution sites
P. atlantica	87	• Syria: Al Hamra, Ain Al-Tina, Al Sarkha, Salim, Qanawat, Al Kafer, Maaria, Al Modawarah, Al Lajat, Palmyra Wadi, Abo Roudjmain 1, Rasm Al Abed, Al Balaas 1-2-3, Abdul Aziz 1-2 and Markab Ali • Turkey: Adana 2
P. palaestina	60	• Syria: Wadi Baradah, Mantaf, Kafer Haya, Al Bara, Ain Al Gazal, Wadi Kandel, Ras Al Baset 1, Al Badrousia, Al Nabiaen, Frolok, Bhamra, Banias, Kadmous, Derekish and Izaz
P. vera	139	• Syria: Izraa Gene bank, Al Moslemia Gene bank and Shahba Gene bank • Tajikistan: Televiska and Dangara 1 -2 -3 -4 -5 • Uzbekistan: Galla Aral • Italy: Bronte 1- 2 – 3 – 4 – 5 - 6
P. lentiscus	22	• Syria: Al Mehwiye • Turkey: Adana 2 • Italy: Bronte 8
P. terebinthus	11	• Syria: Ras Al Baset 2 • Turkey: Adana 1 • Italy: Bronte 6 – 7
P. khinjuk	5	• Syria: Al Balaas 2, Abdul Aziz 1

3.2.2. Plant descriptors

3.2.2.1. *Pistacia vera*

The characterization of Syrian cultivated pistachio female varieties was not included in this thesis because it was already reported in the pervious MSc. study (Ibrahim Basha *et al.,* 2003). Therefore, only wild *P. vera* was characterized according to the IPGRI descriptor list as well as male cultivated pistachios. Table 11 shows the plant descriptors characteristics of *P. vera* for each studied populations which can be assessed as follows:

1. **Tree/Shrub vigor** can be divided into three groups (Figure 26):

   Low: as some female in Bronte 1;

   Intermediate: as some female in Televiska;

   High: as some male in Dangara 1.

Low Intermediate Dense

Figure 26. *P. vera* tree vigor.

1. **Growth habit** can be divided into two groups (Figure 27):

   Tree with single trunk: as some male *P. vera* in Izraa gene bank;

   Tree much branched form base as some female *P. vera* in Galla Aral.

Single trunk Branched form base

Figure 27. *P. vera* growth habit.

2. **Branching habit** can be divided into three groups (Figure 28):

   Sparse as some female *P. vera* in Televiska;

   Intermediate as some male *P. vera* in Bronte 4;

   Dense as some male *P. vera* in Korgan Tubye 2.

Sparse Intermediate Dense

Figure 28. *P. vera* Branching habit.

Table 11. Plant descriptor characters of the *P. vera.*

Site name	Tree	Tree/Shrub vigor	Growth habit	Branching habit
Televiska	Male	Low - Intermediate	Branched form base	Sparse - Intermediate
	Female	Low - Intermediate	Branched form base	Sparse - Intermediate
Dangara 1	Male	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
	Female	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
Dangara 2	Male	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
	Female	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
Korgan Tubye 1	Male	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
	Female	Low- Intermediate	Single trunk - Branched form base	Intermediate
Korgan Tubye 2	Male	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
	Female	Intermediate	Single trunk - Branched form base	Intermediate
Galla Aral	Male	Low- Intermediate	Branched form base	Sparse - Intermediate
	Female	Low- Intermediate	Branched form base	Sparse - Intermediate
Izraa Gene bank	Male	Intermediate	Single trunk	Intermediate
	Female	Intermediate	Single trunk	Intermediate
Al Moslemia Gene bank	Male	Low	Single trunk	Intermediate
	Female	Low	Single trunk	Intermediate
Shahba Gene bank	Male	Intermediate - High	Single trunk	Intermediate
	Female	Intermediate - High	Single trunk	Intermediate
Bronte 1	Male	Low - Intermediate	Single trunk - Branched form base	Sparse - Intermediate
	Female	Low - Intermediate	Single trunk - Branched form base	Sparse - Intermediate
Bronte 2	Male	Low - Intermediate	Single trunk - Branched form base	Sparse - Intermediate
	Female	Low - Intermediate	Single trunk - Branched form base	Sparse - Intermediate
Bronte 3	Male	Low - Intermediate	Single trunk - Branched form base	Sparse - Intermediate
	Female	Low - Intermediate	Single trunk - Branched form base	Sparse - Intermediate
Bronte 4	Male	Intermediate - High	Single trunk - Branched form base	Sparse - Intermediate
	Female	Intermediate - High	Single trunk - Branched form base	Sparse - Intermediate
Bronte 5	Male	Intermediate - High	Single trunk - Branched form base	Sparse - Intermediate
	Female	Intermediate - High	Single trunk - Branched form base	Sparse - Intermediate
Bronte 6	Male	Intermediate - High	Single trunk - Branched form base	Sparse - Intermediate
	Female	Intermediate - High	Single trunk - Branched form base	Sparse - Intermediate

3.2.2.2. *Pistacia atlantica*

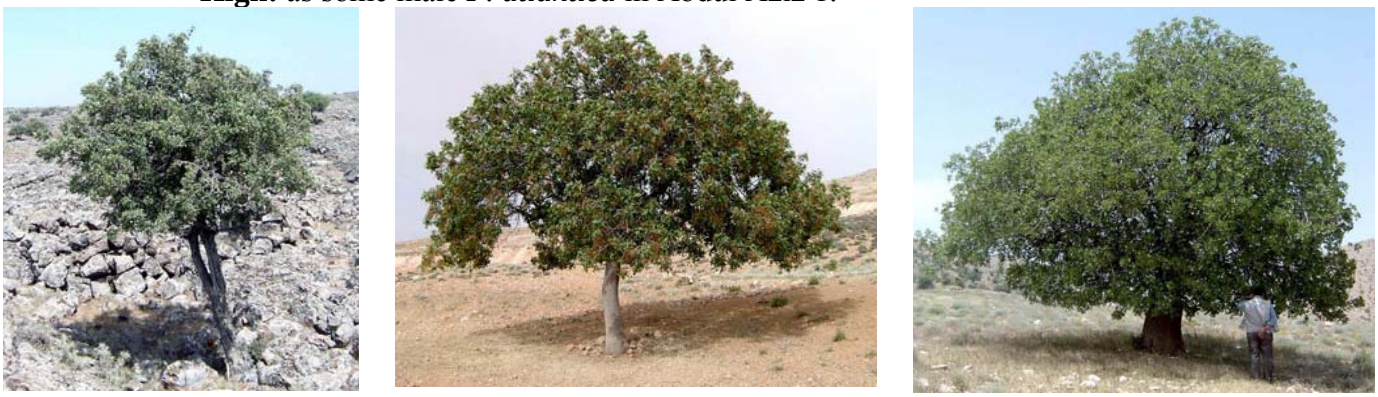
Table 12 shows the common plant descriptors of *P. atlantica* in each studied populations which can be assessed as follows:

4. **Tree/Shrub vigor** can be divided into three groups (Figure 29):

   Low: as some female *P. atlantica* in Al Lajat;

   Intermediate: as some female *P. atlantica* in Al Sarkha;

High: as some male *P. atlantica* in Abdul Aziz 1.



Low Intermediate High

Figure 29. *P. atlantica* tree vigor.

5. **Growth habit** can be divided into two groups (Figure 30):

   Tree with single trunk: as some male *P. atlantica* in Al Hamra;

   Tree much branched form base as some female *P. atlantica* in Salim.

Single trunk Branched form base

Figure 30. *P. atlantica* growth habit.

6. **Branching habit** can be divided into three groups (Figure 31):

   Sparse as some female *P. atlantica* in Palmyra Wadi;

   Intermediate as some male *P. atlantica* in Ain Al-Tina;

   Dense as some male *P. atlantica* in Al Balaas 1.

Sparse Intermediate Dense

Figure 31. *P. atlantica* Branching habit.

Table 12. Plant descriptor characters of the *P. atlantica.*

Site name	Tree	Tree/Shrub vigor	Growth habit	Branching habit
Al Hamra	Male	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
	Female	Intermediate	Single trunk	Dense
Ain Al-Tina	Male	Intermediate - High	Single trunk	Intermediate - Dense
	Female	Intermediate - High	Single trunk	Intermediate - Dense
Al Sarkha	Male	Low - Intermediate	Single trunk	Intermediate - Dense
	Female	Intermediate	Single trunk	Intermediate
Salim	Male	High	Branched form base	Dense
	Female	Intermediate	Branched form base	Intermediate
Qanawat	Male	Intermediate	Branched form base	Sparse - Intermediate
	Female	Intermediate	Branched form base	Sparse - Intermediate
Al Kafer	Male	Intermediate - High	Branched form base	Intermediate - Dense
	Female	Intermediate	Branched form base	Sparse - Intermediate
Maaria	Male	Intermediate	Single trunk	Intermediate
	Female	Intermediate	Single trunk	Intermediate
Al Modawarah	Male	High	Single trunk	Intermediate - Dense
	Female	Intermediate	Single trunk - Branched form base	Intermediate
Al Lajat	Male	Low - Intermediate	Single trunk - Branched form base	Intermediate - Dense
	Female	Low - Intermediate	Single trunk - Branched form base	Intermediate - Dense
Palmyra Wadi	Male	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
	Female	Low - Intermediate	Single trunk - Branched form base	Sparse - Intermediate
Abo Roudjmain 1	Male	Intermediate	Single trunk - Branched form base	Intermediate
	Female	Low - Intermediate	Single trunk - Branched form base	Sparse - Intermediate
Rasm Al Abed	Male	Low	Branched form base	Sparse - Intermediate
	Female	Low	Single trunk - Branched form base	Sparse - Intermediate
Al Balaas 1	Male	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
	Female	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
Al Balaas 2	Male	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
	Female	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
Al Balaas 3	Male	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
	Female	Intermediate - High	Single trunk - Branched form base	Intermediate - Dense
Abdul Aziz 1	Male	High	Single trunk - Branched form base	Intermediate - Dense
	Female	High	Single trunk - Branched form base	Intermediate - Dense
Abdul Aziz 2	Male	High	Single trunk - Branched form base	Intermediate - Dense
	Female	High	Single trunk - Branched form base	Intermediate - Dense
Markab Ali	Male	High	Single trunk - Branched form base	Intermediate - Dense
	Female	High	Single trunk - Branched form base	Intermediate - Dense
Adana 2	Male	High	Single trunk	Dense
	Female	High	Single trunk	Dense

3.2.2.3. *Pistacia palaestina*

Table 13 shows the common plant descriptors of *P. palaestina* in each studied populations which can be assessed as follows:

1. **Tree/Shrub vigor** can be divided into three groups (Figure 32):

   Low: as some female *P. palaestina* in Ain Al Gazal;

   Intermediate: as some female *P. palaestina* in Mantaf;

   High: as some male *P. palaestina* in Frolok.

Low Intermediate Dense

Figure 32. *P. palaestina* tree vigor.

2. **Growth habit** can be divided into two groups (Figure 33):

   Tree with single trunk: as some male *P. palaestina* in Ras Al Baset 1;

   Tree much branched form base as some female *P. palaestina* in Al Badrousia.

Single trunk Branched form base

Figure 33. *P. palaestina* growth habit.

3. **Branching habit** can be divided into three groups (Figure 34):

   Sparse as some female *P. palaestina* in Kadmous;

   Intermediate as some male *P. palaestina* in Wadi Kandel ;

   Dense as some male *P. palaestina* in Banias.

Sparse Intermediate Dense

Figure 34. *P. palaestina* Branching habit.

Table 13. Plant descriptor characters of the *P. palaestina.*

Site name	Tree	Tree/Shrub vigor	Growth habit	Branching habit
Wadi Baradah	Male	Intermediate	Single trunk	Intermediate
	Female	Intermediate	Single trunk	Intermediate
Mantaf	Male	High	Single trunk	Dense
	Female	Intermediate	Branched form base	Intermediate
Kafer Haya	Male	Intermediate	Branched form base	Intermediate
	Female	Intermediate	Branched form base	Intermediate
Al Bara	Male	Intermediate	Branched form base	Intermediate
	Female	Intermediate	Branched form base	Intermediate
Ain Al Gazal	Male	Intermediate	Branched form base	Intermediate
	Female	Low - Intermediate	Branched form base	Sparse - Intermediate
Wadi Kandel	Male	Intermediate	Branched form base	Intermediate
	Female	Intermediate	Branched form base	Intermediate
Ras Al Baset 1	Male	High	Single trunk	Dense
	Female	Intermediate	Branched form base	Intermediate
Al Badrousia	Male	Intermediate	Branched form base	Intermediate
	Female	Intermediate	Branched form base	Intermediate
Al Nabiaen	Male	Intermediate	Branched form base	Intermediate
	Female	Intermediate	Branched form base	Intermediate
Frolok	Male	High	Branched form base	Dense
	Female	High	Branched form base	Dense
Bhamra	Male	Intermediate - High	Branched form base	Intermediate - Dense
	Female	Intermediate - High	Branched form base	Intermediate - Dense
Banias	Male	Intermediate	Branched form base	Intermediate
	Female	Intermediate	Branched form base	Dense
Kadmous	Male	Low	Branched form base	Sparse
	Female	Low	Branched form base	Sparse
Derekish	Male	Intermediate - High	Branched form base	Intermediate - Dense
	Female	Intermediate - High	Branched form base	Intermediate - Dense
Izaz	Male	Intermediate - High	Branched form base	Intermediate
	Female	Intermediate - High	Single trunk	Intermediate

3.2.2.4. *Pistacia terebinthus*

A very few individuals of *P. terebinthus* were found in one location in Syria (Ras Al Baset 2), and was reported in Table 11 The number of individuals was very little. In addition,

some individuals were evaluated and characterized from Turkey and Italy. The common plant descriptors of *P. terebinthus* can be assessed as follows (Figure 35):

1. **Tree/Shrub vigor** can be described as low (as some female in Adana 1) or intermediate (as some male in Bronte 6 and Ras Al Baset 2)
2. **Growth habit** can be described as much branched forms base
3. **Branching habit** can be classified between sparse to intermediate.

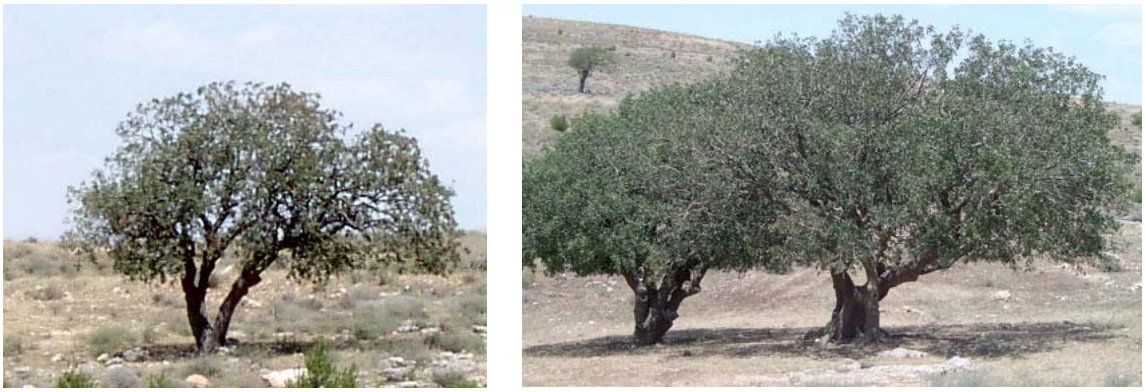
Male Female

Figure 35. Male and female trees of *P. terebinthus.*

3.2.2.5. *Pistacia khinjuk*

This species was found together with *P. atlantica* in two location but with a very few individuals. Therefore only five individuals were evaluated in this study the plant descriptors of *P. khinjuk* can be described as follows (Figure 36):

1. **Tree/Shrub vigor** can be described as intermediate (as some male in Al Balaas 2) or high (as some female in Abdul Aziz 1)
2. **Growth habit** is much branched forms base
3. **Branching habit** can be classified between intermediate to dense.



Male Female

Figure 36. Male and female trees of *P. khinjuk.*

3.2.2.6. *Pistacia lentiscus*

This species was studied into three sites in three countries: Syria (Al Mehwiye), Turkey (Adana 2) and Italy (Bronte 8). According to the plant descriptor, this species can be considered as shrub. The shrub characterization in each studied population can be summarized as follows (Figure 37):

1. **Shrub vigor** can be described as intermediate (as some female in Al Mehwiye) or high (as some male in Adana 2 and Bronte 8)
2. **Growth habit** is much branched forms base
3. **Branching habit** can be classified as dense.

Male

Female

Figure 37. Male and female trees of *P. lentiscus*.

3.2.3. Leaf descriptor

3.2.3.1. *Pistacia vera*

Wild *P. vera* was characterized according to the IPGRI descriptor list as well as male cultivated pistachios. These results can be summarized as follows:

Leaf dimensions: Table 14 shows the maximum and minimum of leaf dimensions of each studied *P. vera* population. The average leaf length ranges from 6.60 cm (wild female in Korgan Tubye 2 site) to 21.00 cm (MV8.2 Syrian cultivated male). According to the leaf width, it ranges from 4.2 cm (MV22.10 Syrian cultivated male) to 21cm (MV8.3 Syrian cultivated male). ANOVA analyses for the length show significant differences between the populations, but the width shows highly significant differences between the populations (Annex 2 - Table 1). On the other hand ANOVA analyses for the length and width show highly significant difference between the individuals (Annex 2 - Table 2). Figure 38 shows the average dimensions of the male and female leaves in each the studied *P. vera* populations and the Syrian cultivated male varieties.

Table 14. The maximum and minimum of leaf dimensions of the *P. vera.*

Site (Population)	Sex	Leaf length		Leaf width	
		Min.	Max.	Min.	Max.
Televiska	Female40	13.00	18.00	11.00	16.57
Galla Aral	Female41	8.00	17.20	6.70	18.00
Dangara 1	Female42	9.50	16.30	11.00	17.40
	Male42	13.50	17.00	13.10	18.50
Dangara 2	Female43	10.50	17.70	7.10	18.50
	Male43	13.50	15.00	13.70	18.30
Korgan Tubye 1	Male44	9.70	16.10	9.30	15.80
Korgan Tubye 2	Female50	6.60	20.80	6.00	17.50
Izraa Gene bank	Male8.1	7.20	8.50	8.00	9.00
	Male8.2	19.20	21.00	17.50	18.00
	Male8.3	19.20	20.00	9.00	21.00
	Male8.4	16.00	18.00	13.00	17.00
	Male8.5	18.00	20.00	6.50	8.50
	Male 8.6	13.00	13.10	7.50	11.00
	Male8.7	11.80	17.50	6.50	11.60
	Male8.8	14.00	16.00	6.50	15.60
	Male8.9	15.10	15.55	9.60	12.60
	Male8.10	12.90	18.60	12.60	16.70
Al Moslemia Gene bank	Male22.2	13.20	14.50	8.50	9.50
	Male22.3	9.50	13.30	7.80	11.40
	Male22.4	11.20	14.30	8.00	12.40
	Male22.8	11.80	13.60	7.80	13.30
	Male22.9	12.90	14.00	10.55	11.40
	Male22.10	11.00	14.50	4.20	12.60
F (population)		2.481*		4.019**	
***P*-value (population)**		0.01941*		0.000462**	
F (individuals)		4.344**		3.614**	
***P*-value (individuals)**		$1.01x10^{-10}$**		$1.08x10^{-08}$**	

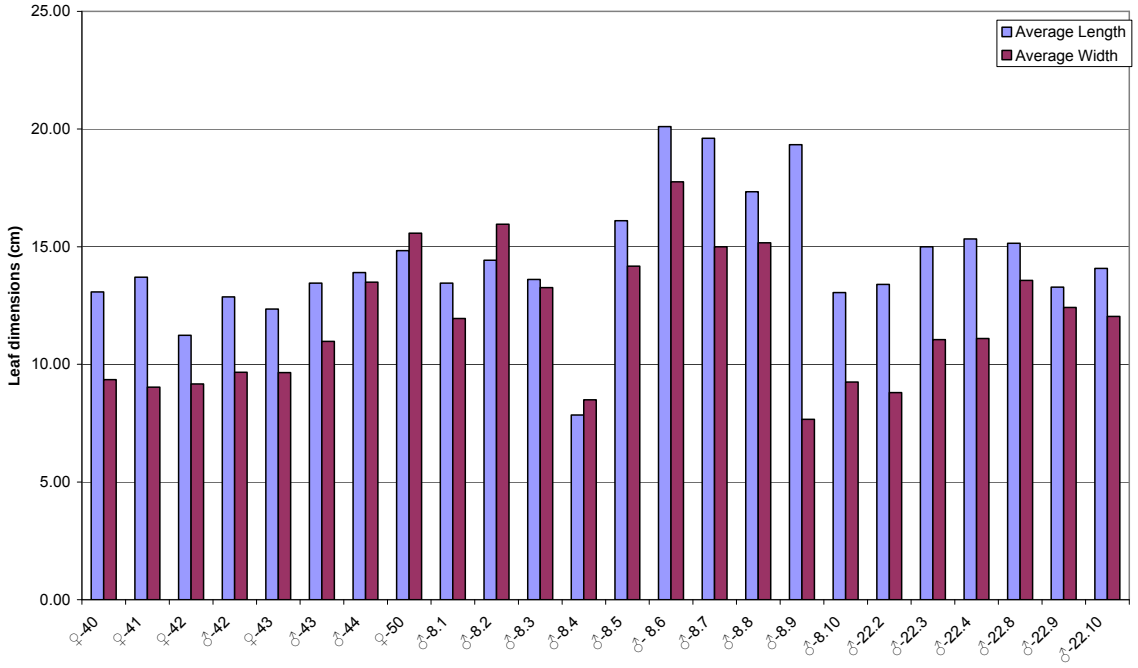


Figure 38. The average leaf dimensions of the *P. vera.*

Terminal leaflet dimensions: Table 15 shows the maximum and minimum values of terminal leaflet dimensions for each studied site. The average leaf length ranges from 3.5 cm (wild female in Korgan Tubye 2 sites) to 15 cm (MV8.3 Syrian cultivated male). According the leaf width ranges from 2.60 cm (wild female in Korgan Tubye 2 sites) to 11 cm (MV8.3 Syrian cultivated male). The length/width ratio ranges between 0.83 (MV8.5 Syrian cultivated male) and 2.57 (wild female Galla Aral site). ANOVA analyses of terminal leaflet length indicated that the differences between the populations are significant, but highly significant for the width and the length /width ratio (Annex 2 - Table 1). On the other hand ANOVA analyses for the length, width and the ratio show highly significant difference between the individuals (Annex 2 - Table 2). Figure 40 shows the average dimensions of the male and female terminal leaflets in these populations and in the Syrian cultivated male varieties.

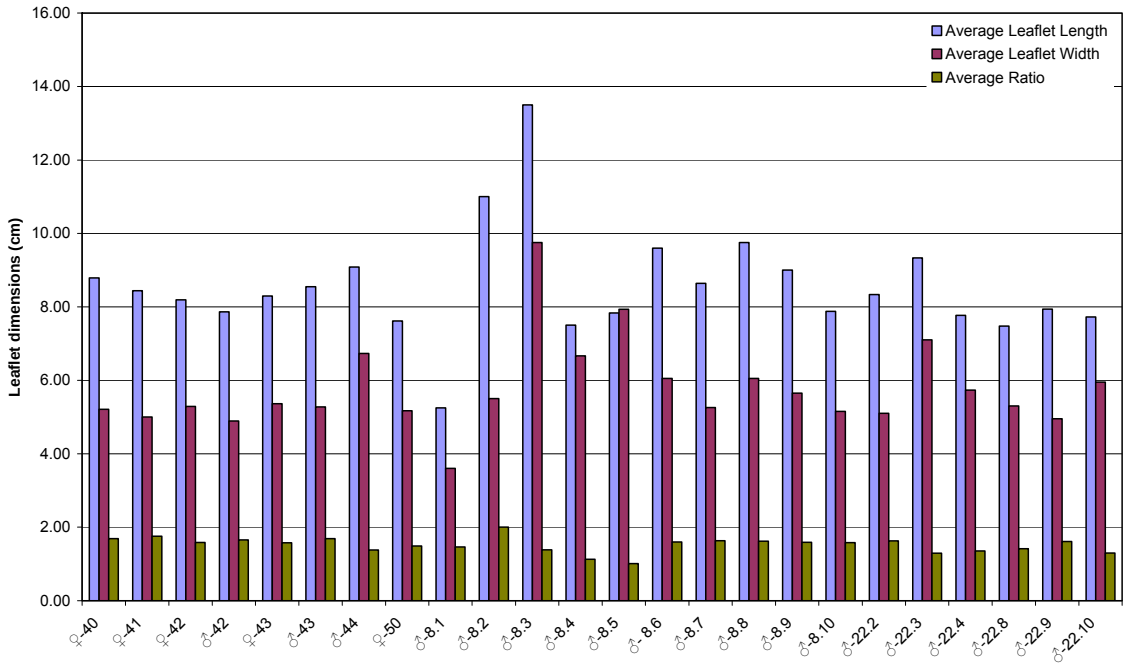


Figure 39. The average terminal leaflet dimensions of the *P. vera*

Table 15. The maximum and minimum of terminal leaflet dimensions of the *P. vera.*

Site (Population)	Sex	Leaflet Length		Leaflet Width		Length/width Ratio	
		Min	Max	Min	Max	Min	Max
Televiska	Female40	7.20	10.70	4.30	6.10	1.45	1.88
Galla Aral	Female41	6.80	10.00	3.70	7.50	1.11	2.57
Dangara 1	Female42	6.00	9.50	3.50	6.80	1.22	2.33
	Male42	6.20	10.70	3.20	6.60	1.29	2.31
Dangara 2	Female43	6.00	12.00	3.50	7.70	1.29	2.00
	Male43	6.40	10.80	3.10	7.00	1.29	2.06
Korgan Tubye 1	Male44	8.00	10.50	5.30	8.50	1.14	1.98
Korgan Tubye 2	Female50	3.50	11.90	2.60	8.00	1.00	1.89
Izraa Gene bank	Male8.1	5.00	5.50	3.50	3.70	1.35	1.57
	Male8.2	10.00	12.00	5.00	6.00	2.00	2.00
	Male8.3	12.00	15.00	8.50	11.00	1.36	1.41
	Male8.4	7.00	8.00	6.00	7.50	1.07	1.25
	Male8.5	7.50	8.00	6.50	9.00	0.83	1.23
	Male 8.6	9.20	10.00	5.70	6.40	1.44	1.75
	Male8.7	7.00	12.30	4.50	6.60	1.53	1.86
	Male8.8	8.50	11.00	5.80	6.30	1.35	1.90
	Male8.9	8.00	10.00	5.50	5.80	1.45	1.72
	Male8.10	6.40	9.00	3.50	6.70	1.34	1.83
Al Moslemia Gene bank	Male22.2	6.00	9.70	4.70	5.60	1.28	1.94
	Male22.3	6.00	11.50	5.30	8.10	1.13	1.46
	Male22.4	7.50	8.30	5.50	6.00	1.32	1.38
	Male22.8	7.00	8.00	5.00	6.00	1.23	1.54
	Male22.9	7.68	8.20	4.50	5.40	1.52	1.71
	Male22.10	6.20	9.00	5.40	6.70	1.15	1.45
F (population)		1.647*		3.255**		3.784**	
***P*-value (population)**		0.12641*		0.003025**		0.000827**	
F (individuals)		2.155**		2.786**		2.404**	
***P*-value (individuals)**		0.000356**		$3.45x10^{-06}$**		5.6610^{-05}**	

Table 16 shows the other morphological characters of the leaves and leaflets, in terms of dominant number of leaflets which were 3 leaflets such as some males in Korgan Tubye 2 site and 5 leaflets such as some females in Galla Aral site. The terminal leaflets sizes are found similar or larger than basal leaflets which were found in all the studied individuals. On the other hand, the terminal leaflets are found in several shapes and apexes (Figure 40):

- Elliptic, such as some wild females in Televiska site;
- Ovate, such as Syrian cultivated male MV 8,3 Izraa Gene bank ;
- Oblong, such as some wild females in Dangara 1 site;
- Round, such as some wild Korgan Tubye 1 site.

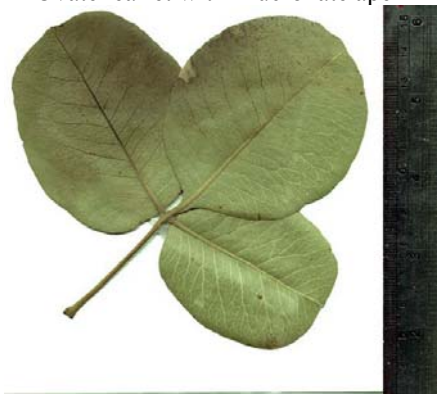
Table 16. Some leaf characters of *P. vera*.

Site (Population)	Sex	Dominant no. of leaflets	Terminal leaflet size	Terminal leaflet shape	Terminal leaflet apex
Televiska	Female40	3 -5	Similar- Larger	Elliptic - Ovate	Acute - Obtuse
Galla Aral	Female41	3 -5	Similar- Larger	Elliptic - Ovate	Acute - Obtuse
Dangara 1	Female42	3 -5	Similar- Larger	Elliptic - Ovate - Oblong	Acuminate - Obtuse
	Male42	3 -5	Similar- Larger	Elliptic	Mucronulate
Dangara 2	Female43	3 -5	Similar- Larger	Elliptic - Ovate	Retuse
	Male43	3 -5	Similar- Larger	Elliptic	Acute
Korgan Tubye 1	Male44	3 -5	Similar- Larger	Elliptic - Ovate - Round	Retuse
Korgan Tubye 2	Female50	3 -5	Similar- Larger	Elliptic - Ovate - Round	Obtuse -Mucronulate
Izraa Gene bank	Male8.1	3 -5	Similar- Larger	Ovate	Mucronulate
	Male8.2	3 -5	Similar- Larger	Ovate	Acuminate
	Male8.3	3 -5	Similar- Larger	Ovate	Obtuse - Retuse
	Male8.4	3 -5	Similar- Larger	Ovate	Cuspidate
	Male8.5	3 -5	Similar- Larger	Oblong	Obtuse
	Male 8.6	3 -5	Similar- Larger	Elliptic	Acute - Obtuse
	Male8.7	3 -5	Similar- Larger	Ovate - Oblong	Retuse
	Male8.8	3 -5	Similar- Larger	Ovate	Obtuse- Retuse
	Male8.9	3 -5	Similar- Larger	Ovate	Mucronate - Obtuse
	Male8.10	3 -5	Similar- Larger	Ovate - Round	Acute
Al Moslemia Gene bank	Male22.2	3 -5	Similar- Larger	Ovate	Obtuse
	Male22.3	3 -5	Similar- Larger	Ovate	Cuspidate
	Male22.4	3 -5	Similar- Larger	Ovate	Cuspidate
	Male22.8	3 -5	Similar- Larger	Ovate	Obtuse
	Male22.9	3 -5	Similar- Larger	Ovate	Acute
	Male22.10	3 -5	Similar- Larger	Ovate - Oblong	Obtuse

Elliptic leaflet with Mucronulate apex

Ovate leaflet with Mucronate apex

Oblong leaflet with acute apex



Round leaflet with obtuse apex

Figure 40. Terminal leaflet shapes of *P.* vera.

3.2.3.2. *Pistacia atlantica*

Leaf dimensions: Table 17 shows the maximum and minimum leaf dimensions of each studied *P. atlantica* populations. The average leaf length ranges from 6.00 cm (male in Rasm Al Abed site) to 22.5 cm (female in Ain Al-Tina site). The leaf width, it ranges from 5.5 cm (female in Al Sarkha site) to 23.00 cm (female in Ain Al-Tina site). ANOVA analyses for each character shows highly significant differences both between populations and between individuals (Annex 2 - Table 3-4). Figure 42 shows the average dimensions of the male and female leaves in each studied *P. atlantica* populations.

Table 17. The maximum and minimum of leaf dimensions of the *P. atlantica*.

Site (Population)	Sex	Leaf length		Leaf width	
		Min.	Max.	Min.	Max.
Al Hamra	Male	12.50	17.50	8.60	12.00
	Female	10.90	19.70	7.00	14.10
Ain Al-Tina	Male	12.40	19.50	9.20	17.50
	Female	7.30	22.50	10.10	23.00
Al Sarkha	Male	18.70	19.30	14.20	17.20
	Female	6.40	19.20	5.50	14.90
Salim	Male	15.20	16.50	9.40	11.90
	Female	8.70	14.30	8.00	10.60
Qanawat	Male	9.40	19.20	8.00	13.40
	Female	8.90	13.50	8.60	10.80
Al Kafer	Male	11.70	16.00	8.00	10.50
Maaria	Female	10.90	17.40	7.50	14.80
Al Modawarah	Male	12.60	17.50	7.20	9.70
	Female	7.90	15.40	7.60	11.00
Al Lajat	Male	11.50	15.60	7.30	12.60
Palmyra Wadi	Male	10.60	15.20	8.00	13.20
	Female	9.50	14.90	7.60	10.40
Abo Roudjmain 1	Male	10.20	19.00	9.80	15.30
	Female	9.50	15.40	9.30	17.00
Rasm Al Abed	Male	6.00	14.20	6.00	12.30
	Female	12.30	14.20	9.20	10.70
Al Balaas 1	Male	8.80	18.20	7.20	13.60
	Female	12.00	15.40	9.20	17.00
Al Balaas 2	Male	10.30	16.50	9.10	14.40
	Female	12.30	14.70	9.10	11.30
Al Balaas 3	Male	10.30	15.60	8.70	14.40
	Female	12.20	17.20	8.80	17.40
Abdul Aziz 1	Male	12.50	15.80	8.70	14.00
	Female	9.20	18.30	8.20	13.70
Abdul Aziz 2	Male	18.20	16.13	16.20	11.84
	Female	11.80	16.00	10.80	14.80
Markab Ali	Female	8.30	15.50	6.20	16.00
Adana 2	Male	13.50	18.70	8.30	14.00
	Female	12.30	15.50	9.20	16.00
F (population)		3.258**		3.803**	
***P*-value (population)**		$1.63x10^{-05}$**		$8.3x10^{-07}$**	
F (individuals)		3.492**		2.950**	
***P*-value (individuals)**		$5.82x10^{-13}$**		$4.04x10^{-10}$**	

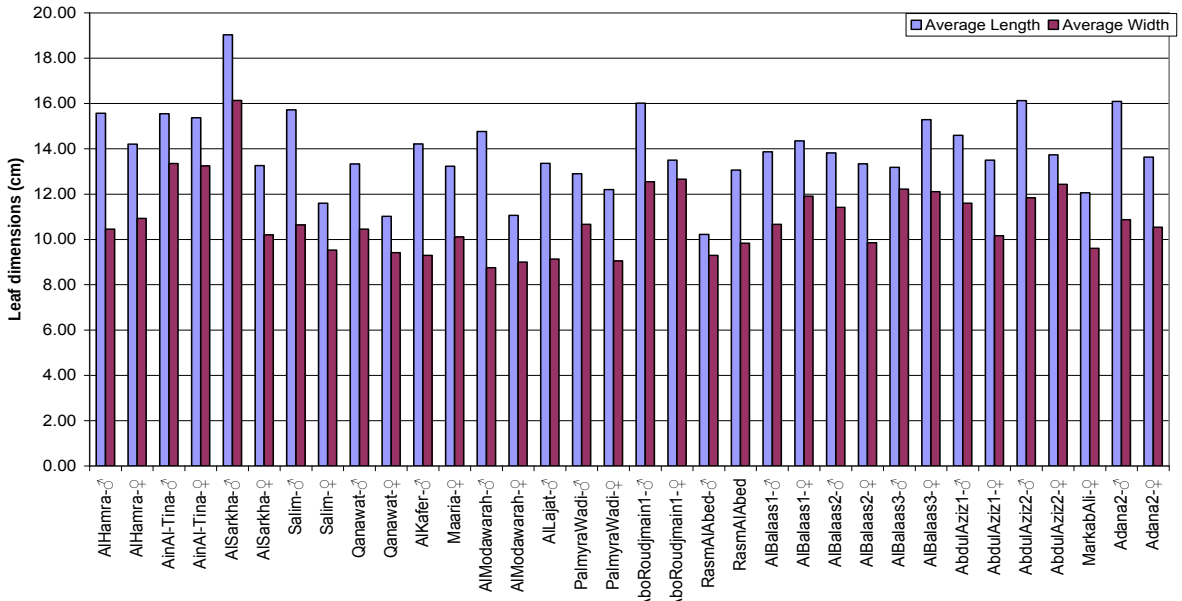


Figure 41. The average leaf dimensions of the *P. atlantica.*

Terminal leaflet dimensions: Table 18 shows the maximum and minimum of terminal leaflet dimensions for each studied site. The average leaf length ranges from 2.8 cm (male in Abdul Aziz 1 and Adana 2 sites) to 12.5 cm (male in Abdul Aziz 2 site). According to the leaf width, it ranges from 1.00 cm (male in Qanawat site) to 6.3 cm (male in Ain Al-Tina site). The length/width ratio ranges between 1.6 (male in Abdul Aziz 1 and Adana 2 sites) and 4 (male in Qanawat site). ANOVA analyses for each character show significant differences both between the population and between individuals (Annex 2 - Table 3-4). Figure 42 shows the average dimensions of the male and female terminal leaflets in these populations.

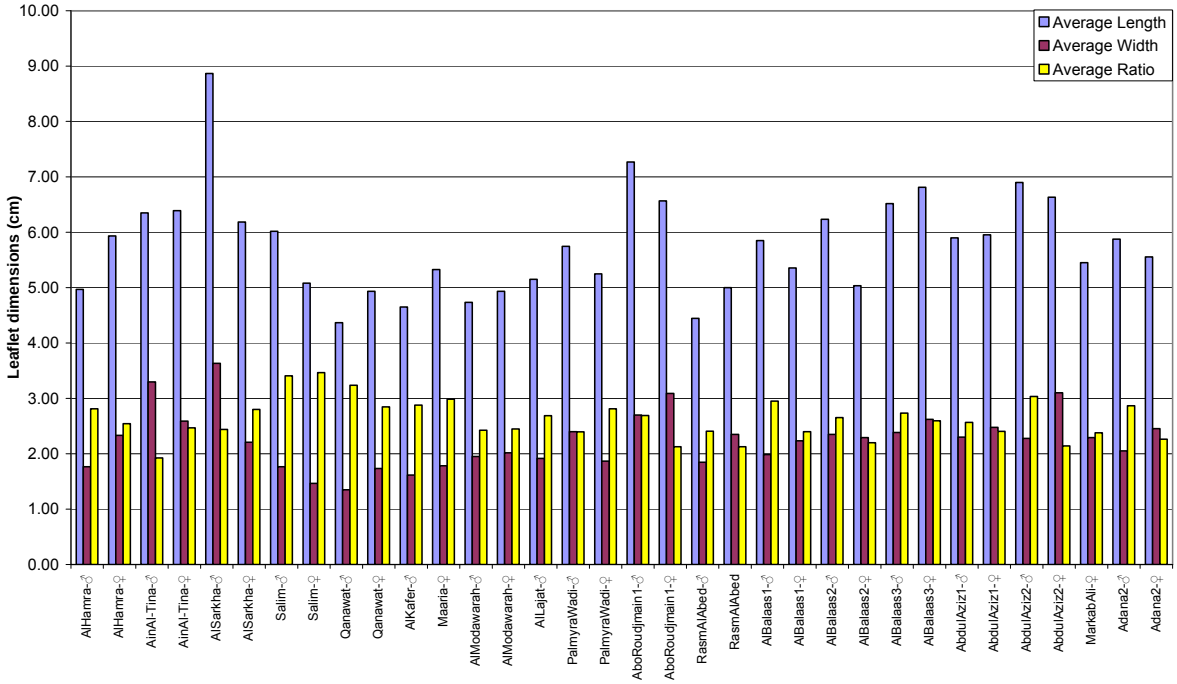


Figure 42. The average terminal leaflet dimensions of the *P. atlantica.*

Table 18. The maximum, and minimum of terminal leaflet dimensions of the *P. atlantica*.

Site (population)	Sex	Terminal leaflet length		Terminal leaflet width		length/width ratio	
		Min.	Max.	Min.	Max.	Min.	Max.
Al Hamra	Male	3.20	6.30	1.50	2.20	2.13	2.86
	Female	4.60	7.80	1.50	3.70	3.07	2.11
Ain Al-Tina	Male	4.50	11.00	2.10	6.30	2.14	1.75
	Female	3.80	9.50	1.50	5.30	2.53	1.79
Al Sarkha	Male	6.70	10.30	3.20	3.90	2.09	2.64
	Female	3.20	8.30	1.10	3.10	2.91	2.68
Salim	Male	5.30	6.70	1.50	1.90	3.53	3.53
	Female	4.50	5.90	1.10	1.90	4.09	3.11
Qanawat	Male	3.00	7.20	1.00	1.80	3.00	4.00
	Female	4.20	5.80	1.50	1.90	2.80	3.05
Al Kafer	Male	3.90	5.50	1.10	2.00	3.55	2.75
Maaria	Female	4.00	7.70	1.20	2.20	3.33	3.50
Al Modawarah	Male	3.90	5.40	1.70	2.70	2.29	2.00
	Female	4.00	6.50	1.70	3.00	2.35	2.17
Al Lajat	Male	3.30	7.00	1.20	2.80	2.75	2.50
Palmyra Wadi	Male	4.00	7.50	1.70	3.10	2.35	2.42
	Female	4.00	7.00	1.70	2.20	2.35	3.18
Abo Roudjmain 1	Male	5.90	8.90	2.00	3.20	2.95	2.78
	Female	5.00	8.60	1.90	4.10	2.63	2.10
Rasm Al Abed	Male	3.70	6.40	1.40	2.90	2.64	2.21
	Female	4.70	5.30	2.00	2.70	2.35	1.96
Al Balaas 1	Male	4.30	8.00	1.50	2.70	2.87	2.96
	Female	4.00	8.60	1.40	4.10	2.86	2.10
Al Balaas 2	Male	3.20	8.40	1.20	2.80	2.67	3.00
	Female	4.20	6.40	2.00	2.70	2.10	2.37
Al Balaas 3	Male	4.80	8.40	1.70	2.80	2.82	3.00
	Female	5.50	8.80	1.90	4.20	2.89	2.10
Abdul Aziz 1	Male	2.80	7.60	1.70	2.80	1.65	2.71
	Female	4.60	7.80	2.20	2.80	2.09	2.79
Abdul Aziz 2	Male	4.40	12.50	1.40	3.50	3.14	3.57
	Female	5.60	7.80	2.70	3.50	2.07	2.23
Markab Ali	Female	3.50	8.80	1.20	3.80	2.92	2.32
Adana 2	Male	2.80	8.30	1.70	2.80	1.65	2.96
	Female	4.70	8.80	2.20	3.80	2.14	2.32
F (population)		3.824**		5.230**		3.179**	
***P*-value (population)**		7.39×10^{-07}**		3.23×10^{-10}**		2.48×10^{-05}**	
F (individuals)		2.875**		2.616**		1.856**	
***P*-value (individuals)**		1.01×10^{-09}**		2.47×10^{-08}**		0.000246**	

Table 19 shows the other morphological characters of the leaves and leaflets, in terms of dominant number of leaflets which are 3 leaflets as some wild males in Balaas 1 site, 5 leaflets (wild female in Palmyra Wadi site), 7 leaflets (wild female in Ain Al-Tina site), 9 leaflets (wild male in Qanawat site) and 11 leaflets (wild male in Al-Jata site). The terminal leaflet sizes were sometimes smaller than basal leaflets as some wild males in Al Hamra site, similar to basal leaflets such as wild female in Maaria site or larger than basal leaflets like some wild females in Rasm Al Abed site. On the other hand, the terminal

leaflets were found in several shapes and apexes. The following examples show the terminal leaflets shapes (Figure 43):

- Ovate, such as some males in Ain Al Tina site;
- Oblong, such as some male in Al kafer site;
- Lanceolate, such as some females in Qanawat site;
- Narrow elliptic, such as some males in Abo Roudjmain 1 site.

Table 19. Some leaf characters of *P. atlantica*.

Site (Population)	Sex	Dominant no. of leaflets	Terminal leaflet size	Terminal leaflet shape	Terminal leaflet apex
Al Hamra	Male	9	Smaller	Ovate	Acute
	Female	7-9	Smaller	Ovate	Mucronulate - Obtuse
Ain Al-Tina	Male	7-9	Smaller	Ovate	Mucronulate
	Female	7	Smaller - Similar	Ovate	Acuminate
Al Sarkha	Male	5-7	Similar - Larger	Ovate	Obtuse
	Female	5-7	Similar - Larger	Ovate	Acuminate -Obtuse
Salim	Male	7-9	Similar - Larger	Oblong	Acuminate
	Female	7-9	Similar - Larger	Oblong	Acuminate
Qanawat	Male	9	Similar - Larger	Oblong	Acuminate
	Female	7-9	Similar - Larger	Oblong	Acuminate
Al Kafer	Male	5-7	Similar	Oblong	Acuminate
Maaria	Female	7-9	Similar	Oblong	Acute
Al Modawarah	Male	7-9	Smaller - Larger	Lanceolate	Obtuse - Acute
	Female	7-9	Smaller - Larger	Lanceolate	Obtuse - Acute
Al Lajat	Male	3-11	Larger	Ovate	Obtuse - Acute
Palmyra Wadi	Male	5-7	Similar - Larger	Narrow elliptic	Acute
	Female	5-7	Similar - Larger	Narrow elliptic	Acuminate
Abo Roudjmain 1	Male	3-7	Smaller – Similar	Narrow elliptic	Obtuse - Acuminate
	Female	5-7	Similar	Narrow elliptic	Acute
Rasm Al Abed	Male	5-7	Larger	Narrow elliptic	Acute
	Female	3-5	Larger	Lanceolate	Acuminate
Al Balaas 1	Male	3-9	Larger	Lanceolate	Acute
	Female	9-11	Smaller	Lanceolate	Acute
Al Balaas 2	Male	7-11	Larger	Lanceolate	Acute
	Female	11	Larger	Lanceolate	Acute
Al Balaas 3	Male	7-9	Larger	Lanceolate	Acute
	Female	7	Similar	Lanceolate	Acute
Abdul Aziz 1	Male	5-7	Larger	Lanceolate	Acute
	Female	7-9	Larger	Narrow elliptic	Acute
Abdul Aziz 2	Male	7	Similar - Larger	Narrow elliptic	Cuspidate
	Female	5-7	Similar - Larger	Narrow elliptic	Acute
Markab Ali	Female	5-7	Similar - Larger	Narrow elliptic	Cuspidate
Adana 2	Male	5-9	Similar - Larger	Lanceolate	Acute
	Female	9-11	Similar - Larger	Lanceolate	Acute

Lanceolate leaflet with acuminate apex | Ovate leaflet with mucronulate apex

Oblong leaflet with acuminate apex | Narrow elliptic with obtuse apex

Figure 43. Terminal leaflet shapes of *P. atlantica*.

3.2.3.3. *Pistacia palaestina*

The terminal leaflet of this species is very small or absent but have 4-6 pairs of basal leaflets, therefore the leaf characterization were only focused on the general characters of the leaves (Figure 44).

Leaf dimensions: Table 20 shows the maximum and minimum of leaf dimensions of each studied *P. palaestina* populations. The average leaf length ranges from 7.1 cm (female in Ain Al Gazal site) to 21.3 cm (female in Al Badrousia site). According to the leaf width, it ranges from 5.5 cm (male in Al Bara site) to 21.6 cm (female in Izaz site). ANOVA analyses for each character show highly significant differences between the populations and individuals (Annex 2 - Table 5-6). Figure 45 shows the average dimensions of the male and female leaves in each studied *P. palaestina* populations.

Very small terminal leaflet No terminal leaflet

Figure 44. leaf shapes of *P. palaestina.*

Table 20. The maximum and minimum of leaf dimensions of the *P. palaestina.*

Site (Population)	Sex	Leaf length		Leaf width	
		Min.	Max.	Min.	Max.
Wadi Baradah	Male	14.00	17.20	7.00	8.60
	Female	13.20	13.80	8.30	10.90
Mantaf	Male	9.90	20.50	7.10	18.10
	Female	10.20	15.90	8.20	12.00
Kafer Haya	Male	10.70	12.80	9.10	10.30
	Female	8.00	17.20	7.30	14.00
Al Bara	Male	9.20	14.50	5.50	9.90
	Female	10.30	14.70	7.20	13.30
Ain Al Gazal	Male	11.60	17.50	7.70	14.00
	Female	7.10	17.30	7.00	14.30
Wadi Kandel	Male	10.30	11.00	7.80	8.00
	Female	10.40	16.50	7.70	10.80
Ras Al Baset 1	Male	12.20	16.50	8.70	13.00
	Female	10.20	21.30	6.10	13.00
Al Badrousia	Female	9.80	21.30	7.90	21.30
Al Nabiaen	Male	10.60	16.10	7.10	10.50
	Female	8.80	15.30	6.80	11.40
Frolok	Male	11.80	18.00	9.70	14.60
	Female	9.20	19.70	6.50	13.00
Bhamra	Male	11.00	15.80	7.50	11.00
	Female	9.80	16.10	6.50	19.50
Banias	Male	12.40	16.50	6.50	10.80
	Female	12.50	16.20	9.50	11.70
Kadmous	Male	11.50	14.00	5.50	9.20
	Female	13.00	20.00	9.60	12.40
Derekish	Female	14.00	20.30	8.10	12.20
	Male	11.60	12.20	7.70	9.00
Izaz	Female	16.00	16.70	12.40	21.60
F (population)		1.974**		2.588**	
***P*-value (population)**		0.0221**		0.002**	
F (individuals)		4.117**		4.219**	
***P*-value (individuals)**		$5.65x10^{-12}$**		$2.49x10^{-12}$**	

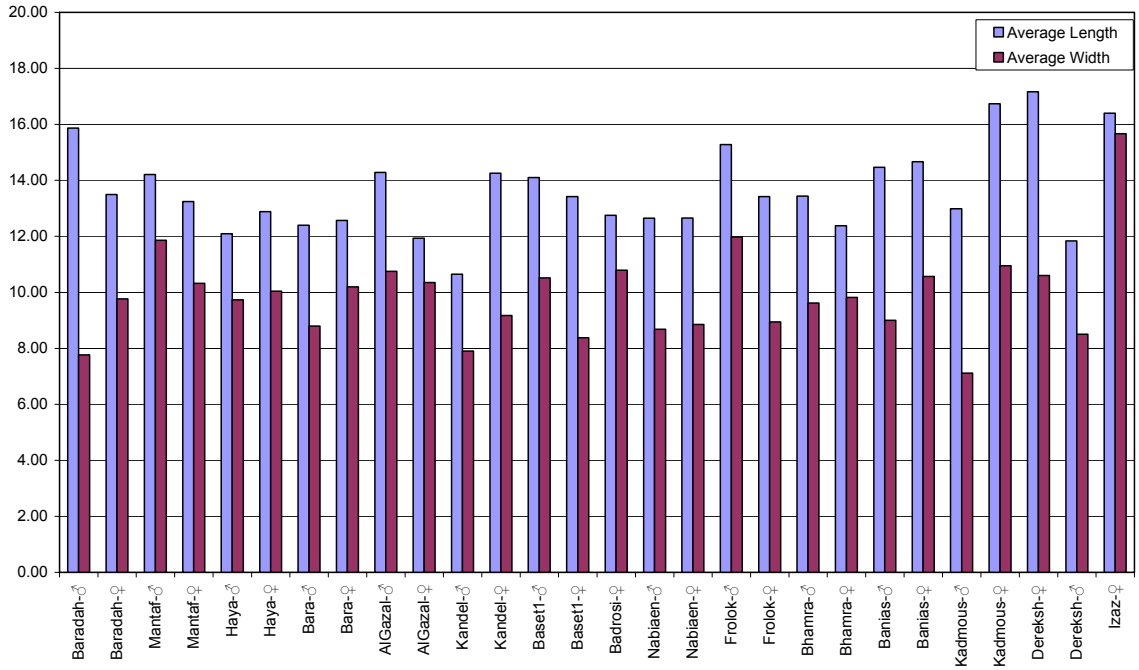


Figure 45. The average leaf dimensions of the *P. palaestina.*

3.2.3.4. *Pistacia terebinthus*

Leaf dimensions: Figure 46 shows the maximum, minimum and average leaf dimensions of each studied *P. terebinthus* populations. The average leaf length ranges from 9.7 cm (female in Ras Al Baset 2 site) to 21.5 cm (female in Adana 1 site). Accordingly the leaf width ranges from 7.9 cm (male in Adana 1 site) to 15.5 cm (female in Adana 1 site). ANOVA analyses for each length character show highly significant differences between the populations were F= 7.446** and P value = $7.65x10^{-04}$ while the width character show only significant differences with F= 3.013* and P value= 0.046 (Annex 2 – Table 7). On the other hand, these characters show highly significant differences between the individuals with F =10.93** and P value= $2.05x10^{-06}$ for length and the F= 6** and P value= $2.3x10^{-04}$ for width (Annex 2 - Table 8).

Leaflet dimensions: Figure 47 shows the maximum, minimum and average leaflet dimensions for each studied *P. terebinthus* populations. The average leaf length ranges from 1.1 cm (male in Ras Al Baset 2 site) to 6 cm (female in Ras Al Baset 2 site). Accordingly the leaf width ranges from 0.3 cm (male in Adana 1 site) to 3.2 cm (female in Ras Al Baset 2 site). The length/width ratio ranges between 1.81 (female in Ras Al Baset 2 site) and 6 (female in Adana 1 site). ANOVA analyses for length and width characters show no significant differences between the populations but highly significant differences between the individuals (Annex 2 - Table 7). On the other hand, ANOVA analyses for the

length/width ratio show no significant differences between the populations or individuals (Annex 2 - Table 8).

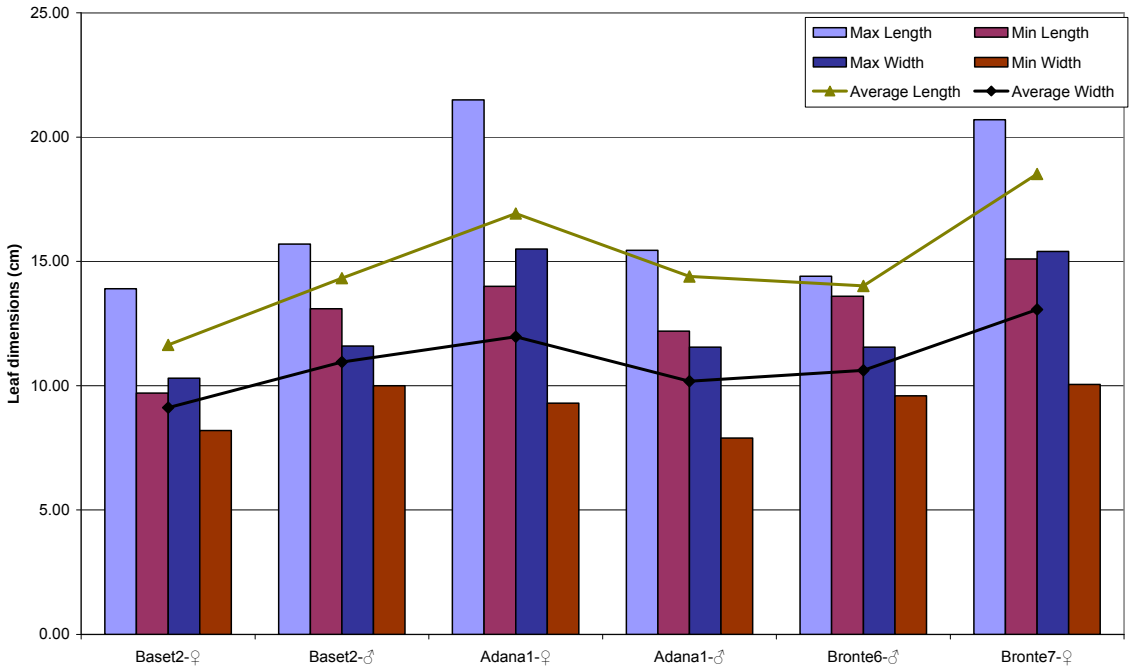


Figure 46. The average leaf dimensions of the *P. terebinthus.*

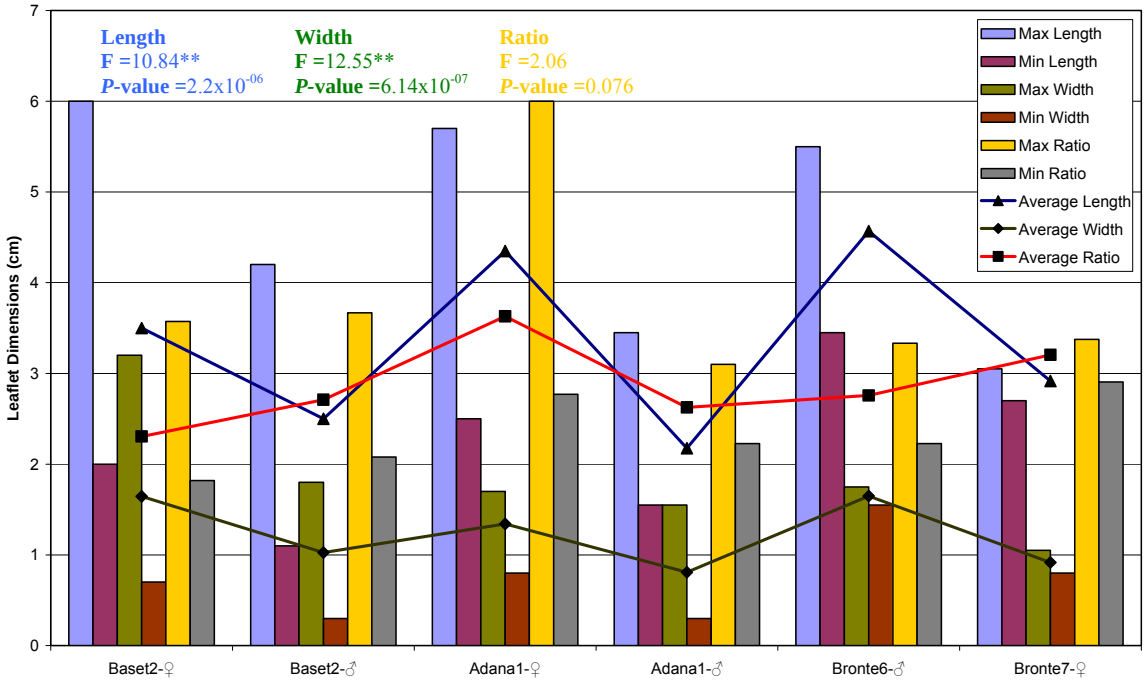


Figure 47. The average leaflet dimensions of the *P. terebinthus.*

Table 21 shows the other morphological characters of the leaves and leaflets, in terms of dominant number of leaflets which ranges between 5 leaflets (wild females in Ras Al Baset 2 site) and 13 leaflets (wild male in Adana 1 site). The terminal leaflet sizes are sometimes smaller than basal leaflets as some wild males in Adana 1 site, similar to basal leaflets such as wild male in Ras Al Baset 2 site or larger than basal leaflets like some wild females in Ras Al Baset 2 site. On the other hand, the terminal leaflets are found mostly in two shapes and apexes. The following examples show the terminal leaflets shapes (Figure 48):

- Elliptic, such as some males in Ras Al Baset 2 site;
- Lanceolate, such as some females in Adana 1 site.

Table 21. Some leaf characters of *P. terebinthus.*

Site (Population)	Sex	Dominant no. of leaflets	Terminal leaflet size	Terminal leaflet shape	Terminal leaflet apex
Ras Al Baset 2	Female	5-11	Similar- Larger	Elliptic - Lanceolate	Mucronulate - Acute
	Male	9-13	Smaller - Similar	Elliptic - Lanceolate	Mucronulate - Acute
Adana 1	Female	9-13	Smaller - Similar	Elliptic - Lanceolate	Mucronulate - Acute
	Male	9-13	Smaller - Similar	Elliptic - Lanceolate	Mucronulate - Acute
Bronte 6	Male	9-13	Smaller - Similar	Elliptic - Lanceolate	Mucronulate - Acute
Bronte 7	Female	9-13	Smaller - Similar	Elliptic - Lanceolate	Mucronulate - Acute

Lanceolate leaflet with acute apex Elliptic leaflet with mucronulate apex

Figure 48. leaf shapes of *P. terebinthus.*

3.2.3.5. *Pistacia khinjuk*

This species is a rare species, it was found associated with *P. atlantica* in two sites. Only 5 individuals were studied morphologically.

Leaf dimensions: Figure 49 shows the maximum, minimum and average leaf dimensions of each studied *P. khinjuk* individual. The average leaf length ranges from 12.1 cm (female in Abdul Aziz 1 site) to 16.2 cm (female in Abdul Aziz 1 site). According to the leaf width, it ranges from 9 cm (male in Al Balaas 2 site) to 17 cm (female in Al Balaas 2 site). ANOVA analyses for each length and width character show no significant differences between the populations (Annex 2 - Table 9). On the other hand, ANOVA analyses for length character shows no significant differences between the individuals, but there is significant difference between the individuals in terms of the width character with F = 6.085** and P value = 0.019 (Annex 2 - Table 10).

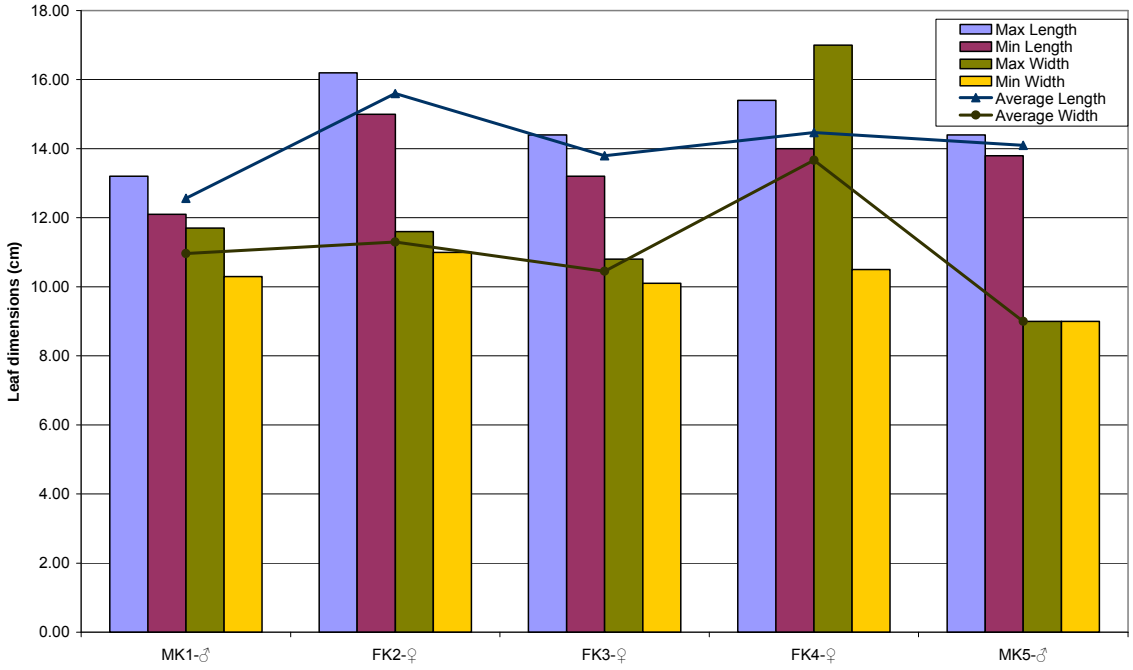


Figure 49. The average leaf dimensions of the *P. khinjuk*.

Leaflet dimensions: Figure 50 shows the maximum, minimum and average leaflet dimensions of each studied *P. khinjuk* individual. The average leaf length ranges from 5 cm (male in Abdul Aziz 1 site) to 8.6 cm (female in Al Balaas 2 site). Accordingly the leaf width ranges from 3.2 cm (male in Al Balaas 2 site) to 5 cm (female in Abdul Aziz 1 site). The length/width ratio ranges between 1.16 (male in Abdul Aziz 1 site) and 1.18 (male in Al Balaas 2 site). ANOVA analyses for length, width and the ratio characters show no significant differences both between the populations and between individuals (Annex 2 - Table 9-10).

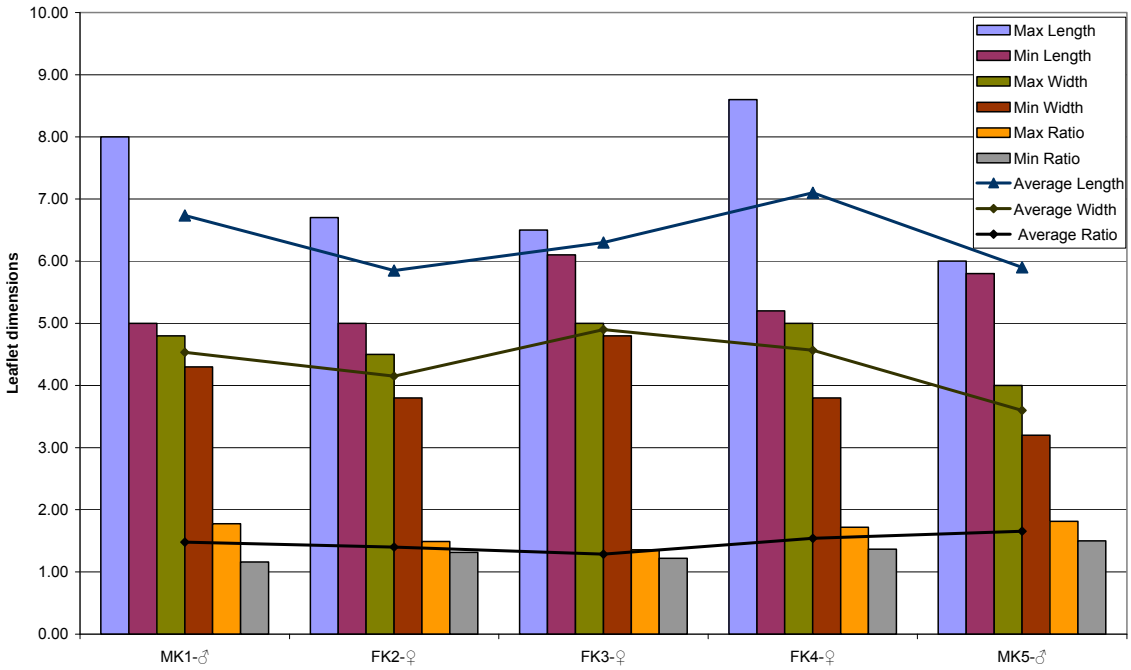


Figure 50. The average leaflet dimensions of the *P. khinjuk*.

Table 22 shows the other morphological characters of the leaves and leaflets, in terms of dominant number of leaflets which ranges between 5-7 leaflets. The terminal leaflet sizes were sometimes similar or larger to basal leaflets. On the other hand, the terminal leaflets are found mostly in ovate shapes and mucronate apexes (Figure 51):

Table 22. Some leaf characters of *P. khinjuk*.

Site (Population)	Sex	Dominant no. of leaflets	Terminal leaflet size	Terminal leaflet shape	Terminal leaflet apex
Abdul Aziz 1	Male 1	5-7	Similar- Larger	Ovate	Mucronate
	Female 2	5-7	Similar- Larger	Ovate	Mucronate
	Female 3	5-7	Similar- Larger	Ovate	Mucronate
Al Balaas 2	Female 4	5-7	Similar- Larger	Ovate	Mucronate
	Male 5	5-7	Similar- Larger	Ovate	Mucronate

Figure 51. The leaf shapes of *P. Khinjuk* (ovate leaflet with mucronate apex.

3.2.3.6. *Pistacia lentiscus*

The terminal leaflet of this species is absent but has 4-6 pairs of basal leaflets, therefore the leaf characterization were only focused on the general characters of the leaves (Figure 53).

Figure 52. The leaf shapes of *P. lentiscus.*

Leaf dimensions: Figure 53 shows the maximum, minimum and average of leaf dimensions for each studied *P. lentiscus* populations. The average leaf length ranges from 2.5 cm (male in Adana 2 site) to 12.6 cm (female in Adana 2 site). Accordingly the leaf width ranges from 4.2 cm (female in Al Mehwiye site) to 7.8 cm (male in Al Mehwiye site). ANOVA analyses for each character show no significant differences between the populations but highly significant differences between individuals with F = 14.128** and P value = $2.89x10^{-13}$ for length and the F = 6.523** and P value = $9.11x10^{-08}$ for width (Annex 2 - Table 11-12).

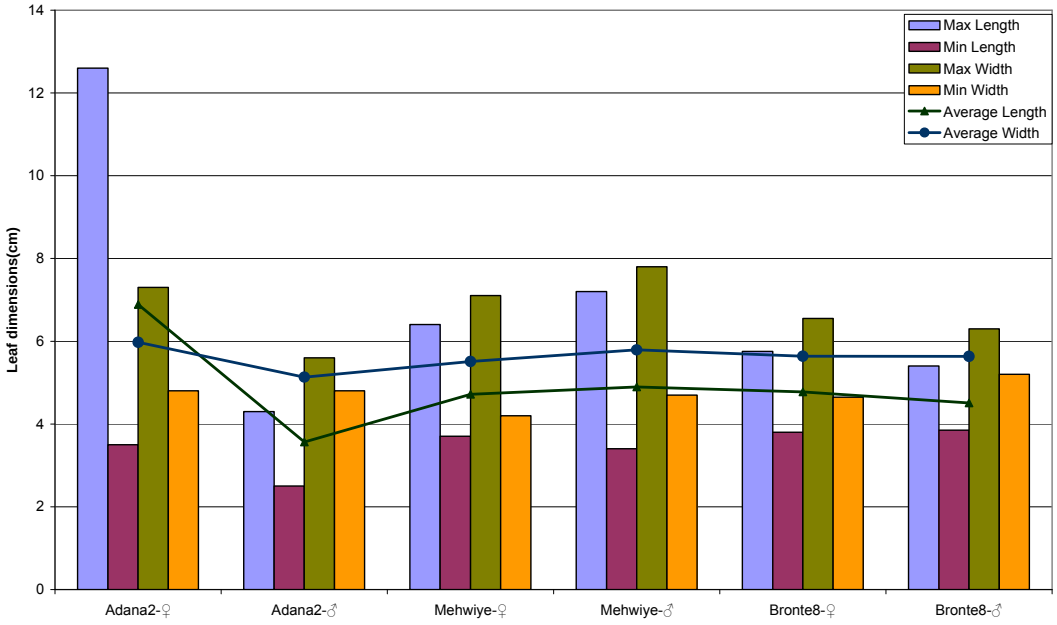


Figure 53. The average leaf dimensions of the *P. lentiscus.*

3.2.4. Nut descriptor

In order to characterize *Pistacia* nuts, the length, width and thickness were measured for 20 nuts of each individual also nut shapes and color after maturity were recorded. Table 23 shows the range of nut dimensions for each *Pistacia* species. ANOVA analyses for each character show highly significant differences between the species (Figure 54). These results can be summarized as follows:

- **Wild *P. vera*;** the average length ranges between 15.77 in Dangara 2 site and 28.28 mm in Televiska site the average width ranges between 8.43 mm in Dangara 2 site and 15.33 mm in Galla Aral site, and the average thickness ranges between 7.56 mm in Dangara 2 site and 14.49 mm in Televiska site. ANOVA analyses for each character show highly significant differences between the populations ($F = 20.6^{**}$ - *P value* = 1.19×10^{-19}) for length, ($F = 19.8^{**}$ – *P-value* = 3.04×10^{-19}) for width and ($F = 23.88^{**}$ - *P-value* = 3.63×10^{-21}) for thickness.
- ***P. atlantica*;** the average length ranges between 5.8 mm in Markab Ali site and 9 mm in Al Kafer site, the average width ranges between 5 mm in Al Kafer site and 7.8 mm in Abo Roudjmain 1 site, and the average thickness ranges between 3.4 mm in Al Kafer site and 7.3 mm in Al Sarkha site. ANOVA analyses for each character show no significant differences between the populations.
- ***P. palaestina*;** the average length ranges between 4.2 mm in Ain Al Gazal site and 5.9 mm in Al Badrousia site, the average width ranges between 3.8 mm in Mantaf site and 5.6 mm in Kafer Haya site, and the average thickness ranges between 3.04 mm in Al Nabiaen site and 4.5 mm in Kafer Haya site. ANOVA analyses for each character show no significant differences between the populations.
- ***P. terebinthus*;** the average length ranges between 5.67 mm in Ras Al Baset 2 site and 7.1 mm in Adana 1 site, the average width ranges between 4.3 mm in Bronte 7 site and 6.8 mm in Adana 1 site, and the average thickness ranges between 3.3 mm in Adana 1 site and 5.3 mm in Adana 1 site. ANOVA analyses for each character show no significant differences between the populations.
- ***P. khinjuk*;** the average length ranges between 8.9 mm in Abdul Aziz 1 site and 10.6 mm in Al Balaas site, the average width ranges between 8.6 mm in Al Balaas site and 9.7 mm in Abdul Aziz 1 site, and the average thickness ranges between 5.64 mm in Abdul Aziz 1 site and 6.5 mm in Al Balaas site. ANOVA analyses for each character show no significant differences between the populations.

- ***P. lentiscus*;** the average length ranges between 1.9 mm in Al Mehwiye site and 3.38 mm in Adana 2 site, the average width ranges between 1.33 mm in Bronte 8 site and 3.38 mm in Adana 2 site, and the average thickness ranges between 1.02 mm in Al Mehwiye site and 1.9 mm in Bronte 8 site. ANOVA analyses for each character show no significant differences between the populations.

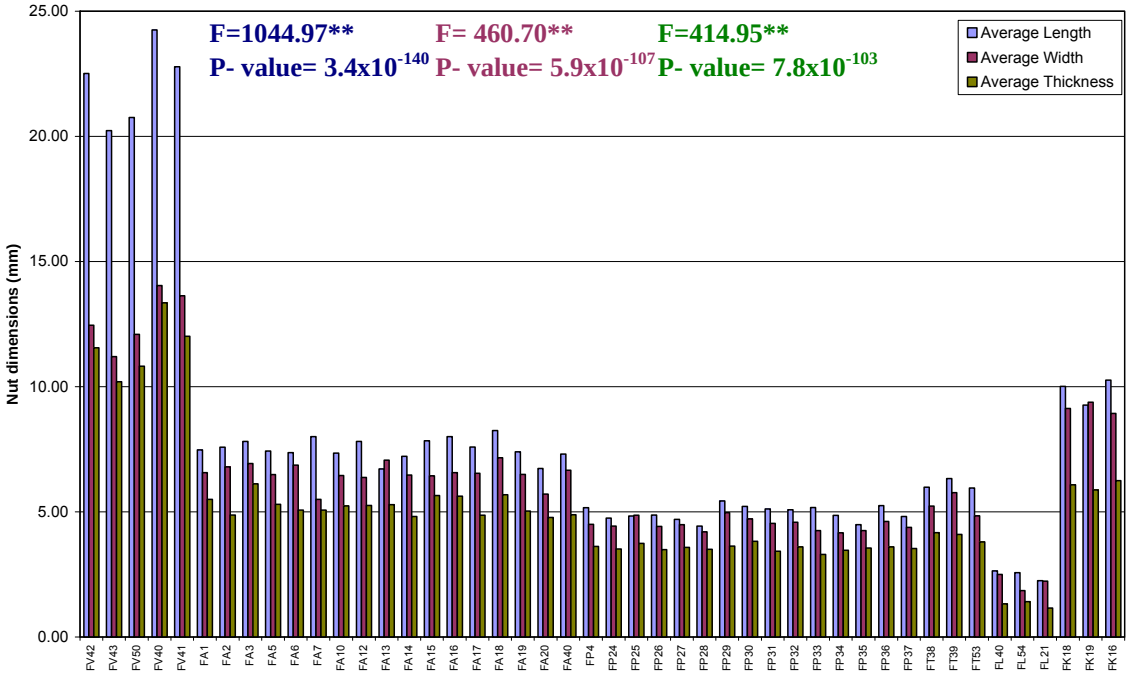


Figure 54. The average dimension of the nuts.

According to the nut shape character and the color after maturity it can be summarized as follows (Figure 55):

- **Wild *P. vera*** most of the nuts of this species were even elongate or narrowly cordate and white or pink were the full maturity colors.
- ***P. atlantica*** the nut shapes of this species were globular or obovoid globular and the color of the mature nuts was dark green.
- ***P. palaestina*** the nut shapes of this species were globular or obovoid globular and the color of the mature nuts was dark green.
- ***P. terebinthus*** the nut shapes of this species were obovoid globular and the color of the mature nuts was dark green.
- ***P. khinjuk*** the nut shapes of this species were globular or obovoid globular and the color of the mature nuts was dark green
- ***P. lentiscus*** the nut shapes of this species were obovoid globular and the color of the mature nuts was black.

Table 23. The range of nut dimensions.

Species	Site (population)	Sample	Length		Width		Thickness	
			max	min	max	min	max	min
P. vera	Dangara 1	FV42	24.28	21.28	14.68	11.14	14.49	9.56
P. vera	Dangara 2	FV43	23.61	15.77	13.00	8.34	11.40	7.56
P. vera	Korgan Tubye 2	FV50	23.76	18.47	13.86	9.62	12.81	7.63
P. vera	Televiska	FV40	28.28	19.14	15.25	12.17	14.94	12.05
P. vera	Galla Aral	FV41	25.92	20.25	15.33	10.59	14.10	10.19
P. atlantica	Al Hamra	FA1	7.70	7.25	7.35	5.75	5.85	5.25
P. atlantica	Ain Al-Tina	FA2	8.15	7.05	7.45	6.35	5.20	4.45
P. atlantica	Al Sarkha	FA3	8.51	7.20	7.78	6.30	7.30	5.50
P. atlantica	Salim	FA5	7.78	6.80	6.80	5.90	5.50	5.01
P. atlantica	Qanawat	FA6	7.80	7.10	7.30	6.60	5.50	4.60
P. atlantica	Al Kafer	FA7	9.00	7.20	6.30	5.00	7.30	3.40
P. atlantica	Al Modawarah	FA10	7.74	7.00	6.78	6.25	5.26	5.20
P. atlantica	Palmyra Wadi	FA12	8.10	7.30	6.99	6.03	5.30	5.22
P. atlantica	Abo Roudjmain 1	FA13	7.70	5.92	7.80	6.50	5.80	4.67
P. atlantica	Rasm Al Abed	FA14	7.50	7.00	6.95	5.95	5.30	4.00
P. atlantica	Al Balaas 1	FA15	8.20	7.30	6.51	6.30	6.40	5.24
P. atlantica	Al Balaas 2	FA16	8.70	7.60	6.80	6.40	6.40	5.19
P. atlantica	Al Balaas 3	FA17	8.20	7.25	6.73	6.40	5.30	4.00
P. atlantica	Abdul Aziz 1	FA18	8.93	7.30	7.49	6.80	6.85	4.80
P. atlantica	Abdul Aziz 2	FA19	8.20	6.90	7.30	5.90	5.90	4.50
P. atlantica	Markab Ali	FA20	7.40	5.80	6.51	5.20	5.10	4.52
P. atlantica	Adana 2	FA40	8.30	6.10	7.40	6.10	5.40	4.27
P. palaestina	Wadi Baradah	FP4	5.40	4.80	4.80	4.20	3.80	3.50
P. palaestina	Mantaf	FP24	5.45	4.40	4.80	3.80	3.55	3.50
P. palaestina	Kafer Haya	FP25	5.19	4.50	5.60	4.30	4.50	3.10
P. palaestina	Al Bara	FP26	5.23	4.20	5.25	3.90	3.50	3.46
P. palaestina	Ain Al Gazal	FP27	5.40	4.20	4.70	4.30	3.64	3.50
P. palaestina	Wadi Kandel	FP28	4.70	4.20	4.40	4.10	3.80	3.20
P. palaestina	Ras Al Baset 1	FP29	5.50	5.40	5.30	4.80	3.80	3.30
P. palaestina	Al Badrousia	FP30	5.90	4.85	5.35	4.05	4.30	3.50
P. palaestina	Al Nabiaen	FP31	5.45	4.80	4.80	4.10	3.63	3.04
P. palaestina	Frolok	FP32	5.40	4.60	5.05	4.05	3.80	3.45
P. palaestina	Bhamra	FP33	5.60	4.60	4.30	4.20	3.55	3.10
P. palaestina	Banias	FP34	5.30	4.30	4.53	3.90	3.60	3.30
P. palaestina	Kadmous	FP35	4.75	4.20	4.90	3.80	3.70	3.47
P. palaestina	Derekish	FP36	5.40	5.05	4.85	4.20	3.80	3.50
P. palaestina	Izaz	FP37	5.19	4.25	4.92	4.00	3.70	3.35
P. terebinthus	Ras Al Baset 2	FT38	6.50	5.67	5.90	4.75	4.80	3.80
P. terebinthus	Adana 1	FT39	7.10	5.80	6.80	5.20	5.30	3.30
P. terebinthus	Bronte 7	FT53	6.51	4.95	5.40	4.30	4.11	3.40
P. lentiscus	Adana 2	FL40	3.38	2.00	3.25	2.10	1.37	1.25
P. lentiscus	Bronte 8	FL54	3.32	2.20	2.12	1.33	1.90	1.03
P. lentiscus	Al Mehwiye	FL21	2.33	1.9	2.26	2.20	1.40	1.02
P. khinjuk	Abdul Aziz 1	FK18	10.35	9.60	9.50	8.75	6.35	5.70
P. khinjuk	Abdul Aziz 1	FK19	9.50	8.90	9.70	8.85	6.10	5.64
P. khinjuk	Al Balaas	FK16	10.60	9.70	9.30	8.60	6.50	5.90

P. vera nuts

P. atlantica nuts

P. palaestina nuts

P. terebinthus nuts

P. khinjuk nuts

P. lentiscus nuts

Figure 55. The nut shapes of the studied *Pistacia* species.

3.3. Molecular markers

Molecular markers were employed recently in several studies of inter- and intra- specific relations of *Pistacia* genotypes and to discriminate between pistachio's varieties (see paragraph 1.8). Three molecular marker techniques were used in this study to assess the extent of genetic diversity in *Pistacia* in both natural and cultivated populations.

3.3.1. *Pistacia vera*

The same 139 wild and cultivated *P. vera* genotypes were analyzed using three molecular marker techniques. The results can be summarized as follows:

3.3.1.1. Amplified Fragment Length Polymorphism (AFLP)

Figure 56 shows an example of one primer pair combination. A total 217 polymorphic bands were generated by 4 primer pair combinations. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 - Table13). Four groups are obtained in this analysis (Table 24, Figure 57):

I. Group one: contains male and female varieties from Italy (Bronte 1 - 2), Turkey (Adana), also female individuals from Uzbekistan (Galla Aral) and male from Tajikistan (Televiska);
II. Group two: contains all male and female varieties from Syria except females in Al Moslemia gene bank site. Also it contains some female individuals from Tajikistan (Dangara1) and some male varieties form Italy (Bronte2);
III. Group three: contains males from Tajikistan (Dangara 2, Korgan Tubye 2) ;
IV. Group four: contains female verities from Italy (Bronte 2 and 3), Iran also male and female individuals from Tajikistan (Televiska, Dangara 1).

Table 24. The countries, site numbers and site names of collected *P. vera* sites.

Country	Site No.	Site name
Syria	2	Ain Al-Tina
	8	Izraa gene bank
	22	Al Moslemia gene bank
	23	Shahba gene bank
Iran	38	Adana
Turkey	39	Iran
Central Asia	41	Galla Aral
	40	Televiska
	42	Dangara 1
	43	Dangara 2
	44	Korgan Tubye 1
	50	Korgan Tubye 2
Italy	52	Bronte 1
	54	Bronte 2
	58	Bronte 3

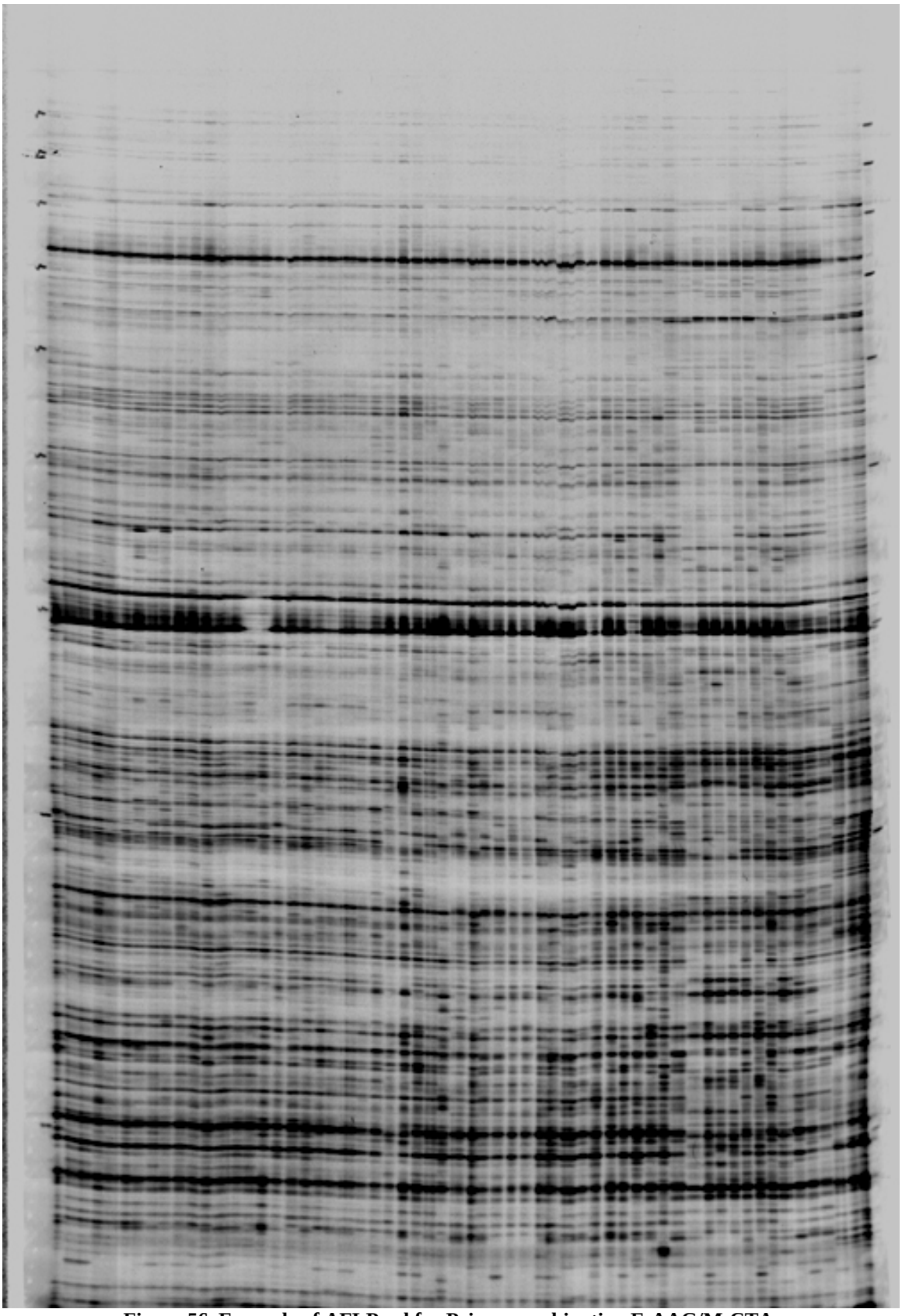


Figure 56. Example of AFLP gel for Primer combination E-AAG/M-CTA.

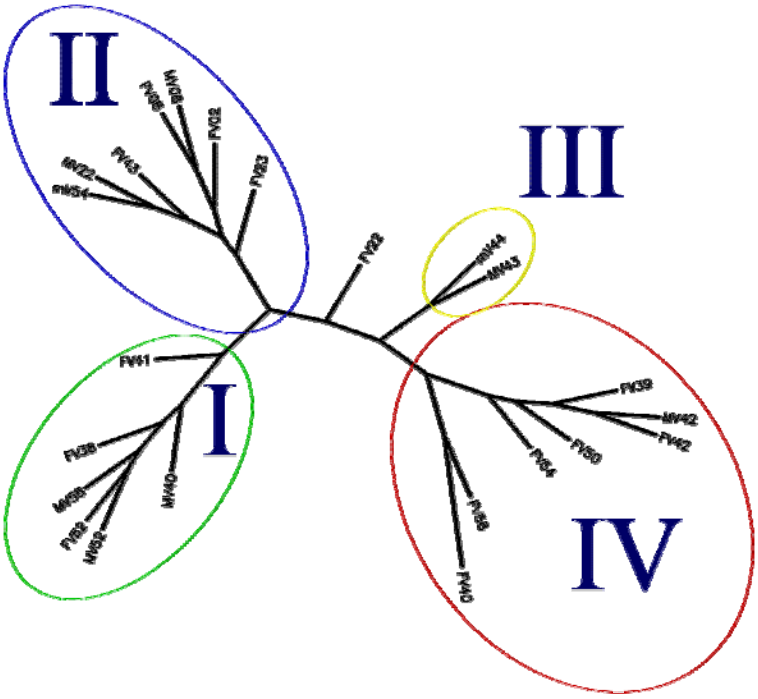


Figure 57. AFLP Unrooted tree based on Nei (1972) genetic distance for *P. vera* according to each collected site.

Figure 58 shows the unrooted relatedness tree among the collected genotypes according to frequency data to their origin country using Nei (1972) genetic distance coefficient which can be divided into 3 groups (Annex 3 - Table17):

I. Group one: contains Syrian male and female varieties, Also Turkish female varieties;
II. Group two: contains Italian male and female varieties;
III. Group three: contains wild male and female individuals from Central Asia and Iranian female varieties.

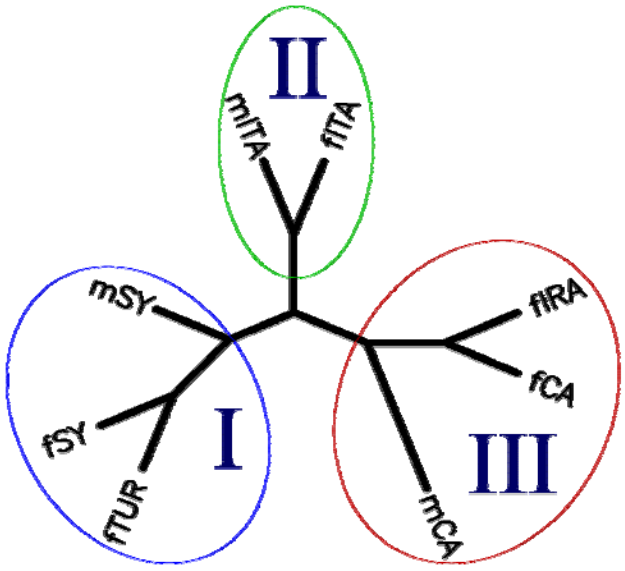


Figure 58. AFLP UPGMA tree based on Nei (1972) genetic distance for *P. vera* according to their origin countries.

Principle component analysis (PCA) confirms clearly the three main groups (Figure 59):

I. Group one: contains Syrian male and female varieties;

II. Group two: contains wild male and female individuals from Central Asia, as well as Turkish and Iranian female varieties;

III. Group three: contains Italian male and female varieties and females of one site in Syria and Tajikistan.

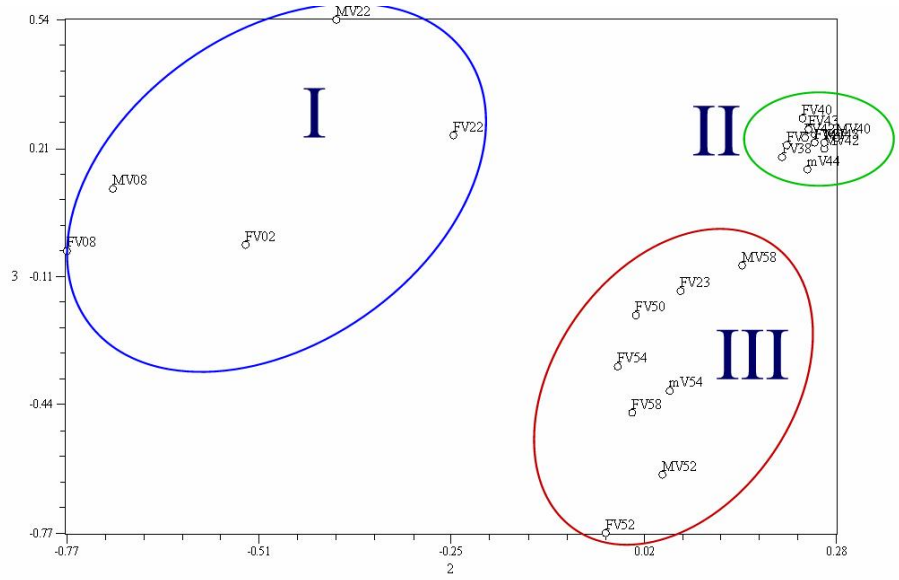


Figure 59. Principle component analysis for *P. vera* based on AFLPdata.

3.3.1.2. Inter Simple Sequence Repeats (ISSR)

Figure 60 shows an example of one ISSR primer. A total 255 polymorphic bands were generated by 6 primers. A binary matrix was created containing 139 rows representing the genotypes and 255 columns representing the polymorphic loci.

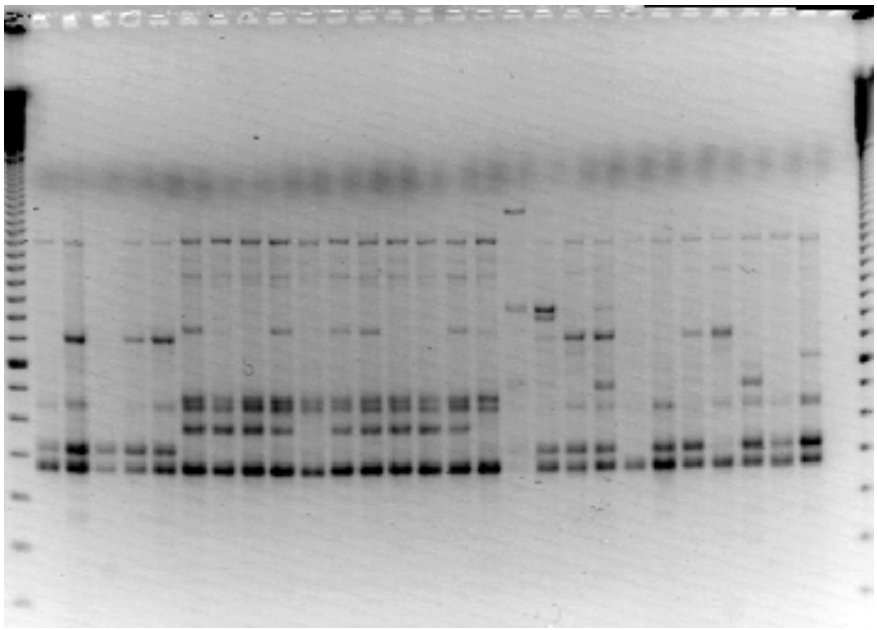


Figure 60. ISSR gel for Primer 847.

The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 - Table14). Five groups are obtained in this analysis (Table 24, Figure 61):

I. Group one: contains all male and female varieties from Italy;
II. Group two: contains some male and female varieties from north Syria (Al Moslemia gene bank and Shahba gene bank);
III. Group three: contains female varieties from Turkey and Iran also male and female individuals of one site in Tajikistan (Televiska);
IV. Group four: contains some male and female varieties from south Syria (Ain Al-Tina, Izraa Gene bank);
V. Group five: contains all male and female individuals from Central Asia.

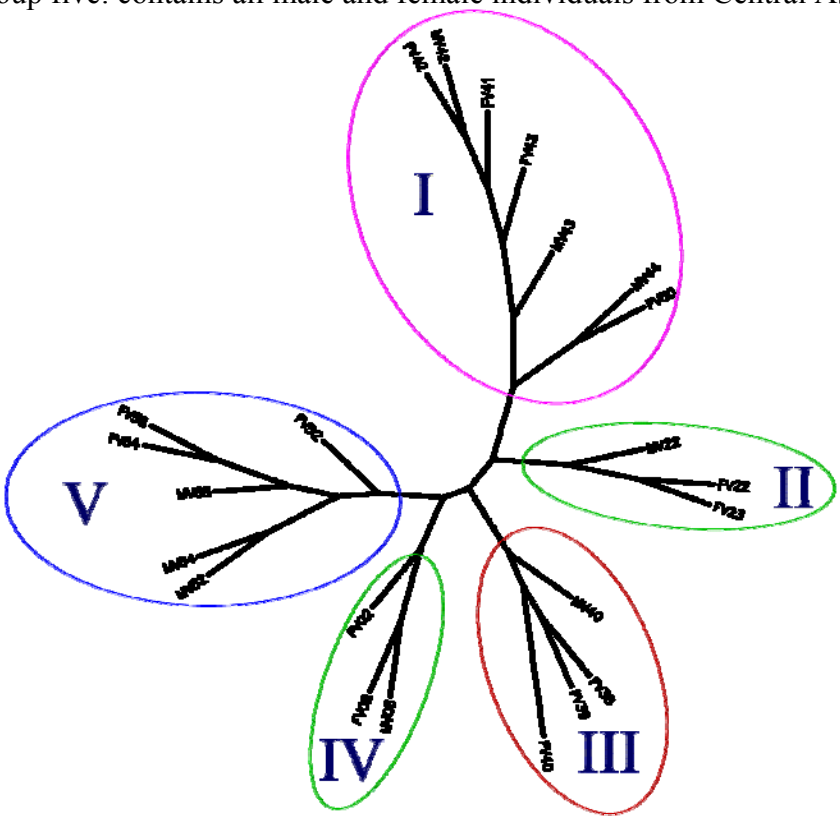


Figure 61. ISSR UPGMA tree based on Nei (1972) genetic distance for *P. vera* according to each collected site.

Figure (62) shows the unrooted relatedness tree among the collected genotypes according to frequency data to their origin country by using Nei(1972) distance coefficient which can be divided into 4 groups (Annex 3 - Table18):

I. Group one: contains Turkish and Iranian varieties;
II. Group two: contains Italian male and female varieties;
III. Group three: contains Syrian male and female varieties;
IV. Group four: contains wild male and female individuals from Central Asia.

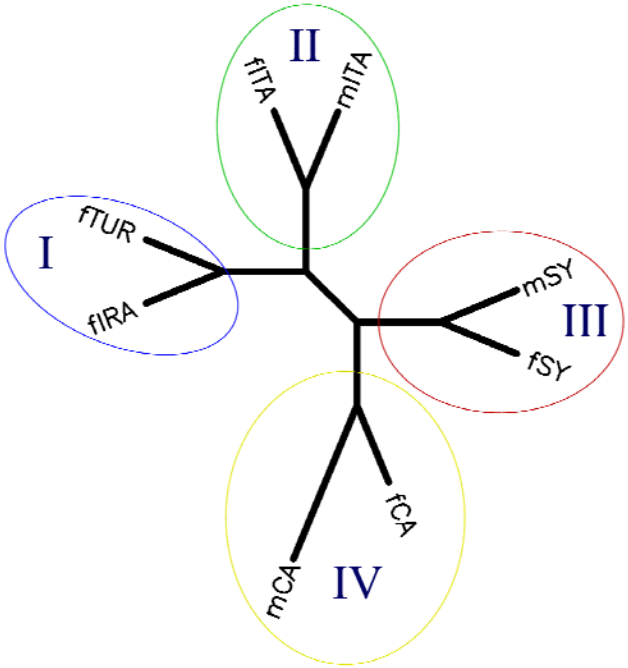


Figure 62. ISSR Unrooted tree based on Nei (1972) genetic distance for *P. vera* according to their origin countries.

Principle component analysis (PCA) confirms clearly the three main groups (Figure 63):

I. Group one: contains wild male and female individuals from Central Asia, as well as Turkish and Iranian female varieties;

II. Group two: contains Syrian male and female varieties;

III. Group three: contains Italian male and female varieties.

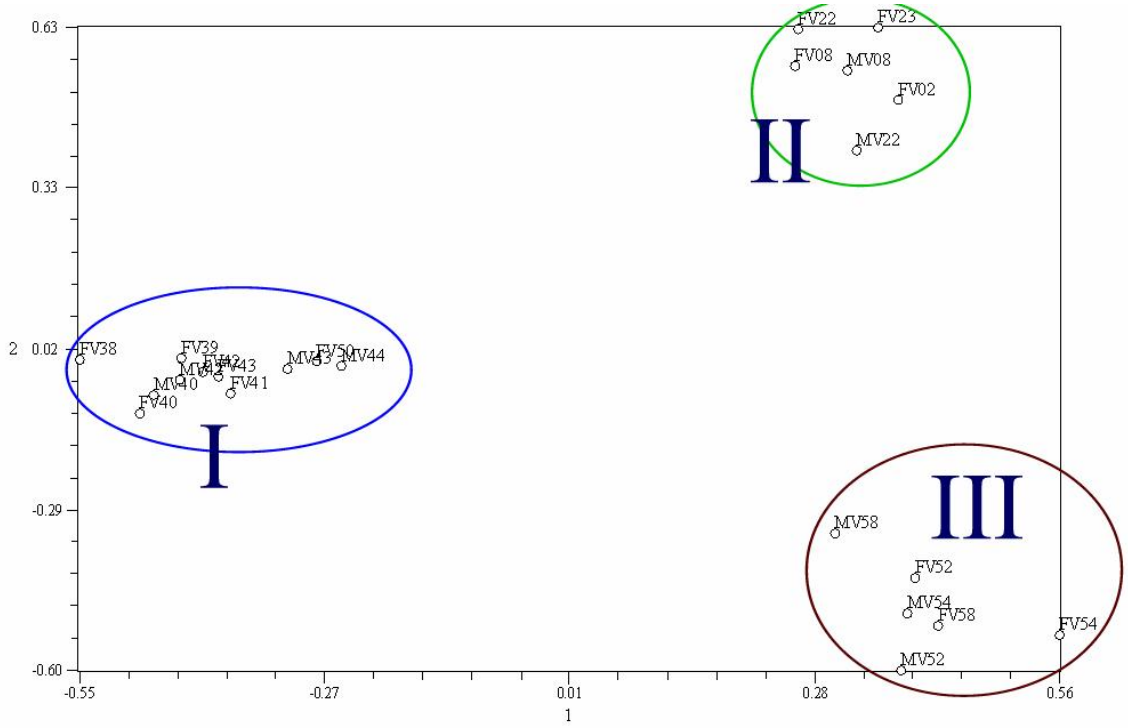


Figure 63. Principle component analysis for *P. vera* based on ISSR data.

3.3.1.3. Microsatellites, Simple Sequence Repeats (SSRs)

Table 25 shows the primers' names and number of alleles studied *P. vera* also the allele size. The total number of primers was 4 out 10 tested primers, since six of them were either monomorphic or did not amplify properly all the *Pistacia* species.

Table 25. Primer used in SSR analysis.

Primer	Loci no.	Alleles no.	Allele size
Ptms-3	1	2	134-146.5
Ptms-7	3	2	160- 178
		5	189-208
		3	217-225
Ptms-10	2	2	140-175
		3	314-378
Ptms-33	1	2	150-184

The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 - Table15). Five, not very sharply divided, groups are obtained in this analysis and two males groups from Italy (Bronte 1 – 2) are not clustered (Table 24, Figure 64):

I. Group one: contains all female varieties from Italy;
II. Group two: contains some female individuals form Tajikistan sites (Dangara 1 – 2, Korgan Tubye 2) and Uzbekistan site (Galla Aral);
III. Group three: contains some female varieties from Syria (Izraa gene bank and Ain Al-Tina);
IV. Group four: contains some male from Syria (Izraa gene bank and Al Moslemia gene bank, Moslemia gene bank and Ain Al- Tina) and Tajikistan (Dangara 1 – 2, Korgan Tubye 1 and Televiska);
V. Group five: contains some female varieties from Syria (Al –Shahba gene bank) and Turkey (Adana) and Tajikistan (Televiska).

Figure 65 shows the unrooted relatedness tree among the collected genotypes according to their origin country by using Nei (1972) genetic distance coefficient and which can be divided into 2 groups (Annex 3 - Table19):

I. Group one: contains all female varieties and individuals which can be divided into two subgroups: (a) Syria, Iran, Turkey, (b) Central Asia and Italy;
II. Group two: contains all male varieties and individuals form Italy, Syria, and Central Asia.

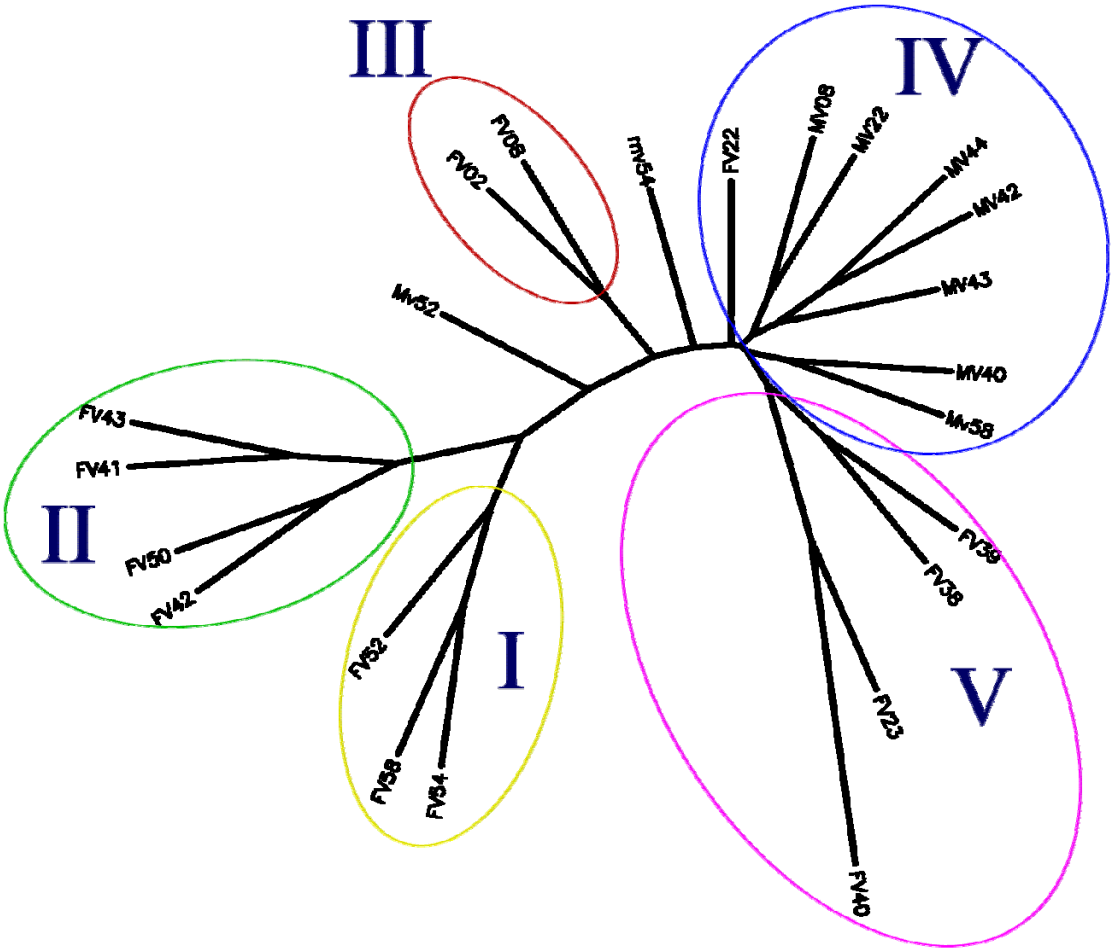


Figure 64. SSR UPGMA tree based on Nei (1972) genetic distance for *P. vera* according to each collected site.

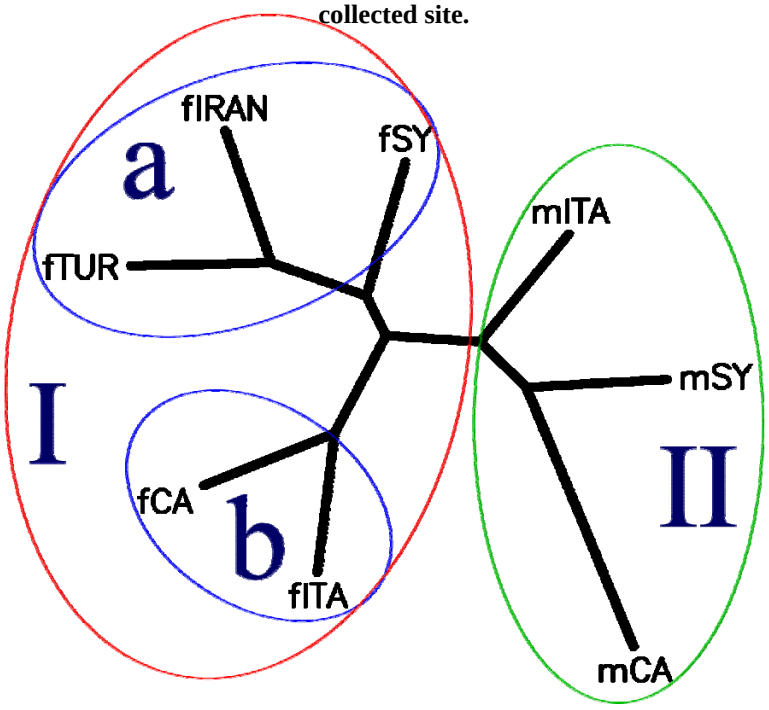


Figure 65. SSR Unrooted tree based on Nei (1972) genetic distance for *P. vera* according to their origin countries.

Principle component analysis (PCA) confirms clearly the three main groups (Figure 66):

I. Group one: contains female individuals from Central Asia;
II. Group two: contains female varieties from Syria and Italy;
III. Group three: contains mainly males from all different sites and some females from Syria.

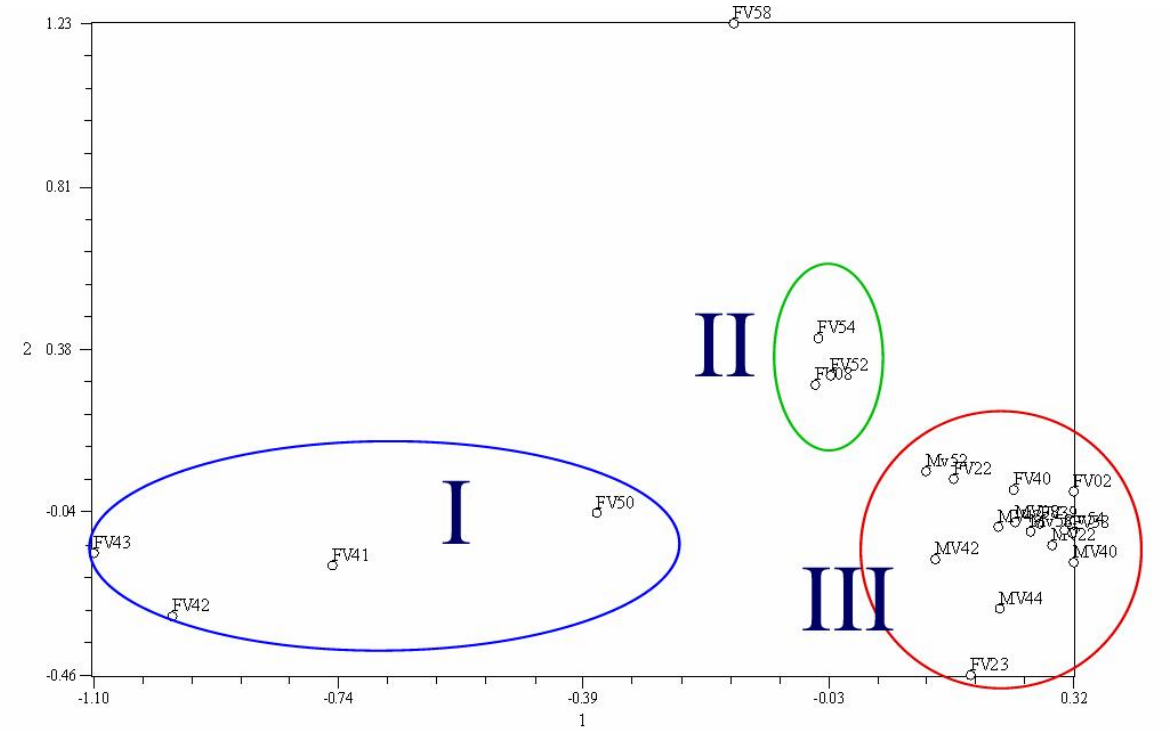


Figure 66. Principle component analysis for pistachio based on SSR data.

3.3.1.4. All markers

Figure 65 shows the genetic relatedness among the genotypes investigated by UPGMA cluster analysis, utilizing the Nei's (1972) genetic distance based on the three molecular marker techniques together. Five groups are obtained in this analysis (Annex 3 - Table16):

I. Group one: contains some male and female varieties from Italy (Bronte1-2);
II. Group two: contains some male and female varieties from Syria (Al Moslemia gene bank and Shahba gene bank, Izraa Gene bank and Ain Al-Tina) and female individuals from Tajikistan (Dangara 2) ;
III. Group three: contains male and female varieties from Turkey (Adana), Tajikistan (Televiska), Uzbekistan (Galla Aral) and Italy (Bronte 2);
IV. Group four: contains some female varieties from Italy (Bronte2-3);
V. Group five: contains male and female individuals from Tajikistan (Dangara 1- 2, Korgan Tubye 1-2, Televiska) and female varieties from Iran.

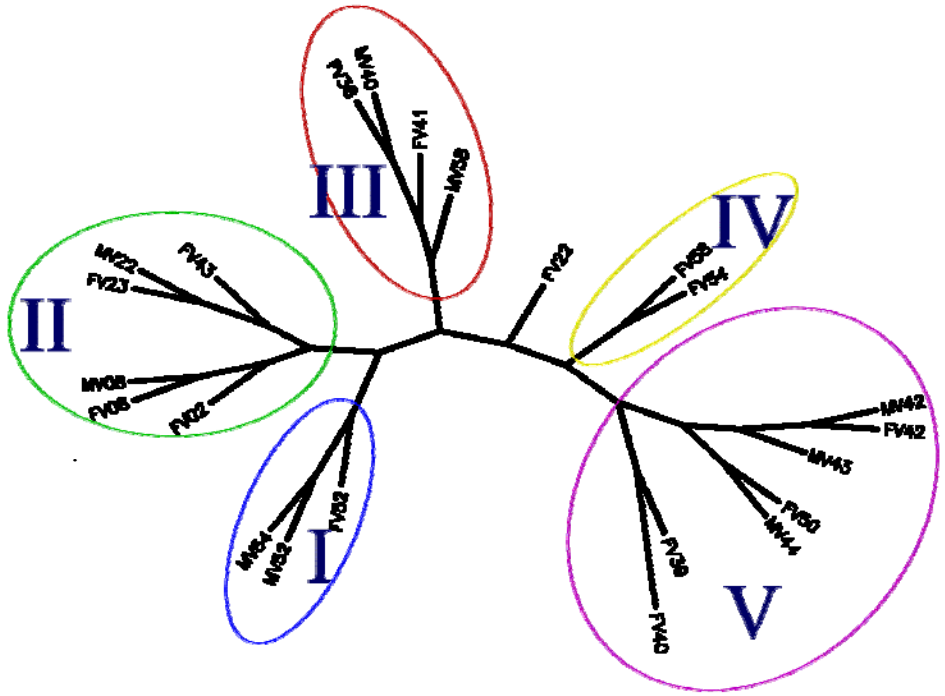


Figure 67. Three marker techniques UPGMA tree based on Nei (1972) genetic distance for *P. vera* according to each collected site.

Figure 64 shows the unrooted relatedness tree among the collected genotype according to their origin country by using Nei distance coefficient based on the three marker techniques together and which can be divided into two groups (Annex 3 – Table20):

I. Group one: contains all female and male varieties from Turkey, Syria and Italy which can be divided into two subgroups: (a) female varieties from Syria and Turkey and (b) male and female varieties from Italy;
II. Group two: contains all female and male varieties from Central Asia and Iran.

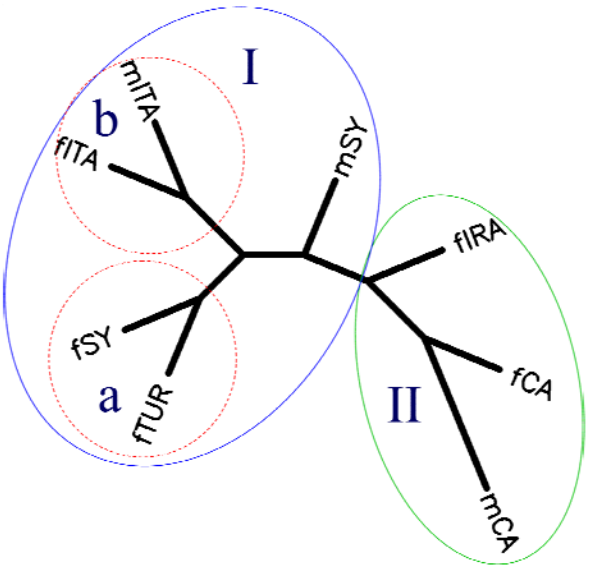


Figure 68. Unrooted tree of three marker techniques based on Nei (1972) genetic distance for *P. vera* according to their origin countries.

The correlations between the three different techniques are calculated based on Mantel test with 1000 permutations. The AFLP and ISSR data are highly significant correlated (r = 0.61). The ISSR and SSR data are highly significant correlated (r = 0.44). Also the SSR and AFLP data are highly significant correlated (r = 0.35) (Table 31).

3.3.2. *Pistacia atlantica*

The same 87 wild *P. atlantica* genotypes were analyzed using three molecular marker techniques from two countries Syrian and Turkey. The results can be summarized as follows:

3.3.2.1. Amplified Fragment Length Polymorphism (AFLP)

Figure 56 shows an example of one primer pair combination. A total 217 polymorphic bands were generated by 4 primer pair combinations. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table21). Four groups are obtained in this analysis (Table 26, Figure 69):

I. Group one: contains all male and female individuals from south Syrian sites and one site from Northeast of Syria (Markab Ali);
II. Group two: contains all male and female individuals from south Turkey (Adana);
III. Group three: contains male and female genotypes from Northeast of Syria and on site from mid of Syria (Abo Roudjmain 1);
IV. Group four: contains male and female genotypes from mid of Syria.

Table 26. The countries, site numbers and site names of collected *P. atlantica* sites.

Country	Site No.	Site name
Syria (South)	1	Al Hamra
	2	Ain Al-Tina
	3	Al Sarkha
	5	Salim
	6	Qanawat
	7	Al Kafer
	9	Maaria
	10	Al Modawarah
	11	Al Lajat
Syria (Middle)	12	Palmyra Wadi
	13	Abo Roudjmain 1
	14	Rasm Al Abed
	15	Al Balaas 1
	16	Al Balaas 2
	17	Al Balaas 3
Syria (Northeast)	18	Abdul Aziz 1
	19	Abdul Aziz 2
	20	Markab Ali
Turkey (South)	37	Adana

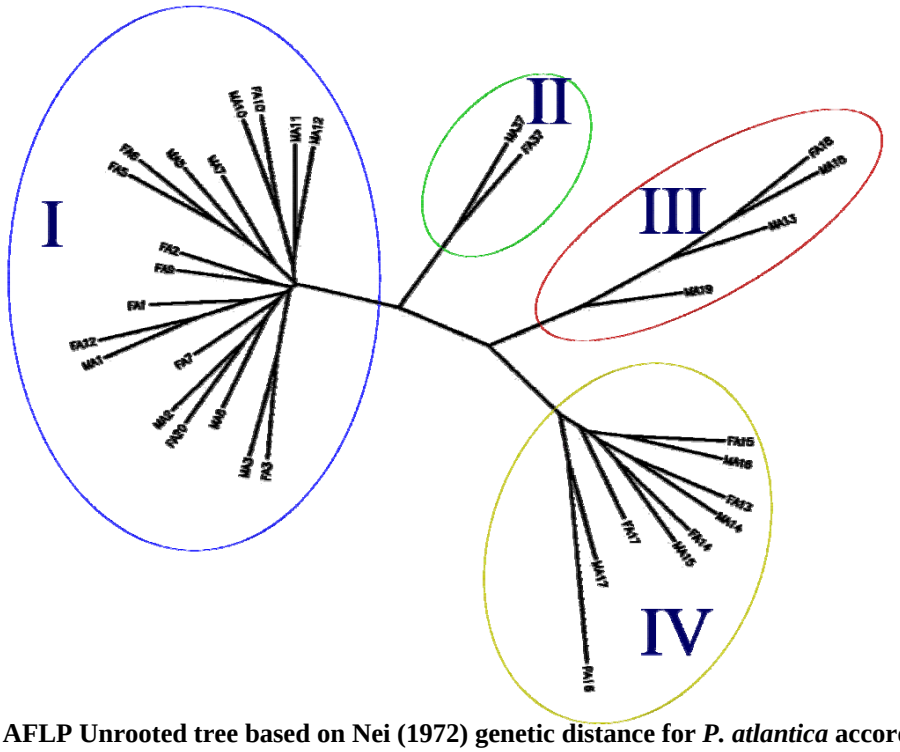


Figure 69. AFLP Unrooted tree based on Nei (1972) genetic distance for *P. atlantica* according to each collected site.

Principle component analysis (PCA) confirms clearly four main groups (Figure 70):

I. Group one: contains female and male individuals from Central of Syria and on site form Northeast of Syria (Abdel Aziz1);

II. Group two: contains female and male individuals from Abdel Aziz2 and Markab Ali sites Northeast Syria;

III. Group three: contains female and male individuals from south Syrian sites; and one site from the central of Syria (Palmyra Wadi);

IV. Group four: contains female and male individuals from Adana Turkey.

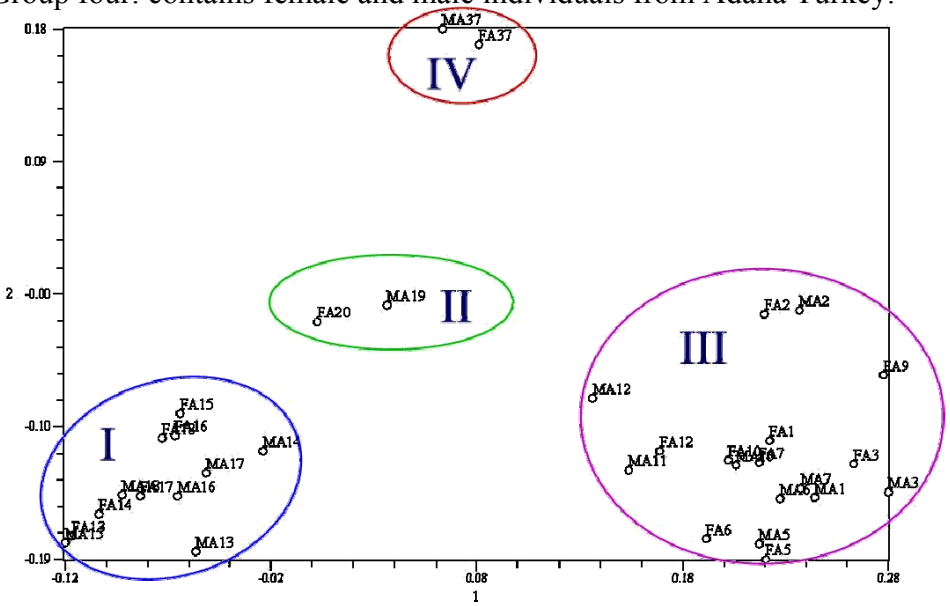


Figure 70. Principle component analysis for *P. atlantica* based on AFLP data.

3.3.2.2. Inter Simple Sequence Repeats (ISSR)

Figure 60 shows an example of one ISSR primer. A total 255 polymorphic bands were generated by 6 primers. A binary matrix was created contains 87 rows representing the genotypes and 255 columns representing the polymorphic loci. The genetic relatedness among the genotypes is investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table22). Five groups are obtained in this analysis (Table 26, Figure 71):

I. Group one: contains male and female individuals from south Syrian sites;
II. Group two: contains male and female individuals from south Syrian sites and some male form mid of Syria (Palmyra Wadi);
III. Group three: contains all male and female individuals from south Turkey (Adana);
IV. Group Four: contains all male and female genotypes from Northeast of Syria sites;
V. Group five: contains all male and female genotypes from mid of Syria.

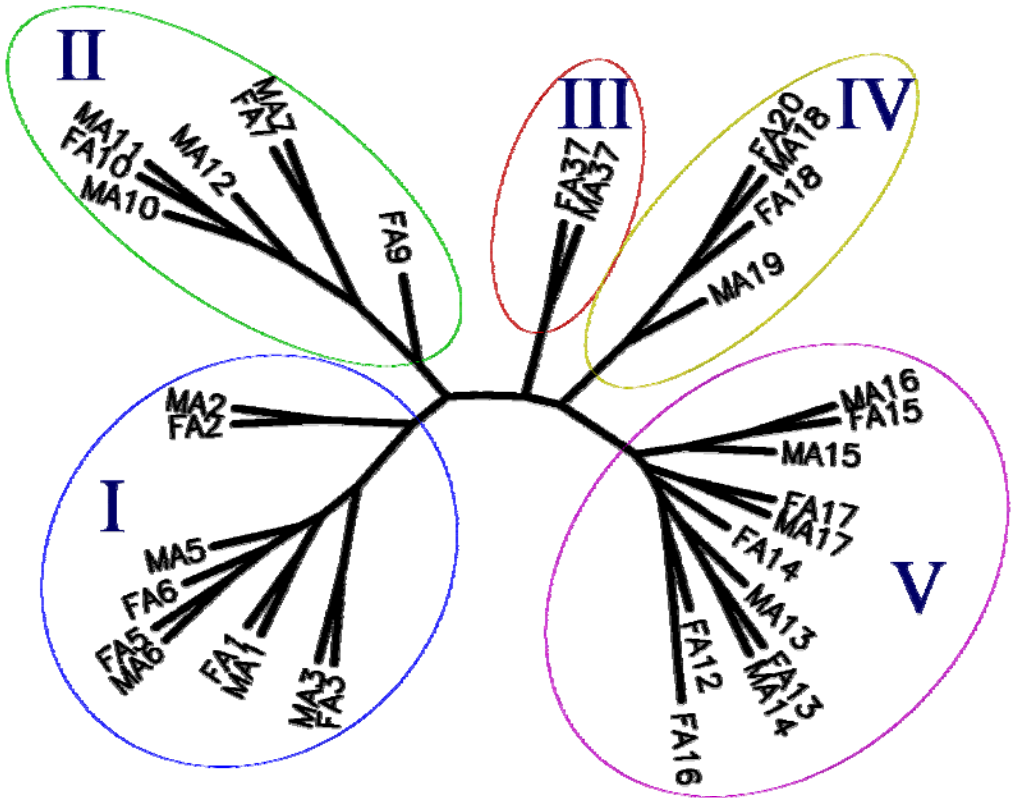


Figure 71. ISSR Unrooted tree based on Nei (1972) genetic distance for *P. atlantica* according to each collected site.

Principle component analysis (PCA) confirms clearly the five main groups (Figure 72):

I. Group one: contains female and male individuals from South of Syria;
II. Group two: contains female and male individuals from South of Syria;
III. Group three: contains female and male individuals from Northeast of Syria;
IV. Group four: contains female and male individuals from Adana Turkey;
V. Group five: contains female and male individuals from mid of Syria.

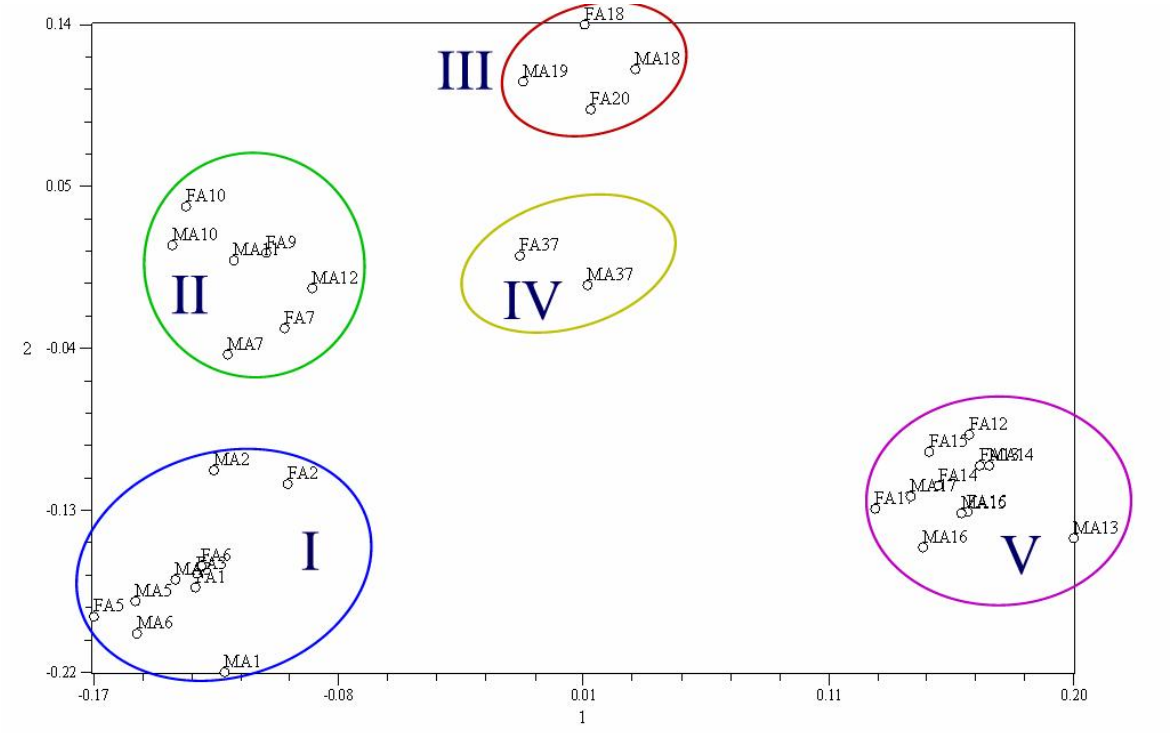


Figure 72. Principle component analysis for *P. atlantica* based on ISSR data.

3.3.2.3. Microsatellites, Simple Sequence Repeats (SSRs)

Table 25 shows the primers' names and number of alleles studied in *P. atlantica* also the allele size. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table 23). Eight groups, not far each other, are obtained in this analysis (Table 26, Figure 73):

I. Group one: contains male individuals from several sites in south and mid of Syria (Al Hamra, Ain Al-Tina, Al Modawarah, Al Lajat, Palmyra Wadi, Abo Roudjmain 1, Rasm Al Abed and Al Balaas 1) and female individuals from one site (Al Balaas 2);
II. Group two: contains male individuals south of Syria (Qanawat and Kafer);
III. Group three: contains some female individuals from Ain Al-Tina and Markab Ali;

IV. Group four: contains some female individuals from south and mid of Syria (Al Hamra, Al Sarkha and Abo Roudjmain 1);

V. Group five: contains male individuals from south of Syria (Salim) and from south of Turkey (Adana);

VI. Group six: contains female individuals from Al Kafer, Al Modawarah, Al Balaas 1 – 3 and Abdul Aziz 1;

VII. Group seven: contains male individuals from Balaas 2 – 3 and and Abdul Aziz 1;

VIII. Group eight: contains female individuals from Syria (Salim, Qanawat, Palmyra Wadi and Rasm Al Abed) and Turkey (Adana).

Also there are some male and female individuals which could not be clustered with the previous groups.

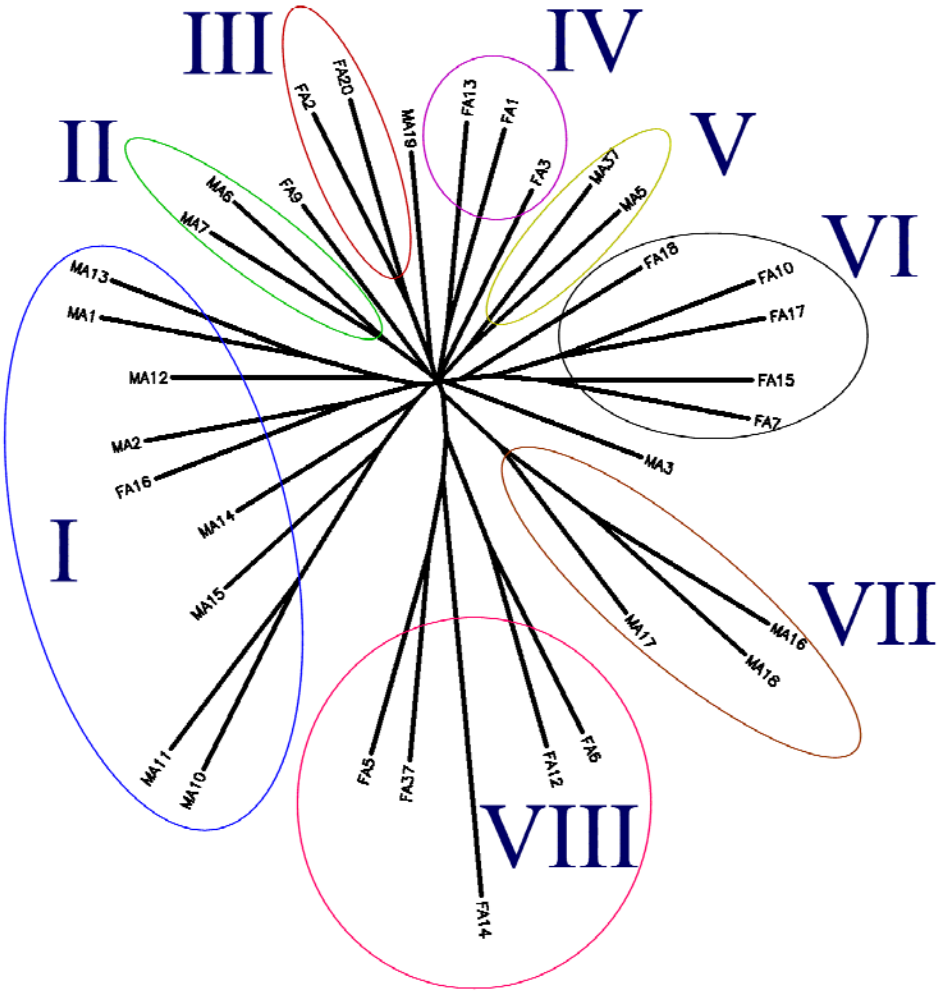


Figure 73. SSR UPGMA tree based on Nei (1972) genetic distance for *P. atlantica* according to each collected site.

Principle component analysis (PCA) confirms clearly the three main groups (Figure 74):

I. Group one: contains female individuals from all of Syria and Turkey;

II. Group two: contains almost all male individuals from all of Syria and Turkey;

III. Group three: contains male individuals from south of Syria (Qanawat and Al-Kafer sites);

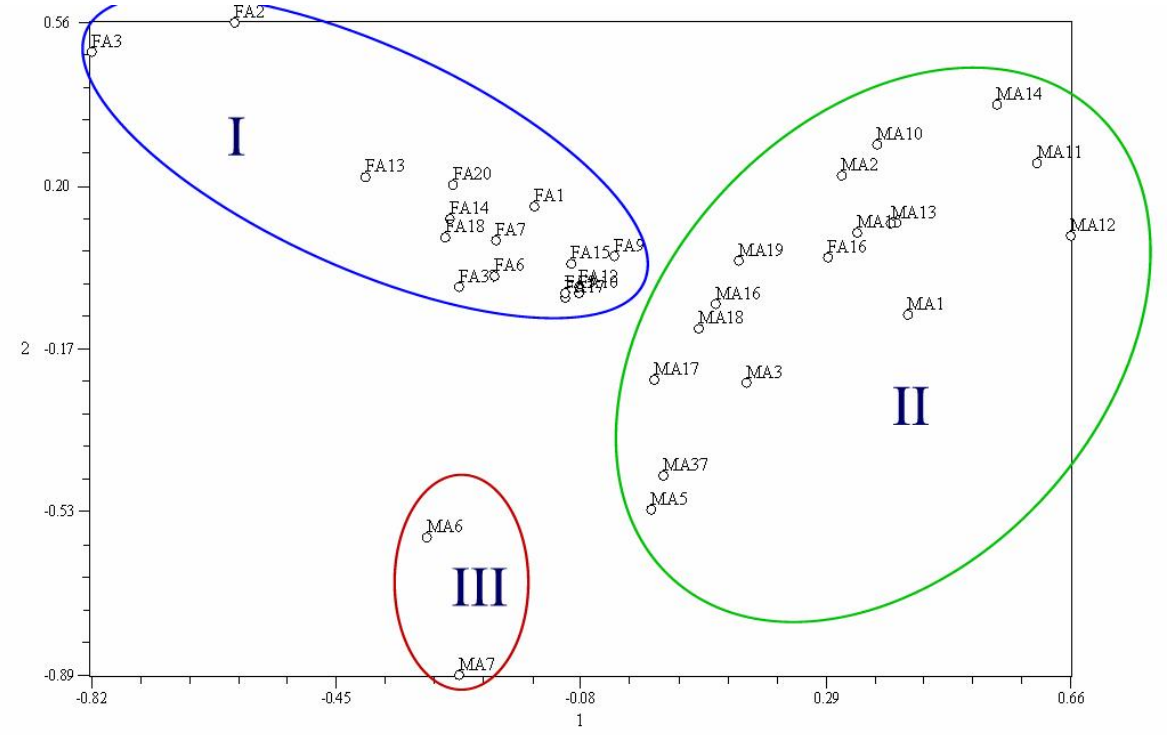


Figure 74. Principle component analysis for *P. atlantica* based on SSR data.

3.3.2.4. All markers

Figure 75 shows the genetic relatedness among the genotypes investigated by UPGMA cluster analysis utilizing Nei's (1972) genetic distance based on the three molecular marker techniques together. Five groups are obtained in this analysis (Annex 3 – Table24):

I. Group one: contains all male and female individuals from some sites in south Syria (Al Hamra, Ain Al-Tina, Al Sarkha, Salim, Qanawat);

II. Group two: contains some male and female individuals from south and mid of Syria (Al Kafer, Al Modawarah, Al Lajat and Palmyra Wadi);

III. Group three: contains female individuals from Markab Ali and Palmyra Wadi;

IV. Group four: contains all male and female individuals from south Turkey (Adana);

V. Group five: contains male and female individuals from mid and Northeast of Syria (Abdul Aziz 1 -2 and Abo Roudjmain 1);

VI. Group six: contains male and female individuals from mid of Syria (Abo Roudjmain 1, Rasm Al Abed and Al Balaas 1 -2 -3).

VII. One site dose not cluster with any group which is Maaria site.

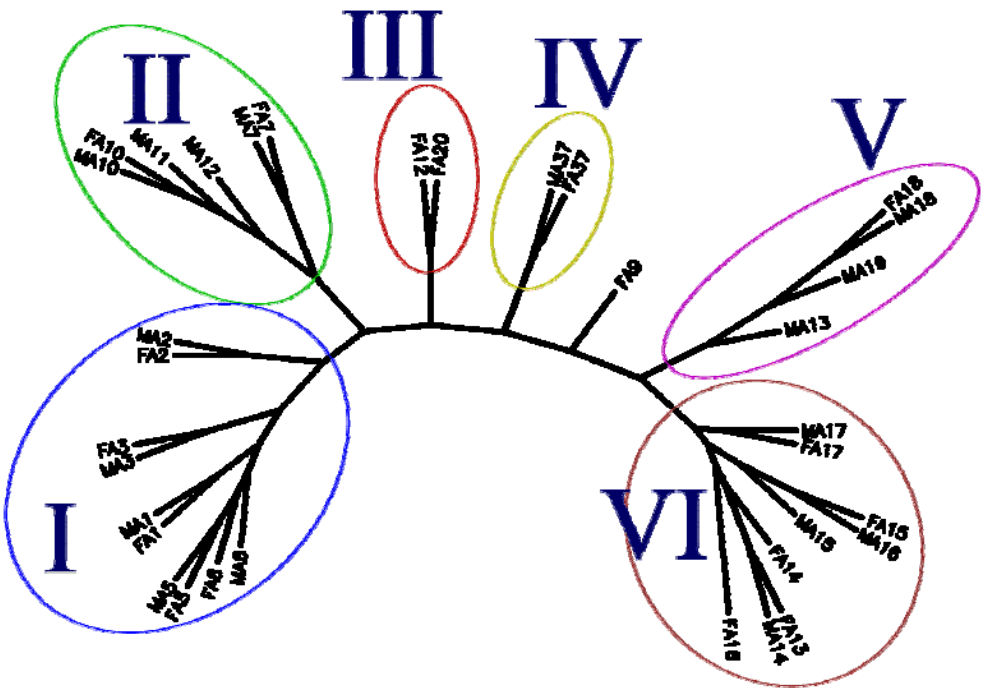


Figure 75. Three marker techniques UPGMA tree based on Nei (1972) genetic distance for *P. atlantica* according to each collected site.

Table 31 shows the correlation between the three different techniques based on Mantel test with 1000 permutations. The AFLP and ISSR data are highly significant correlated (r = 0.68). Also the AFLP and SSR data are highly significant correlated (r = 0.22). On the other hand, the SSR and ISSR data have a poor correlation (r = 0.09) with no significant.

3.3.3. *Pistacia palaestina*

The same 60 wild *P. palaestina* genotypes were analyzed using three molecular marker techniques from Syria. The results can be summarized as follows:

3.3.3.1. Amplified Fragment Length Polymorphism (AFLP)

Figure 56 shows an example of one primer pair combination. A total 217 polymorphic bands were generated by 4 primer pair combinations. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table25). Five groups are obtained in this analysis (Table 27, Figure 71):

I. Group one: contains male and female individuals from Wadi Baradah, Ras Al Baset 1, Wadi Kandel, Mantaf, Kafer Haya, Al Bara and Ain Al Gazal;
II. Group two: contains all male and female individuals from Frolok, Banias and Derekish;

III. Group three: contains male and female genotypes from Frolok, Kadmous and Derekish;

IV. Group four: contains male and female genotypes from Mantaf, Al Bara, Al Nabiaen and Bhamra;

V. Group five: contains male and female genotypes from Kafer Haya, Ain Al Gazal, Wadi Kandel and Bhamra.

Table 27. The countries, site numbers and site names of collected *P. palaestina* sites.

Country	Site No.	Site name
Syria	4	Wadi Baradah
	24	Mantaf
	25	Kafer Haya
	26	Al Bara
	27	Ain Al Gazal
	28	Wadi Kandel
	29	Ras Al Baset 1
	30	Al Badrousia
	31	Al Nabiaen
	32	Frolok
	33	Bhamra
	34	Banias
	35	Kadmous
	36	Derekish

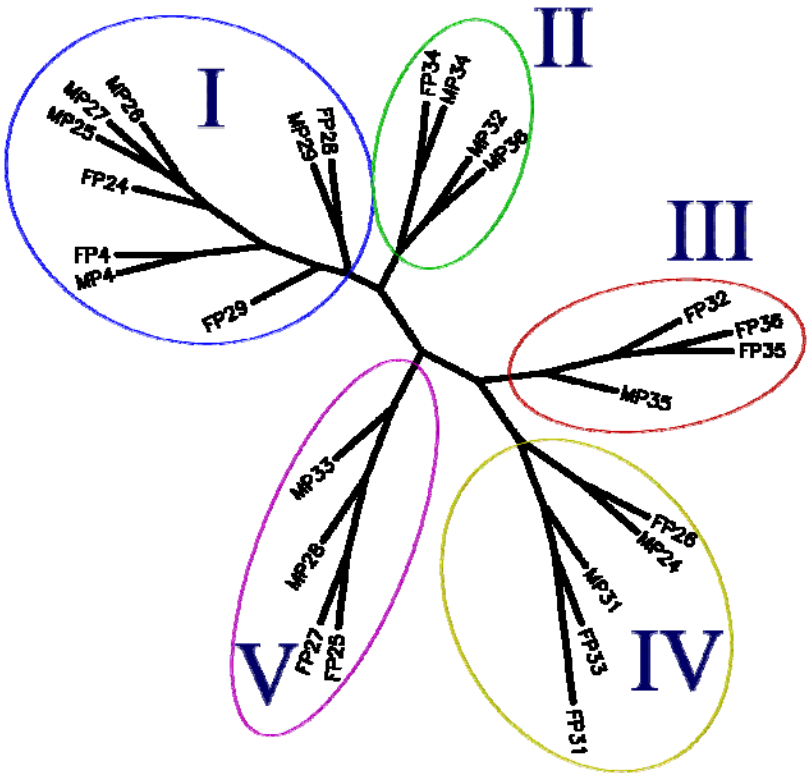


Figure 76. AFLP Unrooted tree based on Nei (1972) genetic distance for *P. palaestina* according to each collected site.

Principle component analysis (PCA) confirms clearly the three main groups (Figure 77):

I. Group one: contains male and female individuals from one site in Syria Wadi Baradah;

II. Group two: contains male and female individuals in Syria (Mantaf, Kafer Haya, Al Bara, Ain Al Gazal and Wadi Kandel);

III. Group three: contains male and female individuals in Syria (Ras Al Baset 1, Al Badrousia, Al Nabiaen, Frolok, Bhamra, Banias, Kadmous and Derekish).

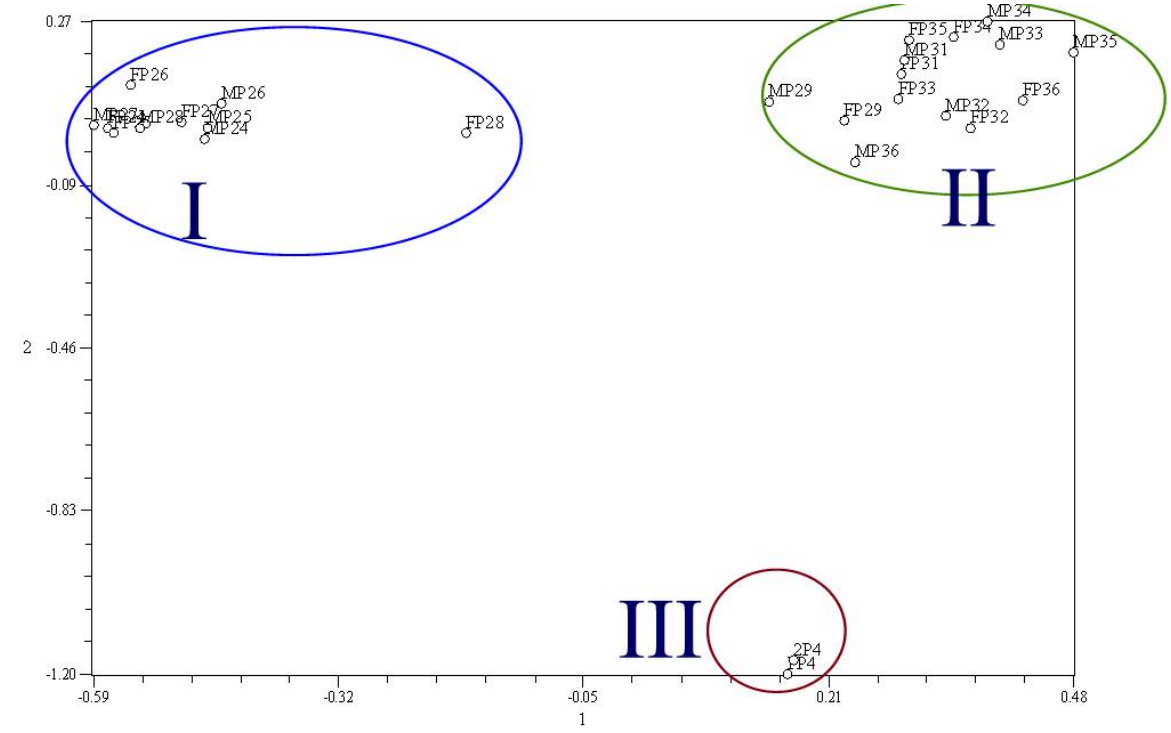


Figure 77. Principle component analysis for *P. palaestina* based on AFLP data.

3.3.3.2. Inter Simple Sequence Repeats (ISSR)

Figure 60 shows an example of one ISSR primer. A total 255 polymorphic bands were generated by 6 primers. A binary matrix is created contains 60 rows representing the genotypes and 255 columns representing the polymorphic loci. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table 26). Three groups are obtained in this analysis (Table 27, Figure 78):

I. Group one: contains male and female individuals from Al Bara, Ain Al Gazal, Wadi Kandel and Ras Al Baset 1;

II. Group two: contains male and female individuals from Wadi Baradah, Mantaf, Kafer Haya and Derekish;

III. Group three: contains all male and female individuals from Al Nabiaen, Frolok, Bhamra, Banias, Kadmous and Derekish.

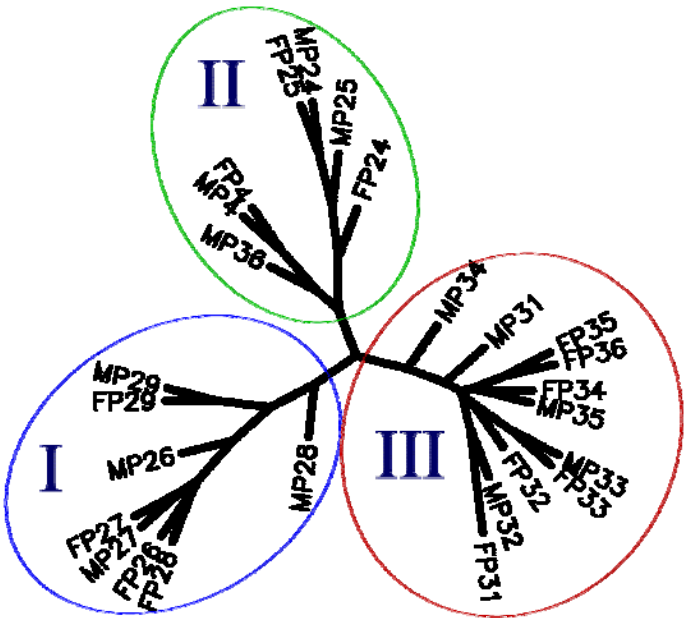


Figure 78. ISSR Unrooted tree based on Nei (1972) genetic distance for *P. palaestina* according to each collected site.

Principle component analysis (PCA) confirms clearly the three main groups (Figure 79):

I. Group one: contains male and female individuals in Syria (Al Bara, Ain Al Gazal, Wadi Kandel and Ras Al Baset 1);

II. Group two: contains male and female individuals in Syria (Mantaf, Kafer Haya, Al Badrousia, Al Nabiaen, Frolok, Bhamra, Banias, Kadmous and Derekish);

III. Group three: contains male and female individuals from one site in Syria Wadi Baradah.

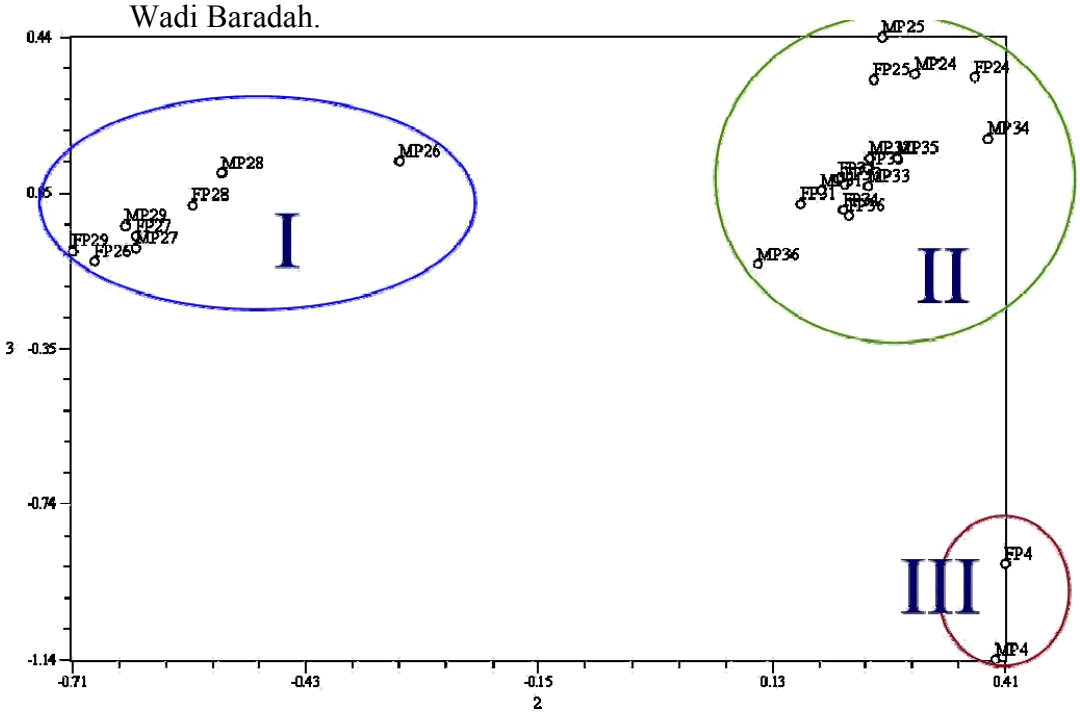


Figure 79. Principle component analysis for *P. palaestina* based on ISSR data.

3.3.3.3. Microsatellites, Simple Sequence Repeats (SSRs)

Table 25 shows the primers' names and number of alleles studied in *P. palaestina* also the allele size. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table 27). Two groups are obtained in this analysis (Table 27, Figure 80):

I. Group one: contains all male individuals from all Syrian sites except some female genotypes from Mantaf site. This group can be divided into 3 subgroups as follows:
   a. Subgroup Ia: contains male individuals from Banias and Kafer Haya and the female individuals from Mantaf site;
   b. Subgroup Ib: contains male individuals from Wadi Baradah, Mantaf, Ain Al Gazal, Frolok, Kadmous and Derekish;
   c. Subgroup Ic: contains male individuals from Ras Al Baset 1, Al Bara, Wadi Kandel, Al Nabiaen and Bhamra.

II. Group two: contains all female individuals from all Syrian sites. This group can be divided into 2 subgroups as follows:
   a. Subgroup IIa: contains female individuals from Al Bara, Ain Al Gazal, Wadi Kandel, Frolok and Banias;
   b. Subgroup IIb: contains female individuals from Wadi Baradah, Kafer Haya, Ras Al Baset 1, Al Badrousia, Al Nabiaen, Bhamra, Kadmous and Derekish.

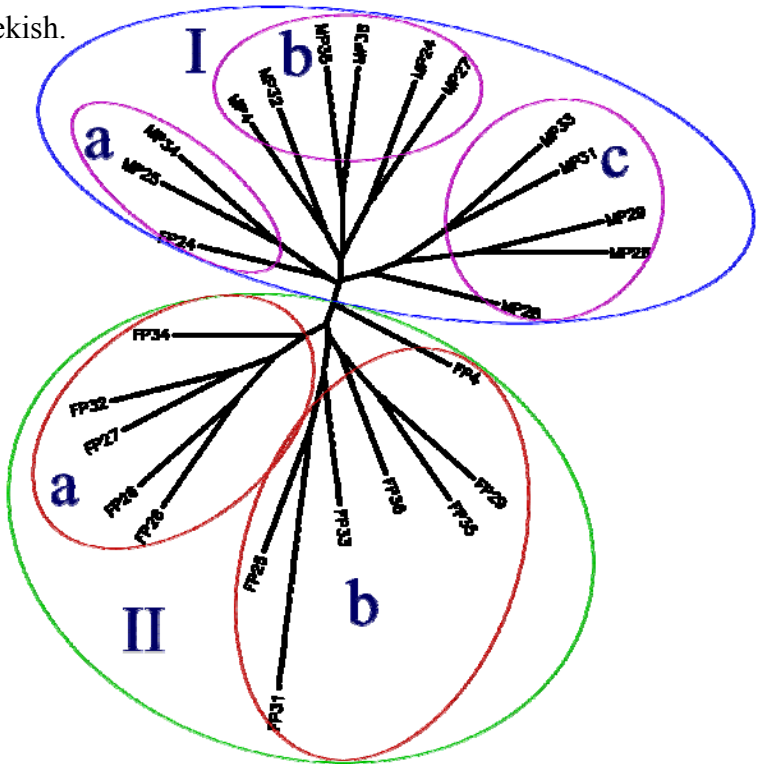


Figure 80. SSR UPGMA tree based on Nei (1972) genetic distance for *P. palaestina* according to each collected site.

Principle component analysis (PCA) confirms clearly the six main groups (Figure 81):

I. Group one: contains female individuals in Syria (Al Bara, Wadi Kandel);
II. Group two: contains female individuals in Syria (Ain Al Gazal, Frolok and Banias);
III. Group three: contains female individuals in Syria (Kadmous and Derekish);
IV. Group four: contains female individuals in Syria (Mantaf, Kafer Haya, Al Badrousia, Al Nabiaen, , Bhamra and Ras Al Baset 1)
V. Group five: contains male individuals in Syria (Wadi Baradah, Kafer Hayam, Frolok, Banias, Kadmous and Derekish)
VI. Group six: contains male and female individuals from one site in Syria (Mantaf, Al Bara, Ain Al Gazal, Wadi Kandel, Ras Al Baset 1, Al Badrousia, Al Nabiaen and Bhamra).

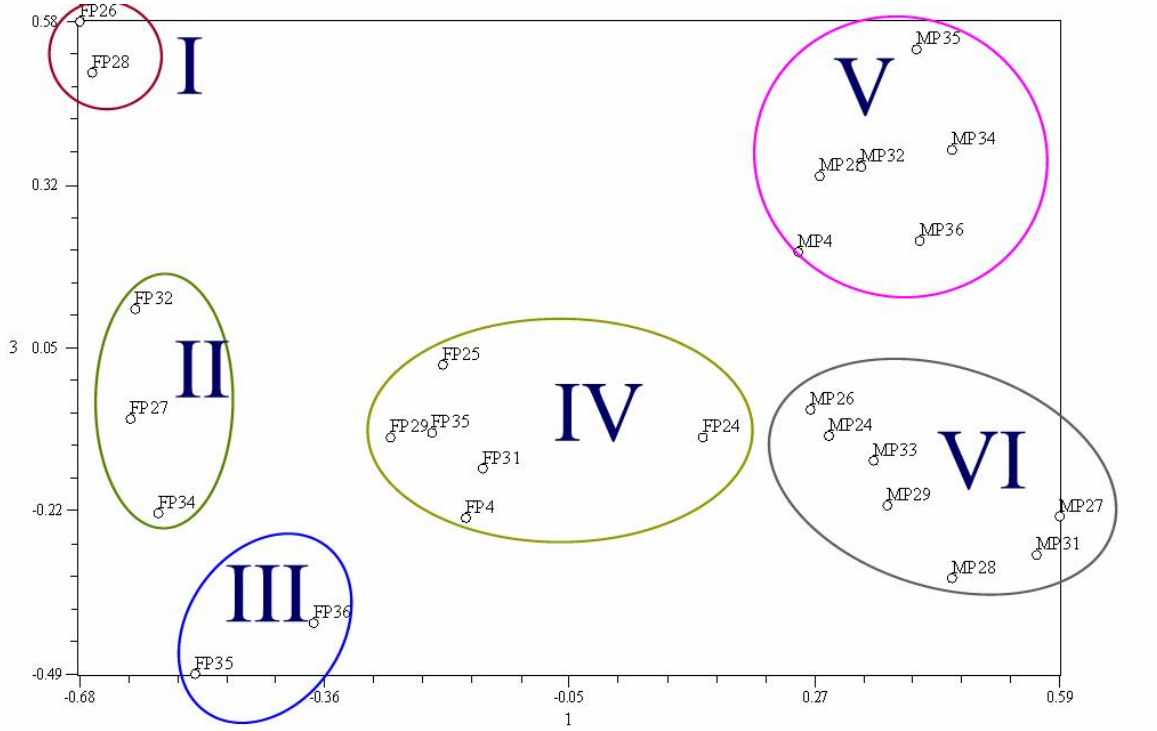


Figure 81. Principle component analysis for *P. palaestina* based on ISSR data.

3.3.3.4. All markers

Figure 82 shows the genetic relatedness among the genotypes investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance based on the three molecular marker techniques together. Five groups are obtained in this analysis (Annex 3 – Table 28):

I. Group one: contains male and female individuals from some Al Bara, Ain Al Gazal, Wadi Kandel and Ras Al Baset 1 sites;
II. Group two: contains some male and female individuals from Frolok and Banias sites;

III. Group three: contains male and female individuals from Wadi Baradah, Mantaf and Kafer Haya;

IV. Group four: contains all male and female individuals from Mantaf, Kafer Haya and Derekish;

V. Group five: contains male and female individuals from Bhamra, Al Nabiaen, Frolok, Kadmous and Derekish;

VI. Group six: contains male and female individuals from Ain Al Gazal and Wadi Kandel.

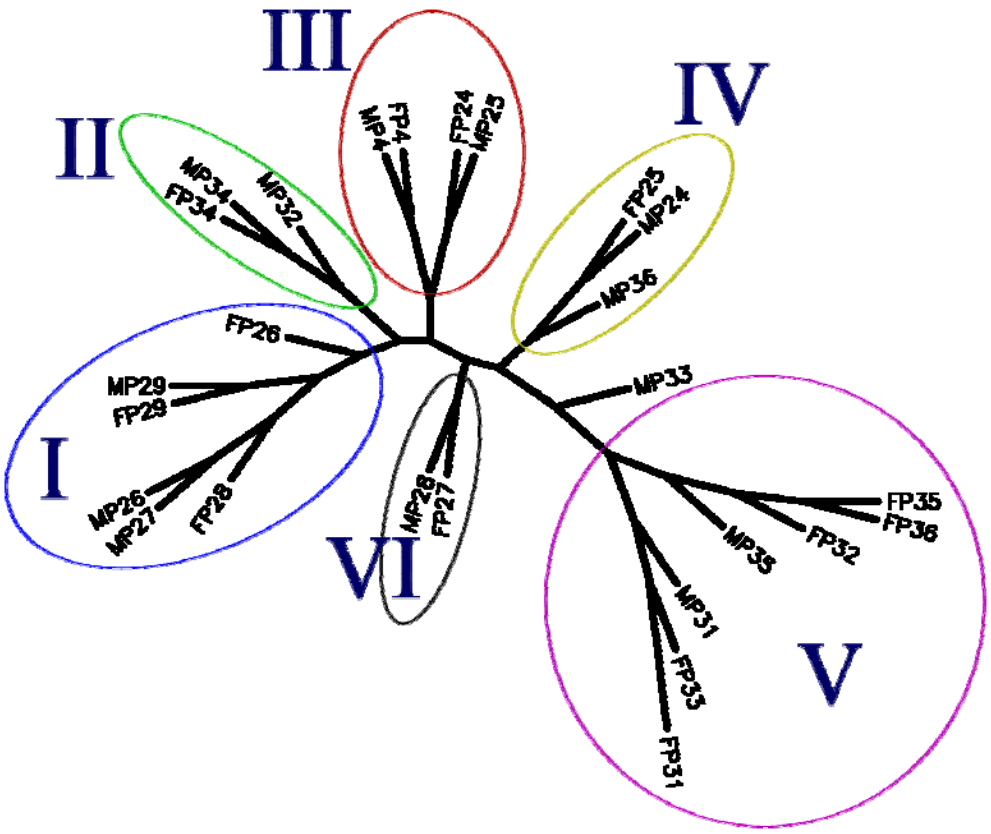


Figure 82. Three marker techniques UPGMA tree based on Nei (1972) genetic distance for *P. palaestina* according to each collected site.

Table 31 shows the correlation between the three different techniques based on Mantel test with 1000 permutations. The AFLP and ISSR data are highly significant correlated (r = 0.73). The AFLP and SSR data are highly significant correlated (r = 0.38). Also the SSR and ISSR data are highly significant correlated (r = 0.28).

3.3.4. *Pistacia terebinthus*

The same 12 wild *P. terebinthus* genotypes were analyzed using three molecular marker techniques from three countries Syria, Turkey and Italy. The results can be summarized as follows:

3.3.4.1. Amplified Fragment Length Polymorphism (AFLP)

Figure 56 shows an example of one primer pair combination. A total 217 polymorphic bands were generated by 4 primer pair combinations. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table29). Three groups are obtained in this analysis (Table 28, Figure 83):

I. Group one: contains all female individuals from Italy (Bronte 7) and Turkey ;
II. Group two: contains all male individuals from Italy (Bronte 8) and Turkey;
III. Group three: contains all Syrian male and female genotypes.

Table 28. The countries, site numbers and site names of collected *P. atlantica* sites.

Country	Site No.	Site name
Syria	29	Ras Al Baset 2
Turkey	37	Adana 1
Italy	59	Bronte 6
	60	Bronte 7

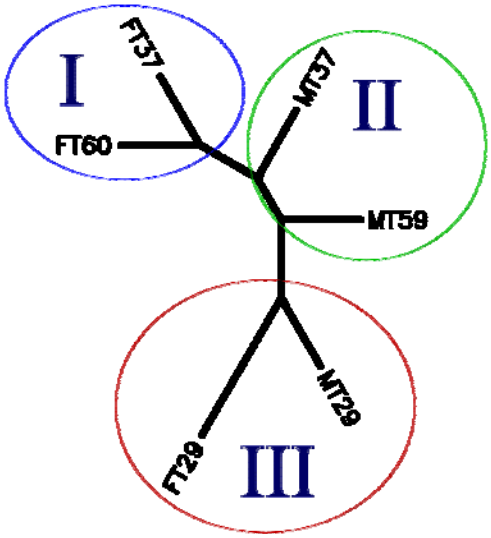


Figure 83. AFLP Unrooted tree based on Nei (1972) genetic distance for *P. terebinthus* according to each collected site.

Principle component analysis (PCA) confirms clearly the three main groups (Figure84):

I. Group one: contains male and female individuals from Italy;
II. Group two: contains male and female individuals from Turkey;
III. Group three: contains male and female individuals from Syria.

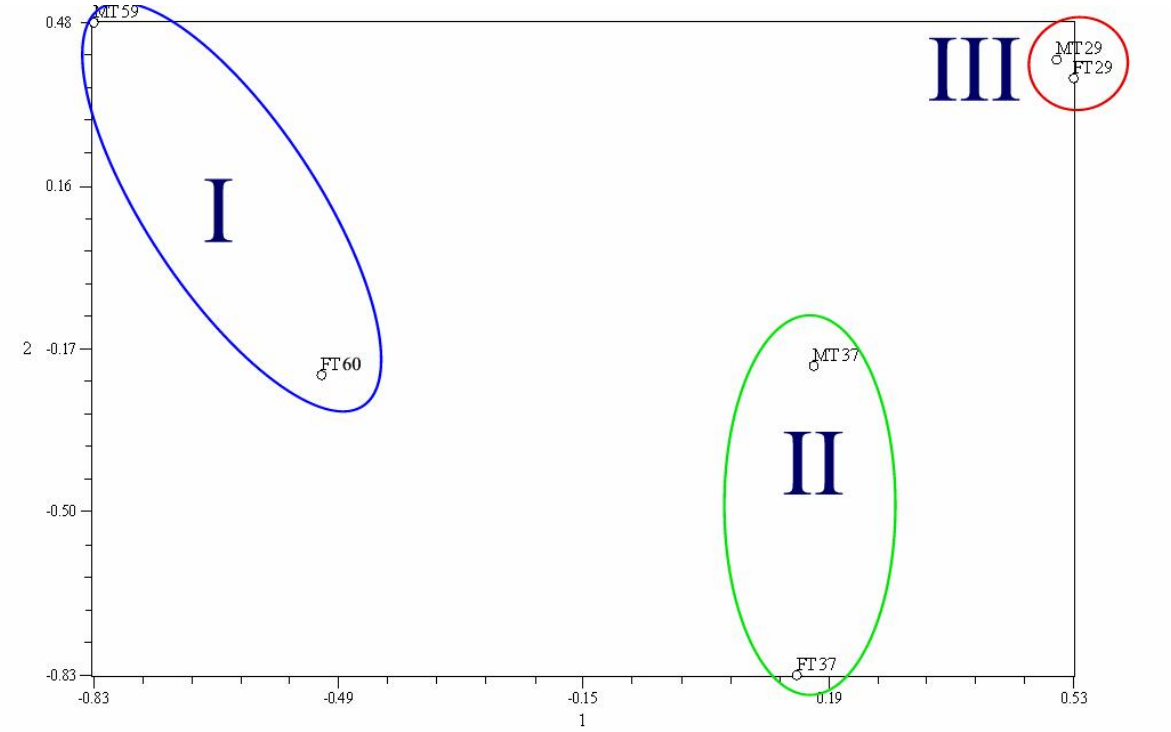


Figure 84. Principle component analysis for *P. terebinthus* based on AFLP data.

3.3.4.2. Inter Simple Sequence Repeats (ISSR)

Figure 60 shows an example of one ISSR primer. A total 255 polymorphic bands were generated by 6 primers. A binary matrix was created contains 12 rows representing the genotypes and 255 columns representing the polymorphic loci. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table 30). Three groups are obtained in this analysis (Table 28, Figure 85):

I. Group one: contains all male and female individuals Turkey;

II. Group two: contains all male and female individuals from Syria;

III. Group three: contains all male and female individuals from Italy.

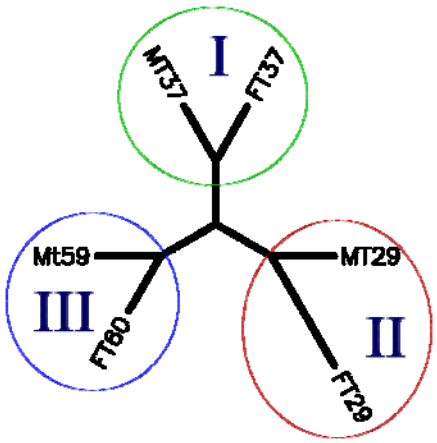


Figure 85. ISSR Unrooted tree based on Nei (1972) genetic distance for *P. terebinthus* according to each collected site.

Principle component analysis (PCA) confirmsclearly the three main groups (Figure 86):

I. Group one: contains male and female individuals from Syria;

II. Group two: contains male and female individuals from Italy;

III. Group three: contains male and female individuals from Turkey.

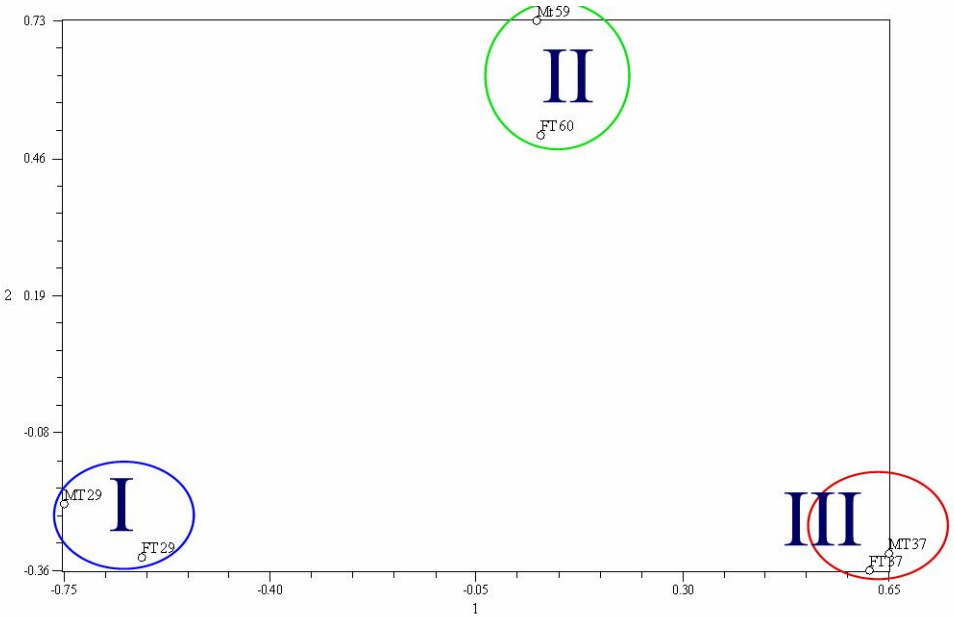


Figure 86. Principle component analysis for *P. terebinthus* based on ISSR data.

3.3.4.3. Microsatellites, Simple Sequence Repeats (SSRs)

Table 25 shows the primers' names and number of alleles studied in *P. terebinthus* also the allele size. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table 31). Three groups are obtained in this analysis (Table 28, Figure 87):

I. Group one: contains all male and female individuals Turkey;

II. Group two: contains all male and female individuals from Syri;

III. Group three: contains all male and female individuals from Italy.

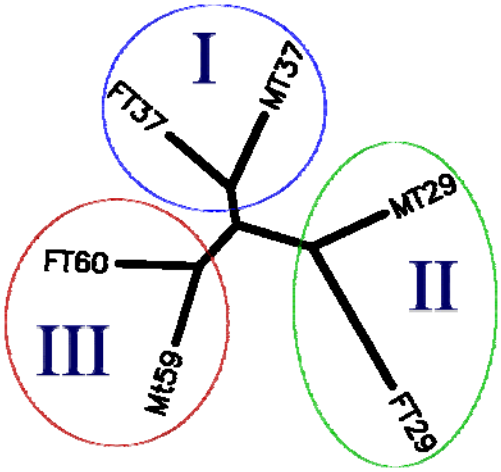


Figure 87. SSR UPGMA tree based on Nei (1972) genetic distance for *P. terebinthus* according to each collected site.

Principle component analysis (PCA) confirms clearly the three main groups (Figure 88):

I. Group one: contains male and female individuals from Turkey;

II. Group two: contains male and female individuals from Syria;

III. Group three: contains male and female individuals from Italy.

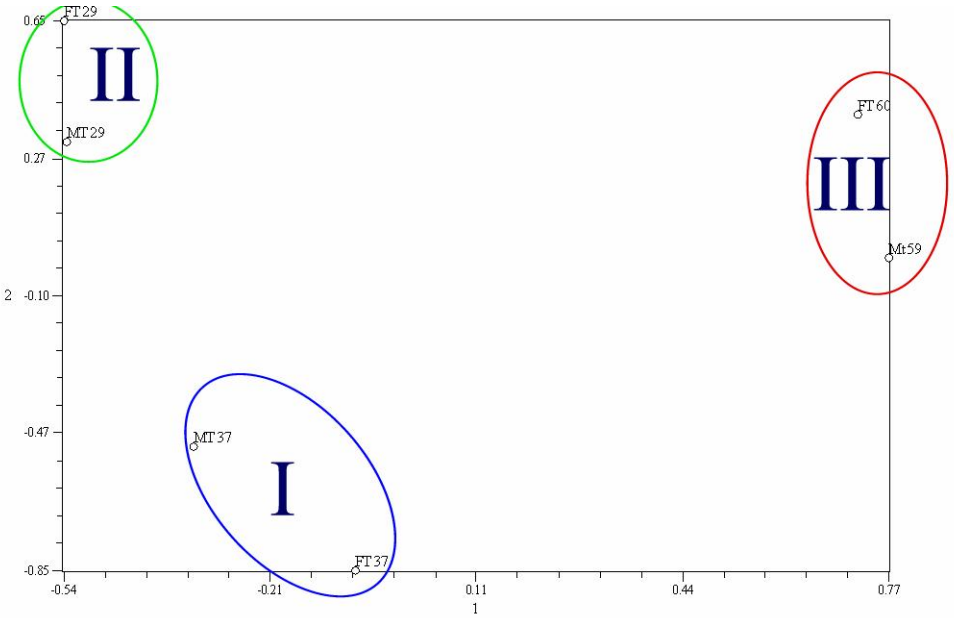


Figure 88. Principle component analysis for *P. terebinthus* based on SSR data.

3.3.4.4. All markers

Figure 89 shows the genetic relatedness among the genotypes investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance based on the three molecular marker techniques together. Three groups are obtained in this analysis (Annex 3 – Table32):

I. Group one: contains all male and female individuals Turkey;

II. Group two: contains all male and female individuals from Syria

III. Group three: contains all male and female individuals from Italy.

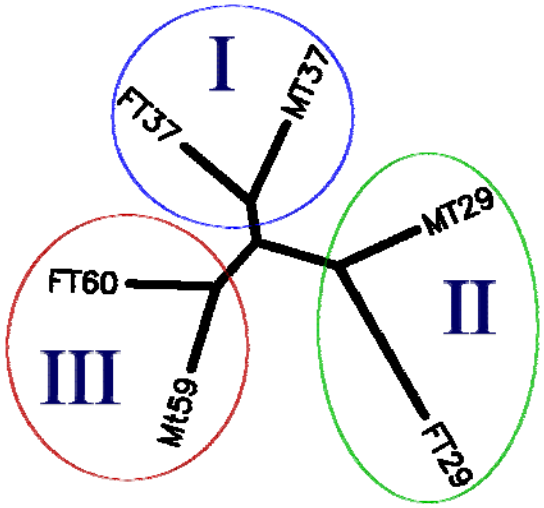


Figure 89. Three marker techniques UPGMA tree based on Nei (1972) genetic distance for *P. terebinthus* according to each collected site.

Table 31 shows the correlation between the three different techniques based on Mantel test with 1000 permutations. The AFLP and ISSR data are highly significant correlated (r = 0.60). Also the AFLP and SSR data are highly significant correlated (r = 0.64). On the other hand, the SSR and ISSR data are significantly correlated (r = 0.70).

3.3.5. *Pistacia khinjuk*

The same 5 wild *P. khinjuk* genotypes were analyzed using three molecular marker techniques from Syria. The results can be summarized as follows:

3.3.5.1. Amplified Fragment Length Polymorphism (AFLP)

Figure 56 shows an example of one primer pair combination. A total 217 polymorphic bands were generated by 4 primer pair combinations. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table 33). Two groups are obtained in this analysis (Table 29, Figure 90):

I. Group one: contains all female individuals from Syria ;
II. Group two: contains all male individuals from Syria.

On the other hand, principle component analysis (PCA) obtains two groups for first group for males and the second for the females in Abdul Aziz 1 site (Figure 91).

Table 29. The countries, site numbers and site names of collected *P. khinjuk* sites.

Country	Site No.	Site name
Syria	16	Al Balaas 2
	18	Abdul Aziz 1

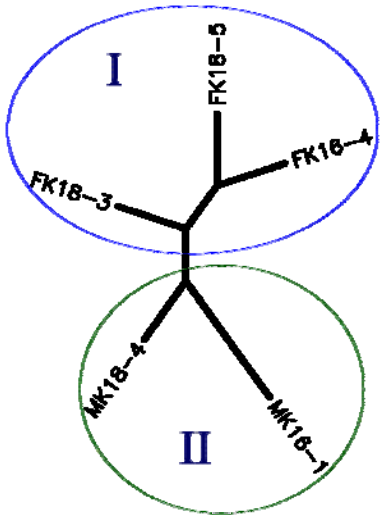


Figure 90. AFLP Unrooted tree based on Nei (1972) genetic distance for *P. khinjuk* according to each collected site.

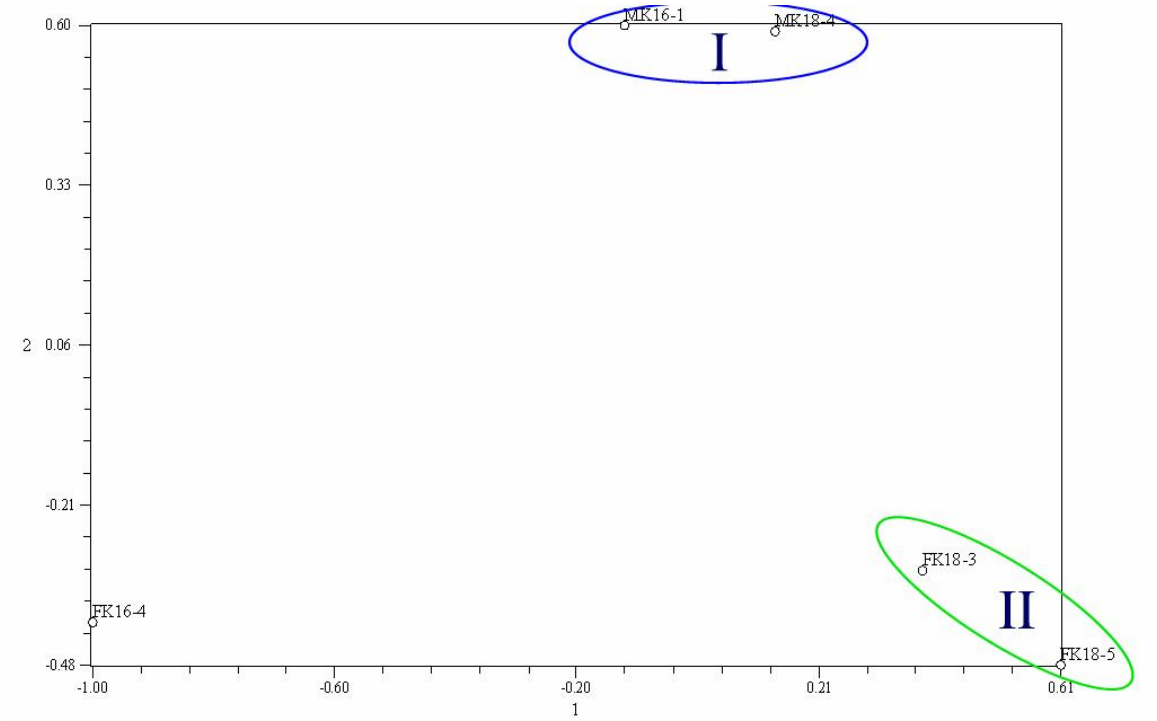


Figure 91. Principle component analysis for *P. khinjuk* based on AFLP data.

3.3.5.2. Inter Simple Sequence Repeats (ISSR)

Figure 60 shows an example of one ISSR primer. A total 255 polymorphic bands were generated by 6 primers. A binary matrix is created contains 5 rows representing the genotypes and 255 columns representing the polymorphic loci. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table 34). Two groups are obtained in this analysis (Table 29, Figure 92):

I. Group one: contains all female individuals from Syria;

II. Group two: contains all male individuals from Syria.

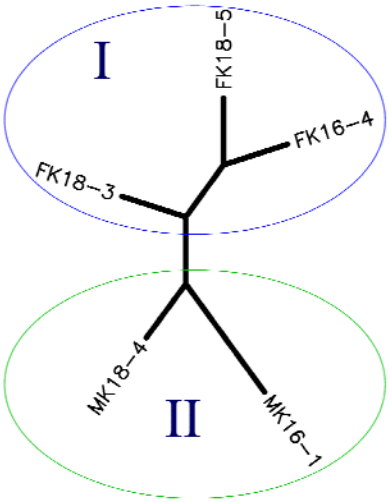


Figure 92. ISSR Unrooted tree based on Nei (1972) genetic distance for *P. khinjuk* according to each collected site.

Principle component analysis (PCA) confirms clearly the same two groups, first group for the females but one sample is not included and the second for the males (Figure 93).

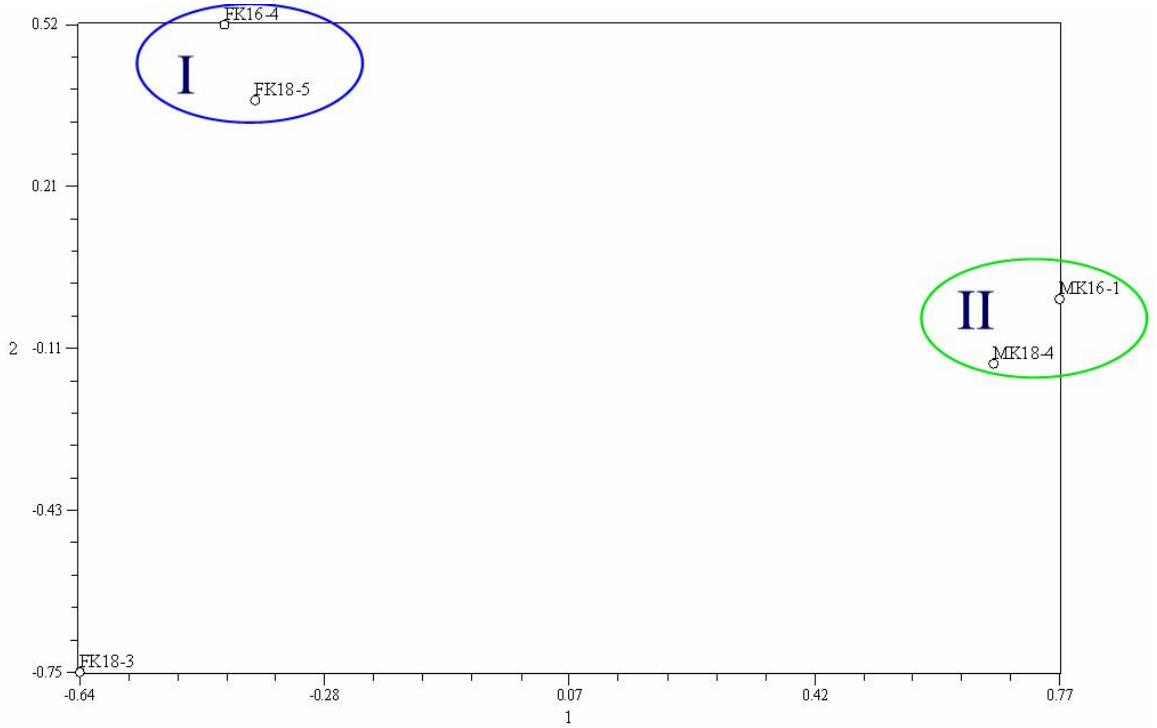


Figure 93. Principle component analysis for *P. khinjuk* based on ISSR data.

3.3.5.3. Microsatellites, Simple Sequence Repeats (SSRs)

Table 25 shows the primers' names and number of alleles studied in *P. khinjuk* also the allele size. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table 35). Two groups are obtained in this analysis (Table 29, Figure 94):

I. Group one: contains all male individuals Syria;

II. Group two: contains all female individuals from Syria.

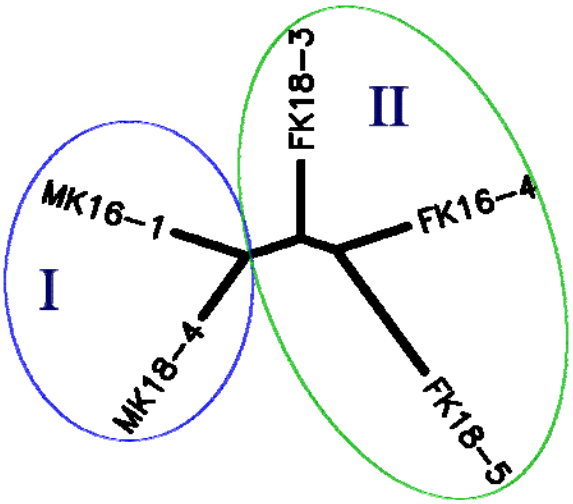


Figure 94. SSR UPGMA tree based on Nei (1972) genetic distance for *P. khinjuk* according to each collected site.

Principle component analysis (PCA) confirms clearly the same two groups, first group for the females but one sample is not included and the second for the males (Figure 95).

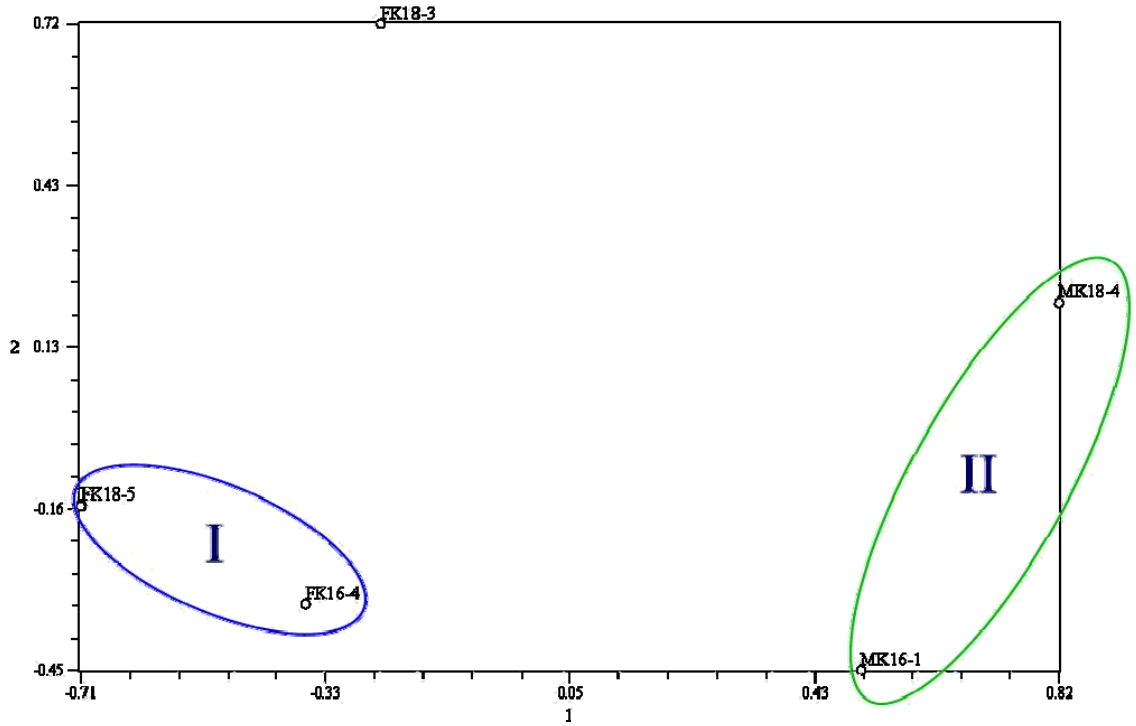


Figure 95. Principle component analysis for *P. khinjuk* based on SSR data.

3.3.5.4. All markers

Figure 96 shows the genetic relatedness among the genotypes investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance based on the three molecular marker techniques together. Two groups are obtained in this analysis (Annex 3 – Table36):

I. Group one: contains all female individuals Syria;

II. Group two: contains all male individuals from Syria.

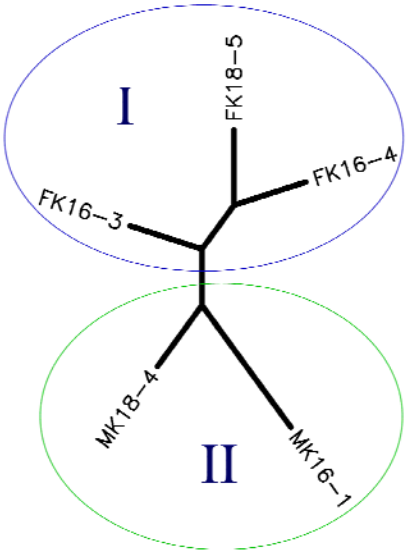


Figure 96. Three marker techniques UPGMA tree based on Nei (1972) genetic distance for *P. khinjuk* according to each collected site.

Table 31 shows the correlation between the three different techniques based on Mantel test with 1000 permutations. The AFLP and ISSR techniques are not significantly correlated (r = 0.28) and the AFLP and SSR techniques are not significantly correlated (r = 0.23). Also the SSR and ISSR techniques are significantly correlated (r = 0.78).

3.3.6. *Pistacia lentiscus*

The same 22 wild *P. lentiscus* genotypes were analyzed using three molecular marker techniques from three countries Syria, Turkey and Italy. The results can be summarized as follows:

3.3.6.1. Amplified Fragment Length Polymorphism (AFLP)

Figure 56 shows an example of one primer pair combination. A total 217 polymorphic bands were generated by 4 primer pair combinations. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table37). Three groups are obtained in this analysis (Table 30, Figure 97):

I. Group one: contains all female individuals from Turkey and Italy;
II. Group two: contains all male individuals from Turkey and Italy;
III. Group three: contains all male and female individuals from Syria.

Table 30. The countries, site numbers and site names of collected *P. lentiscus* sites.

Country	Site No.	Site name
Syria	21	Al Mehwiye
Turkey	40	Adana 2
Italy	54	Bronte 8

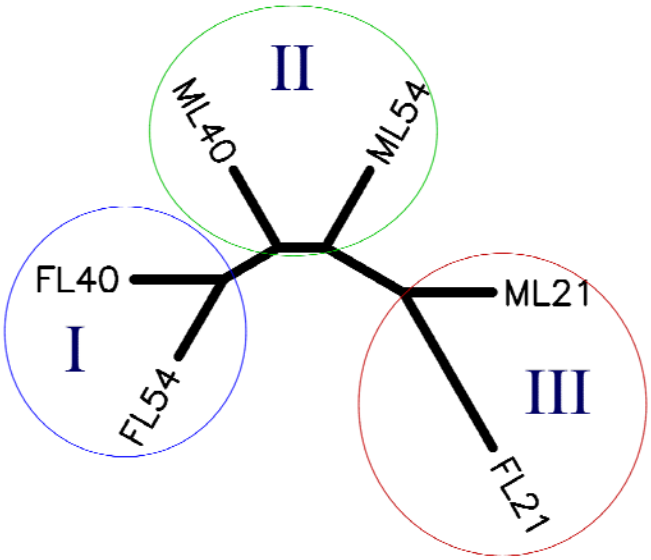


Figure 97. AFLP Unrooted tree based on Nei (1972) genetic distance for *P. lentiscus* according to each collected site.

Principle component analysis (PCA) confirms clearly the three main groups (Figure98):

I. Group one: contains male and female individuals from Syria;

II. Group two: contains male and female individuals from Turkey;

III. Group three: contains male and female individuals from Italy.

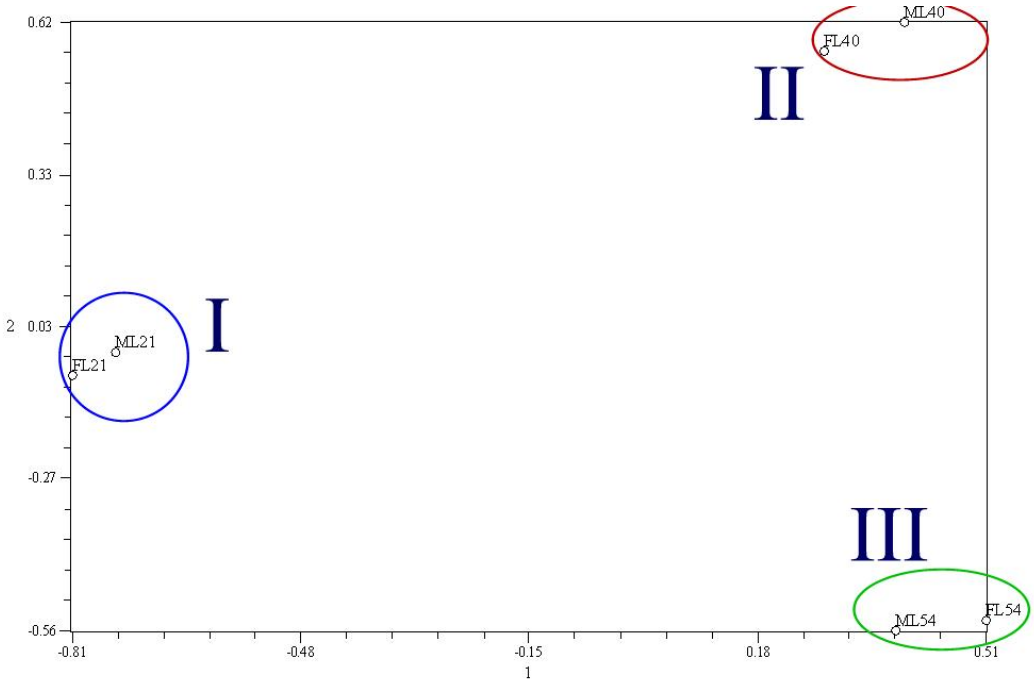


Figure 98. Principle component analysis for *P. lentiscus* based on AFLP data.

3.3.6.2. Inter Simple Sequence Repeats (ISSR)

Figure 60 shows an example of one ISSR primer. A total 255 polymorphic bands were generated by 6 primers. A binary matrix is created contains 22 rows representing the genotypes and 255 columns representing the polymorphic loci. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table 38). Three groups are obtained in this analysis (Table 30, Figure 99):

I. Group one: contains all male and female individuals from Italy;

II. Group two: contains all male and female individuals from Turkey;

III. Group thee: contains all male and female individuals from Syria.

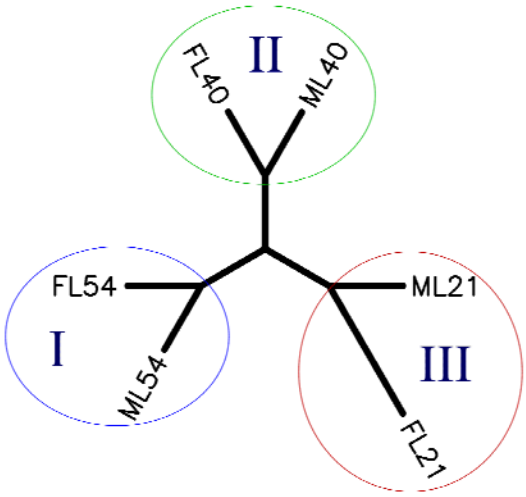


Figure 99. ISSR Unrooted tree based on Nei (1972) genetic distance for *P. lentiscus* according to each collected site.

Principle component analysis (PCA) confirms clearly the three main groups (Figure100):

I. Group one: contains male and female individuals from Italy;

II. Group two: contains male and female individuals from Turkey;

III. Group three: contains male and female individuals from Syria.

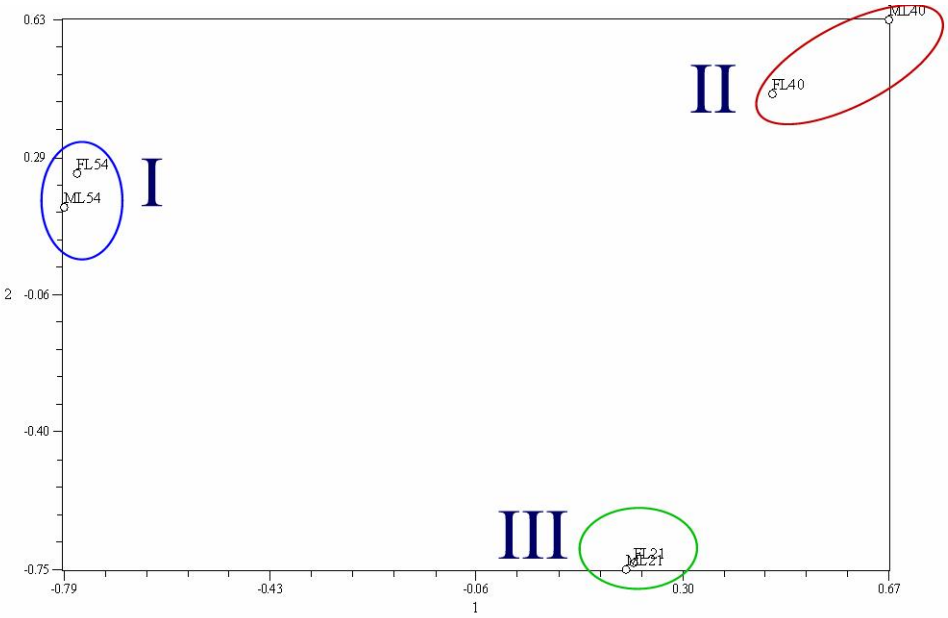


Figure 100. Principle component analysis for *P. lentiscus* based on ISSR data.

3.3.6.3. Microsatellites, Simple Sequence Repeats (SSRs)

Table 25 shows the primers' names and number of alleles studied in *P. lentiscus* also the allele size. The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance (Annex 3 – Table 39). Three groups are obtained in this analysis (Table 30, Figure 101):

I. Group one: contains all male and female individuals from Italy;

II. Group two: contains all male and female individuals from Turkey;

III. Group thee: contains all male and female individuals from Syria.

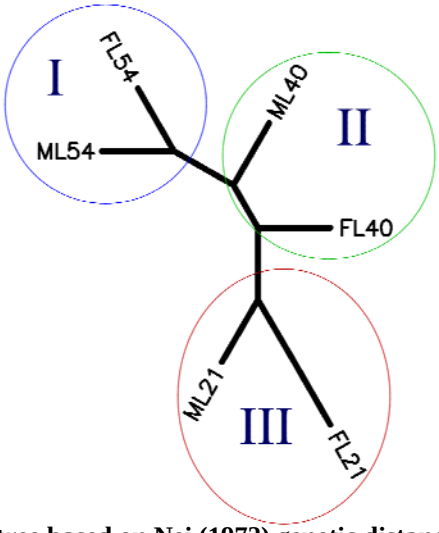


Figure 101. SSR UPGMA tree based on Nei (1972) genetic distance for *P. lentiscus* according to each collected site.

Principle component analysis (PCA) confirms clearly the three main groups (Figure 102):

I. Group one: contains male and female individuals from Syria;

II. Group two: contains male and female individuals from Turkey;

III. Group three: contains male and female individuals from Italy.

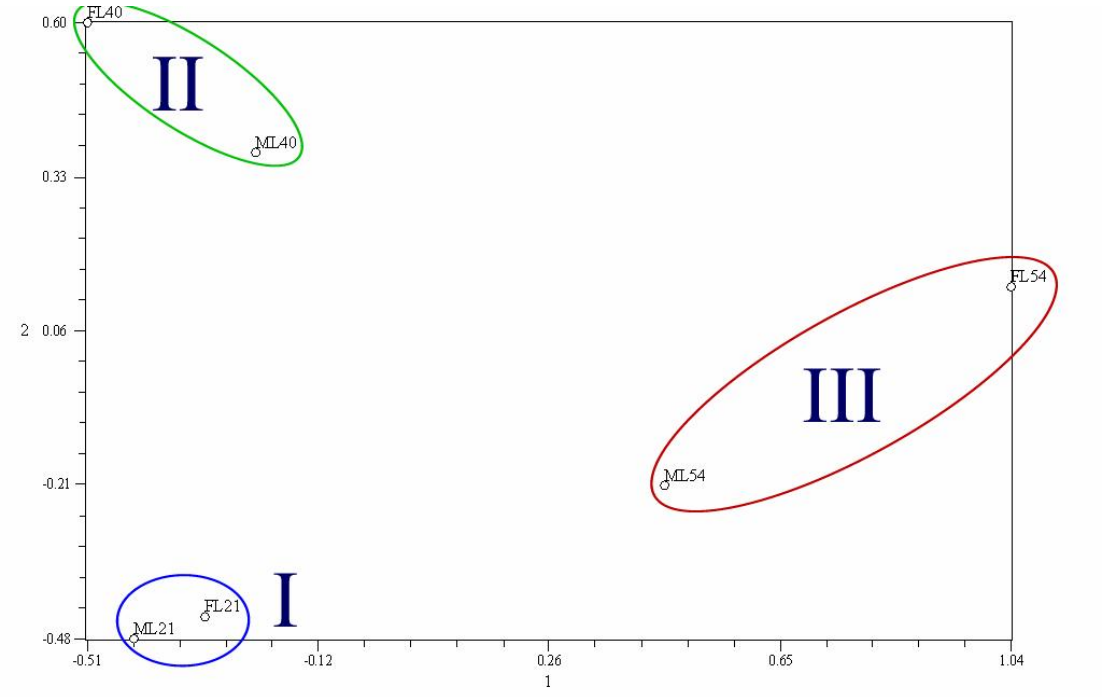


Figure 102. Principle component analysis for *P. lentiscus* based on ssr data.

3.3.6.4. All markers

Figure 103 shows the genetic relatedness among the genotypes investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance based on the three molecular marker techniques together. Three groups are obtained in this analysis (Annex 3 – Table40):

I. Group one: contains all female individuals from Turkey and Italy;

II. Group two: contains all male individuals from Turkey and Italy;

III. Group three: contains all male and female individuals from Syria.

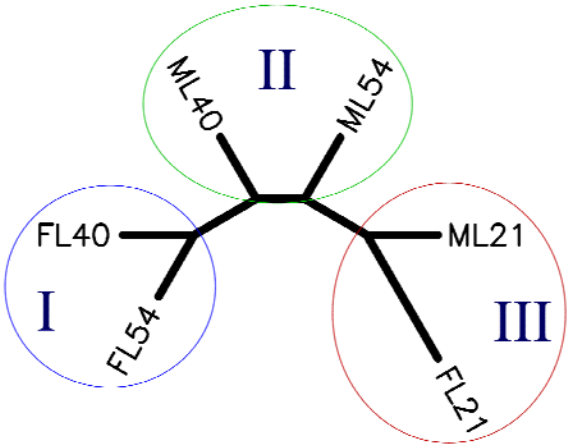


Figure 103. Three marker techniques UPGMA tree based on Nei (1972) genetic distance for *P. lentiscus* according to each collected site.

Table 31 shows the correlation between the three different techniques based on Mantel test with 1000 permutations. The AFLP and ISSR techniques are significantly correlated (r = 0.85). On the other hand, the AFLP and SSR techniques are highly significant correlated (r = 0.66). Also the SSR and ISSR techniques are highly significant correlated (r = 0.78).

3.3.7. *Pistacia* spp.

Frequencies of each studied *Pistacia* species were calculated for each molecular marker binary code matrix and the genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance.

3.3.7.1. Amplified Fragment Length Polymorphism (AFLP)

The genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance based on AFLP technique (Figure 104). Two groups are obtained in this analysis (Annex 3 – Table 41):

I. Group one: contains three species *P. atlantica* and *P. vera* (wild and cultivated) and *P. khinjuk* and this group can be divided into two subgroups:
   a. Subgroup Ia: contains two species which are *P. atlantica* and cultivated *P. vera*;
   b. Subgroup Ib: contains two species which are *P. khinjuk* and wild *P. vera*

II. Group two: contains three species *P. palaestina*, *P. terebinthus* and *P. lentiscus*.

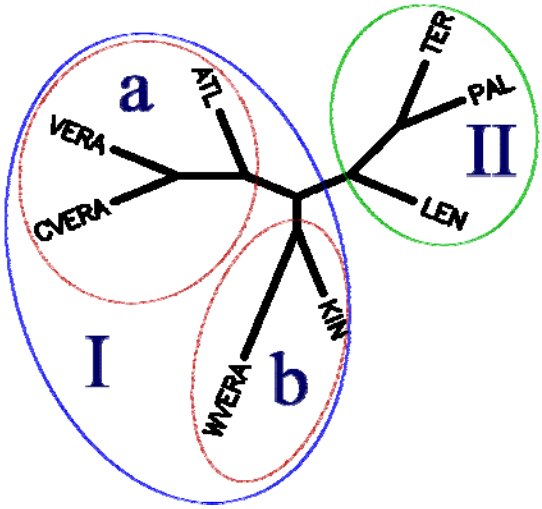


Figure 104. AFLP UPGMA Unrooted tree based on Nei (1972) genetic distance for *Pistacia* spp.

Principle component analysis (PCA) confirms clearly the three main groups while *P. lentiscus* is not clustered (Figure 105):

I. Group one: contains *P. atlantica* and *P. khinjuk*;

II. Group two: contains wild and cultivated *P. vera*;

III. Group three: contains *P. palaestina* and *P. terebinthus*.

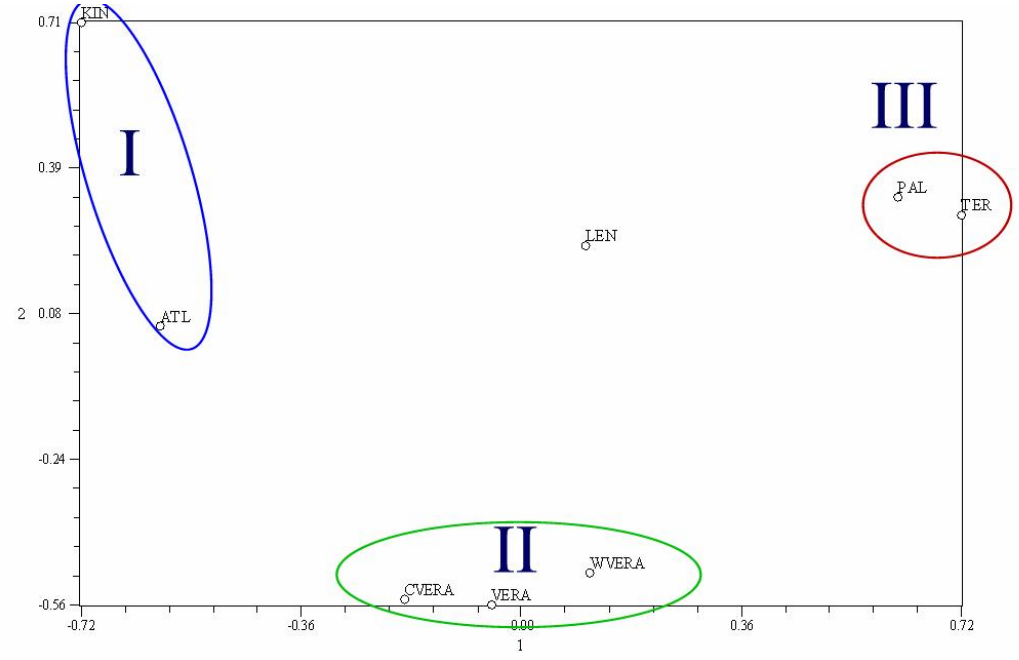


Figure 105. Principle component analysis for *Pistacia* based on AFLP data.

3.3.7.2. Inter Simple Sequence Repeats (ISSR)

Figure 106 shows the genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's genetic distance based on the ISSR techniques. Two groups are obtained in this analysis, while *P. khinjuk* and *P. atlantica* are not clustered with any group (Annex 3 – Table 42):

I. Group one: contains three species *P. palaestina, P. terebinthus* and *P. lentiscus*;

II. Group two: contains wild and cultivated *P. vera.*

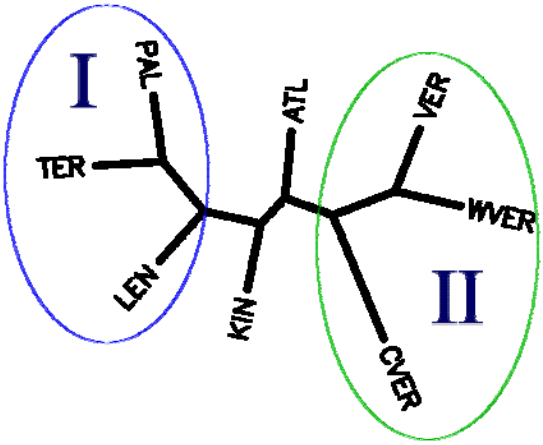


Figure 106. ISSR UPGMA Unrooted tree based on Nei (1972) genetic distance for *Pistacia* spp.

Principle component analysis (PCA) confirms clearly the three main groups while *P. lentiscus* do not clustered (Figure 107):

I. Group one: contains *P. palaestina* and *P. terebinthus*;

II. Group two: contains *P. atlantica* and *P. khinjuk*;

III. Group three: contains wild and cultivated *P. vera*.

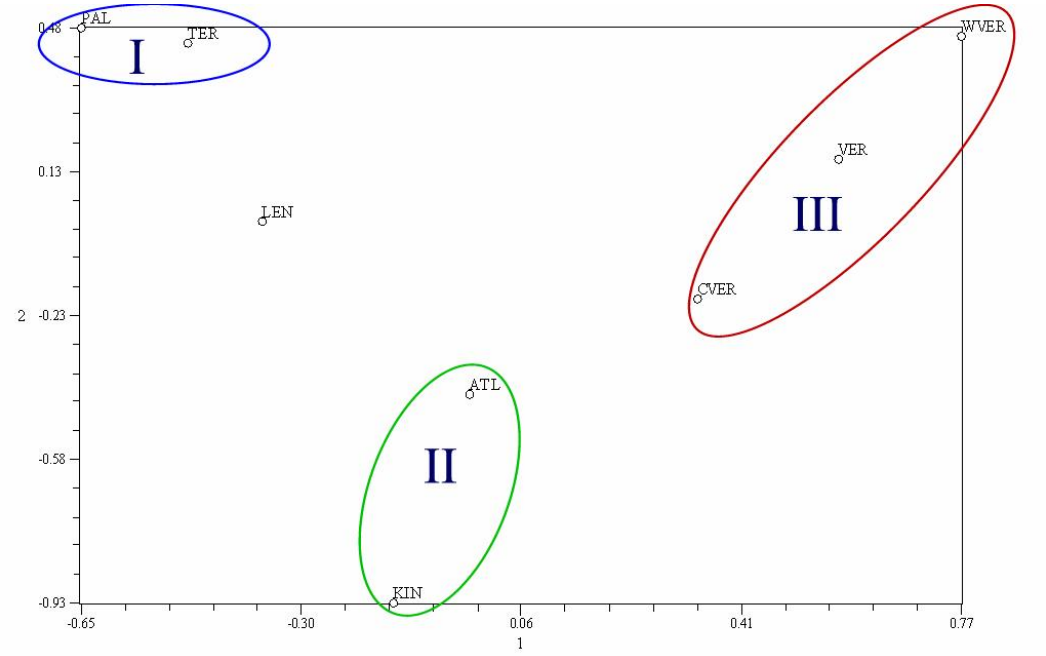


Figure 107. Principle component analysis for *Pistacia* based on ISSR data.

3.3.7.3. Microsatellites, Simple Sequence Repeats (SSRs)

Figure 108 shows the genetic relatedness among the genotypes was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance based on the SSR

techniques. Three groups are obtained in this analysis, while *P. lentiscus* are not clustered with any group (Annex 3 – Table 43):

I. Group one: contains two species *P. khinjuk* and *P. atlantica*;

II. Group two: contains two species *P. palaestina* and *P. terebinthus*;

III. Group three: contains wild and cultivated *P. vera.*

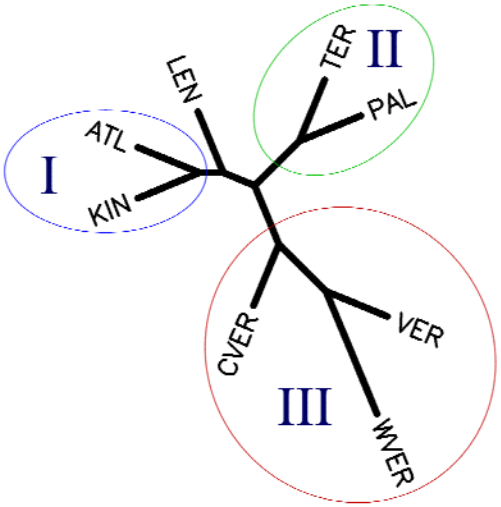


Figure 108. SSR UPGMA Unrooted tree based on Nei (1972) genetic distance for *Pistacia* spp.

Principle component analysis (PCA) confirms clearly the three main groups while *P. lentiscus* is not clustered (Figure 109):

I. Group one: contains wild and cultivated *P. vera*;

II. Group two: contains *P. atlantica* and *P. khinjuk*;

III. Group three: contains *P. palaestina* and *P. terebinthus*.

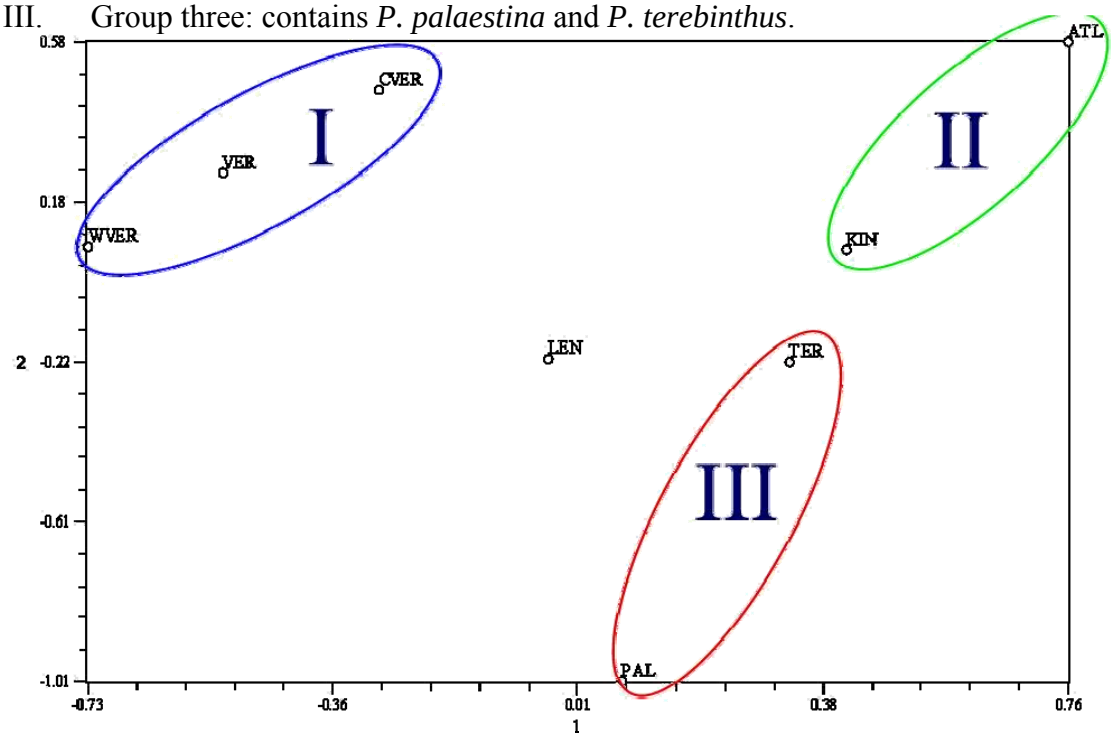


Figure 109. Principle component analysis for *Pistacia* based on ISSR data.

3.3.7.4. All markers

Figure 110 shows the genetic relatedness among the *Pistacia* which was investigated by UPGMA cluster analysis based on Nei's (1972) genetic distance based on the three molecular marker techniques together. Two groups are obtained in this analysis (Annex 3 – Table 44):

I. Group one: contains three species contains three species *P. palaestina, P. terebinthus* and *P. lentiscus*;
II. Group two: *P. atlantica* and *P. vera* (wild and cultivated) and *P. khinjuk* and this group can be divided into two subgroups:
    a. Subgroup Ia: contains two species which are *P. khinjuk* and wild *P. vera*;
    b. Subgroup Ib: contains two species which are *P. atlantica* and cultivated *P. vera*.

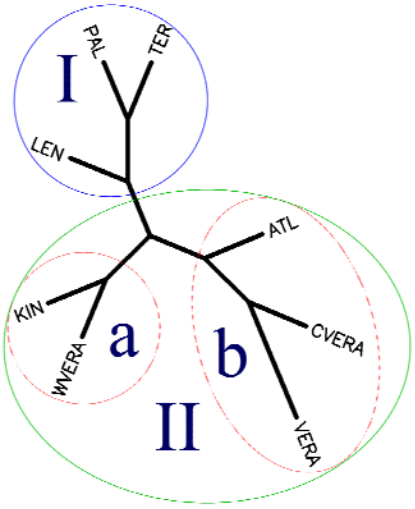


Figure 110. Three marker techniques UPGMA tree based on Nei (1972) genetic distance for *Pistacia* spp.

Table 31 shows the correlation between the three different techniques based on Mantel test with 1000 permutations. The correlation between the AFLP and ISSR techniques are very highly significant correlated (r = 0.89). Also between the AFLP – ISSR techniques (r = 0.69) and AFLP – SSR techniques (r = 0.67) are highly significant correlated.

Table 31. Correlation value between the three different techniques based on Mantel test for each species

Species	Molecular marker technique	AFLP		ISSR		SSR	
		r	P	r	P	r	P
P. vera	**AFLP**	**-**	**-**				
	ISSR	**0.61****	**0.00**	**-**	**-**		
	SSR	**0.35****	**0.00**	**0.44****	**0.00**	**-**	**-**
P. atlantica	**AFLP**	**-**	**-**				
	ISSR	**0.68****	**0.00**	**-**	**-**		
	SSR	**0.22****	**0.01**	**0.09**	**0.1**	**-**	**-**
P. palaestina	**AFLP**	**-**	**-**				
	ISSR	**0.73****	**0.00**	**-**	**-**		
	SSR	**0.38****	**0.00**	**0.28****	**0.00**	**-**	**-**
P. terebinthus	**AFLP**	**-**	**-**				
	ISSR	**0.60****	**0.00**	**-**	**-**		
	SSR	**0.64****	**0.00**	**0.70***	**0.04**	**-**	**-**
P. khinjuk	**AFLP**	**-**	**-**				
	ISSR	**0.28**	**0.2**	**-**	**-**		
	SSR	**0.23**	**0.2**	**0.78**	**0.06**	**-**	**-**
P. lentiscus	**AFLP**	**-**	**-**				
	ISSR	**0.85***	**0.02**	**-**	**-**		
	SSR	**0.66****	**0.01**	**0.72****	**0.00**	**-**	**-**
Pistacia	**AFLP**	**-**	**-**				
	ISSR	**0.89****	**0.00**	**-**	**-**		
	SSR	**0.69****	**0.00**	**0.67****	**0.00**	**-**	**-**

** Highly significant correlation at P ≤0.01
* Significant correlation at P ≤0.05

3.4. Molecular marker versus ecogeographic and morphological data

The climatic data were used to form a matrix contains all distributed sites for each species and the dissimilarity between the climatic characters for each site were calculated and compared with the molecular dissimilarity matrixes obtained from each molecular marker for each species. Table 32 shows the correlation between the climatic data and the molecular variation of each species based on Mantel test with 1000 permutations. The results can be summarized as follows:

1. ***P. vera*****:** All used molecular markers show highly significant correlation with the climatic data for each studied site where the samples are collected;
2. ***P. atlantica*****:** All used molecular markers show significant correlation with the climatic data for each studied site. r value ranges between 0.37-0.53;
3. ***P. palaestina*****:** The AFLP and ISSR molecular markers show highly significant correlation with the climatic data for each studied site. r value is 0.39 for AFLP and 0.52 for ISSR On the other hand SSR molecular marker is not correlated;
4. ***P. terebinthus*****:** The AFLP and ISSR molecular markers show correlation with the climatic data for each studied site but not significant. r value is 0.25 for AFLP and

0.74 for ISSR. On the other hand SSR molecular marker is significant correlation with the climatic data r =0.67.

5. ***P. khinjuk*:** All used molecular markers show good correlation with the climatic data for each studied site but not significant. r value ranges between 0.47-0.54;
6. ***P. lentiscus*:** All used molecular markers show good correlation with the climatic data for each studied site but not significant. r value ranges between 0.45 - 0.52.

The quantitive morphological characters of leaves were also compared with the molecular markers data for male and female groups in the each site. The correlation between the three different techniques based on Mantel test with 1000 permutations (Table 32). The results show that there are no correlations between the leaves and leaflets dimensions and any of the used molecular marker techniques.

Also quantitive morphological characters of nuts were compared with the molecular markers data for female groups in the each site. The correlation between the three different techniques based on Mantel test with 1000 permutations (Table 32). The results show that there are no correlations between the nuts dimensions and any of the used molecular marker techniques, except in the case of SSR technique and the nut dimensions in *P. palaestina* and *P. terebinthus* which are significantly correlated (r =0.46).

Table 32. The correlation value between the molecular marker techniques and the climatic data and morphological characters

Species	Molecular marker technique	Climatic characters		Leaves characters		Nuts characters	
		r	P	r	P	r	P
P. vera	AFLP	0.48**	0.00	0.012	0.48	0.38	0.14
	ISSR	0.58**	0.00	0.05	0.4	0.19	0.30
	SSR	0.5**	0.00	-0.06	0.3	0.30	0.14
P. atlantica	AFLP	0.38*	0.02	0.13	0.09	-0.02	0.48
	ISSR	0.37*	0.03	0.06	0.19	-0.02	0.45
	SSR	0.53*	0.02	0.05	0.30	-0.08	0.31
P. palaestina	AFLP	0.39**	0.00	0.03	0.31	0.05	0.29
	ISSR	0.52**	0.00	0.02	0.42	-0.2	0.1
	SSR	-0.2	0.4	0.03	0.37	0.46*	0.02
P. terebinthus	AFLP	0.25	0.35	-0.43	0.06	0.05	0.29
	ISSR	0.74	0.08	-0.13	0.3	-0.2	0.1
	SSR	0.67*	0.04	-0.18	0.25	0.46*	0.02
P. khinjuk	AFLP	0.47	0.07	0.01	0.45	0.19	0.2
	ISSR	0.5	0.06	0.04	0.35	0.46	0.16
	SSR	0.54	0.06	0.03	0.37	0.41	0.08
P. lentiscus	AFLP	0.45	0.07	0.17	0.18	0.20	0.2
	ISSR	0.52	0.06	0.01	0.21	0.45	0.16
	SSR	0.50	0.06	0.13	0.33	0.39	0.08

** Highly significant correlation at P ≤0.01

* Significant correlation at P ≤0.05

4. Chapter four: Discussion

4.1 Ecogeographic survey

Even if 54 different sites were selected in several countries such as Syria, Tajikistan, Uzbekistan, Turkey and Italy, which represent the area of distribution of the wild and cultivated *Pistacia*, this study was focused mainly on Syria and Tajikistan. In fact, these countries have different aspects in term of *Pistacia* distribution. In Syria there is no presence of wild *Pistacia vera*, but it is the third or fourth world leading pistachio countries (FAO, 2006). Moreover, some of other *Pistacia* species, such as *P. atlantica*, *P. palaestina*, *P. terebinthus*, *P. khinjuk* and *P. lentiscus*, are wildly distributed in Syria (Post, 1932; Khalife, 1958; Mouterde, 1966). On the other hand, in Central Asia and Tajikistan there are pure stands of *Pistacia vera* which are not yet studied in any of the other *Pistacia* programs (Kayimov *et al.*, 1998). Turkey and Italy were included into this study to obtain some samples to be compared either with the Syrian wild *Pistacia* spices, which have minor distribution like *P. terebinthus* and *P. lentiscus*, or with cultivated and wild pistachio. All the sites have been selected in accord with the literature review. Regular visits were paid to each site in order to identify the populations' distribution. The Geographical Positioning System (GPS) was used to have the accurate position of each population and several distribution and soil maps were created.

The *Pistacia* genus was found in different climatic areas. Cultivated *P. vera*, *P. atlantica* and *P. khinjuk* were found in arid and semi-arid Syrian sites with mean annual rainfall ranging between 191 and 417 mm, as previously mentioned by (Zohary, 1996), whereas *P. palaestina*, *P. terebinthus* and *P. lentiscus* were found in sub humid and humid Syrian sites with mean annual rainfall ranging between 457 and 1280 mm. While the Turkish and Italian sites were located in sub humid sites and contains cultivated *P. vera*, *P. atlantica*, *P. terebinthus* and *P. lentiscus* with mean annual rainfall ranging between 500 and 752 mm. On the other hand, the wild *Pistacia vera* were found in Central Asia semi arid and sub humid zones with mean annual rainfall ranging between 368 and 619 mm. These results indicate that pistachio is a drought resistant tree and flourishing in arid and semi-arid zones. Herrera (1997) mentioned that pistachio is a xerophytic tree; nevertheless good economical production need to provide enough soil humidity during end of winter, spring and early summer, to cover the water demand of the vegetative growth and formation of the inflorescence bud for the next year. Mielke & True (1979) reported that good pistachio fruiting require between 150-500 mm of annual rainfall.

Evidences indicated that a long time ago *Pistacia atlantica* were grown in large parts of Syria (Nahal, 1996b), nowadays, it can only be found in small patches or in isolated areas and it is actually threatened in most of these areas (Zohary, 1973; Nahal, 1996a-b-c). Also Zohary (1996) reported that *Pistacia khinjuk* is associated species to *Pistacia atlantica* in southwest Asia but Sankary (1981) mention that the presence of *P. khinjuk* in Syria is rare and localize in Northeast of Syria. These information agreed with the results of this study and a few individuals were found in Abdel Aziz Mountain.

Pistacia terebinthus and *Pistacia palaestina* are close relatives and Engler (1883) considered *P. palaestina* as a variety of *P. terebinthus*. On the other hand, *P. terebinthus* is native to central and western parts of the Mediterranean, while *P. palaestina* is native to eastern part of the Mediterranean and some European countries such as Greece, Turkey (Mazzola *et al*., 1996; Zohary, 1996; Atli *et al.*, 2001a,b; Batlle *et al.,* 2001; Zakynthinos & Rouskas, 2001). The results of present study confirmed that *P. terebinthus* were found in one site near the Turkish border while a wider distribution of *P. palaestina* is in Syria. These two species were distributed in sub-humid and humid zones in Syria, while only *P. terebinthus* was distributed in sub-humid zones in Turkey and Italy.

Pistacia lentiscus is evergreen shrub wildly present in Syria and found in the costal sub-humid zones, also this species was found in Sicily (Italy) and Turkey. These results agreed with previous reports and flora (Gussone, 1844; Post, 1932; Mouterde, 1966).

According to the results of present soil survey study, *Pistacia* species were found in a wide range of soils, but especially in those very shallow, moderately developed, non-acid with clay-enriched subsoil, and also on no significant soil profile development or poorly developed soils of semi-deserts. Most of the studied sites are stony soils. The slope were varying between level to gently undulating <8% and steeply dissected to mountainous >30%. These results agree with several authors who describe the soils of Pistacia species. Such as Hendricks & Ferguson (1995), Herrera (1997) and Rieger (2002) who emphasized that successful pistachio cultivation can be reached in most soil types even poor marginal soils. Also Anwar & Rabbani (2001) mentioned that *P. atlantica* grows in dry rocky lands in Pakistan. Talhouk *et al.*, (2001) found this species in Lebanon limited to the region of Arsal which is a semi arid highland and have a severe desertification and soil erosion problems. Khaldi & Khoudja (1996) and El-Ghawawi (2001) have reported that wild *Pistacia* species are particularly resistant to drought and tolerant to poor soils and *P. atlantica* is a good rootstock for pistachio varieties. *P. terebinthus* can grow in the stony

and calcareous soil of the dry areas which penetrate deeply in the soil through even rock cracks (Atli *et al.*, 2001b).

4.2. Morphological characterization

4.2.1. *Pistacia vera*

The Morphological characterization results showed differences among the individuals and populations of wild studied *P. vera* and the male varieties. The results about plant descriptor characters, for wild pistachio, showed that individuals were ranked between low vigor growth and high vigor growth; moreover most of the wild individuals branched from the base, while the cultivated ones have a single trunk, with the branching habit ranging between sparse and dense. Ibrahim Basha *et al*. (2003) obtained similar results in Syrian varieties but the tree vigor ranged between intermediate and high vigor due to agricultural services applied in the orchards.

The leaf and leaflet dimensions, shapes and apex were characterized and showed significant and highly significant difference. The average leaf length ranged between 6.60 and 21.00 cm and the leaf width ranged between 4.2 and 21 cm. While the leaflet length ranged between 3.5 and 15 cm and the leaflet width ranged between 2.60 and 11 cm. the dominant number of leaflets which were 3 or 5 leaflets. The terminal leaflets sizes were found similar or larger than basal leaflets. The terminal leaflets were found in several shapes and apexes. Nut dimensions were also measured and showed highly significant difference in size. Nut length ranged between 15.77 and 28.28 mm. Nut width ranged between 8.43 and 15.33 mm and the average thickness ranged between 7.56 and 14.49 mm. On the other hand, most of the wild nut shapes were either elongate or narrowly cordate. Almost similar ranges of dimensions were reported by Zohary (1996), Hadj-Hassan (2001), and Kayimov (2001).

4.2.2. *Pistacia atlantica*

The Morphological characterization results showed differences among the individuals and population of *P. atlantica* in Syria. The plant growth vigor ranged between low and high vigor growth tree. These trees were either branched form base or had single trunk, while the branching habit ranged between sparse and dense. These differences were due to environmental and soil conditions for each population as demonstrated by Sankary (1981) and Nahal (1995).

The leaf and leaflet dimensions, shapes and apex were characterized and showed highly significant difference. The average leaf length ranged between 6.00 and 22.5 cm and the leaf width ranged between 5.5 and 23 cm. While the leaflet length ranged between 2.8 and 12.5 cm, and the leaflet width ranged between 1 and 6.3 cm. The dominant number of leaflets ranged between 3 and 11 leaflets. The terminal leaflets were found in several shapes and apexes. Nut dimensions were also measured and showed significant difference in size. These results agreed with those of Kafkas *et al.* (2002) in his survey of wild *Pistacia* in Turkey. Nut length ranged between 5.8 and 9 mm. Nut width ranged between 5 and 7.8 mm and the average thickness ranged between 3.4 and 7.3 mm. On the other hand, most of the nut shapes were globular or obovoid globular. Atli *et al.* (2001a) reported similar nut dimension in Turkey populations.

4.2.3. *Pistacia palaestina*

The morphological characterization results showed differences among the individuals and populations of *P. palaestina* in Syria. The plant growth vigor ranged between low and high vigor growth tree. Most of these trees were branched from base, while the branching habit ranged between sparse and dense. These differences were probably due to environmental and soil conditions for each population rather than genetically determined as indicated by (Hadj Ibrahim *et al*., 1998; Nahal *et al*., 1995).

The terminal leaflet of this species is very small or absent but have 4-6 pairs of basal leaflets. The leaf dimensions showed highly significant difference between populations. The average leaf length ranged between 7.1 and 21.3 cm and the leaf width ranged between 5.5 and 21.6 cm. Nut dimensions were also measured and showed significant difference between populations in size. Nut length ranged between 4.2 and 5.9 mm. Nut width ranged between 3.8 and 5.6 mm and the average thickness ranged between 3.04 and 4.5 mm. On the other hand, most of the nut shapes were globular or obovoid globular. Atli *et al.* (2001a) reported same nut dimension of nuts in Turkey. Also Zohary mentioned (1996) general information about *P. palaestina* characters which agreed with our results.

4.2.4. *Pistacia terebinthus*

The Morphological characterization data showed differences among the individuals and populations of *P. terebinthus* in Syria, Turkey and Italy. The plant growth vigor ranged between low and intermediate vigor growth tree. These trees were branched form base,

while the branching habit ranged between sparse and intermediate. These differences due to environmental and soil conditions for each population.

The leaf and leaflet dimensions, shapes and apex were characterized and showed highly significant difference. The average leaf length ranged between 9.7 and 21.5 cm and the leaf width ranged between 7.9 and 15.5 cm. While the leaflet length ranged between 1.1 and 6 cm and the leaflet width ranged between 0.3 and 3.2 cm. The dominant number of leaflets ranged between 5 and 11 leaflets. The terminal leaflets were found in several shapes and apexes. Nut dimensions were also measured and showed no significant difference between populations in size. These results agreed with those of Kafkas *et al.* (2002) in his survey of wild *Pistacia* in Turkey. Nut length ranged between 5.67 and 7.1mm. Nut width ranged between 4.3 and 6.8mm and the average thickness ranged between 3.3 and 5.3 mm. On the other hand, most of the nut shapes were obovoid globular. Atli *et al.* (2001b) reported similar nut dimension of nuts in Turkey.

4.2.5. *Pistacia khinjuk*

The Morphological characterization results showed differences among the individuals and populations of *P. khinjuk* in Syria. The plant growth vigor ranged between intermediate and high vigor growth tree. These trees were branched form base, while the branching habit ranged between intermediate and dense. These differences due to environmental and soil conditions for each population.

The leaf and leaflet dimensions, shapes and apex were characterized and showed no significant difference between populations. The average leaf length ranged between 12.1 and 16.2 cm and the leaf width ranged between 9 and 17 cm. While the leaflet length ranged between 5 and 8.6 cm and the leaflet width ranged between 3.2 and 5 cm. The dominant number of leaflets ranged between 5 and 7 leaflets. The terminal leaflets were found in several shapes and apexes. Nut dimensions were also measured and showed no significant difference between populations in size. Nut length ranged between 8.9 and 10.6 mm. Nut width ranged between 8.6 and 9.7 mm and the average thickness ranged between 5.64 and 6.5 mm. On the other hand, most of the nut shapes were globular or obovoid globular. Atli *et al.* (2001a) reported larger nut dimension of nuts in Turkey but Zohary (1996) mentioned smaller nut dimensions, on other hand the leaflets dimensions obtained in this study agreed with those described by Zohary (1996).

4.2.6. *Pistacia lentiscus*

The Morphological characterization results showed differences among the individuals and populations of *P. lentiscus* in Syria. The plant growth vigor ranged between intermediate and high vigor growth shrub. These shrubs were branched form base, while the branching habit can be classified as dense. These differences are due to environmental and soil conditions.

The terminal leaflet of this species is absent but has 4-6 pairs of basal leaflets. The leaf dimensions showed highly significant differences between populations. The average leaf length ranged between 2.5 and 12.6 cm and the leaf width ranged between 4.2 and 7.8 cm. Nut dimensions were also measured and showed no significant difference in size. Nut length ranged between 1.9 and 3.38 mm. Nut width ranged between 1.33 and 3.38 mm and the average thickness ranged between 1.02 and 1.9 mm. On the other hand, most of the nut shapes were obovoid globular. Atli *et al.* (2001a) and Zohary (1996) reported similar leaf and nut dimensions.

4.3. Molecular markers

A total 217 polymorphic bands AFLP were generated by 4 primer pair combinations using AFLP technique. As well as 255 polymorphic bands were generated by 6 ISSR primers This large number of polymorphic bands proved that the primer combinations were successfully chosen, this result agree with Hartl and Seefelder (1998) that mentioned the AFLP techniques as helpfully generating a large number of polymorphic bands.

The SSR alleles have almost in the same size found by Ahmad *et al*. (2003). Even if in our case the alleles has a wider range than pervious mentioned reference, maybe due to the higher number of studied species in this study. It should be underlined that the markers used were designed for just *P. vera*.

4.3.1. *Pistacia vera*

The genetic relatedness among the genotypes was investigated using AFLP data which clustered the populations into four groups (see paragraph 3.4.1.1). The obtained clusters shown that some of the wild *Pistacia vera* individuals from Central Asia were distributed all over the groups. AFLP data prove that there is wide variation between the females in the Syrian gene banks; therefore several field gene banks located in different sites and in several countries, insure the conservation of a wide range of variation. On the other hand, the relatedness among the collected genotypes, according to their country of origin, divided the accessions into three major groups. The first group contains Syrian and Turkish

varieties, due to the fact that Turkey and Syria are a neighbor countries and the pistachio cultivation is flourish in north of Syria and Southeast of Turkey (Ibrahim Basha *et al.*, 2003). Not surprising, the Italian varieties grouped together in separate group and the third group contains the Iranian and Central Asia individuals. Hence, the genetic and the geographic distances were in agreement. On the other hand, the principle component analysis (PCA) of the molecular data clearly grouped the Syrian varieties in one group, the Turkish and Iranian varieties with the Central Asia individuals together, and a third group contains Italian and Syrian varieties. This is probably due to the fact that pistachio was introduced into Italy in 30 A.D. by Romans from Syria, according to Mina Palumbo (1882) or during the Arab occupation in 9^{th} and 10^{th} centuries (Fabbri & Valenti, 1997). Similar results were suggested by Kafkas *et al*., (2006) that found the Syrian and Italian varieties grouped together in a molecular investigation of several pistachio varieties.

The ISSR data, used to find genetic relatedness among the genotypes and varieties, clustered the samples into five groups (see paragraph 3.4.1.2). Also this technique discriminated the individuals according to their country of origin and put the Turkish and Iranian varieties into the same group and the Syrian, Italian and Central Asia each one in a separate group. On other hand, the principle component analysis (PCA) confirmed clearly the existence of just three main groups in which Central Asia, Turkish and Iranian have one group, but The Syrian and Italian were separated in two different groups.

On the other hand, the SSR data clustered the genotypes and varieties into five groups according to their genetic relatedness (see paragraph 3.4.1.3). All the male individuals are grouped together while the females are divided into four groups. Looking to the country of origin, the female group could be divided in two subgroups: (a) contain Syria, Iran, Turkey, (b) Central Asia and Italy. While the principle component analysis (PCA) confirmed clearly three main groups, first group contains female individuals from Central Asia, the second group contains female varieties from Syria and Italy, and the third group contains mainly males from all different sites and some females from Syria and Iran.

The genetic relatedness among the genotypes and varieties detected by analyzing the data obtained from all the three techniques together clustered the genotypes into five groups (see paragraph 3.4.1.4). While the genetic relatedness among the genotypes and varieties according to their origin country has got two groups, the first group has Turkish, Syrian and Italian varieties and the second group has Iranian varieties and Central Asia wild individuals.

The correlations between the three different techniques have shown a highly significant consistence between the different markers typology ranged between 0.35 and 0.66. Similar results, of high significant correlation between the results obtained with different molecular techniques, were found on pistachio varieties detected either with RAPD, AFLP or ISSR (Kafkas, 2006).

The results showed that all the three marker systems were able to reveal variability between pistachio varieties and the genotypes. This result agreed with several pervious studies on pistachio. Hence, the choice of a molecular marker typology could depend only by personal preferences, i.e. financial point or laboratories technical availability (Ibrahim Basha *et al.*, 2006; Ahmad *et al*., 2003; Kafkas *et al*., 2006).

4.3.2. *Pistacia atlantica*

The genetic relatedness among the genotypes was investigated using AFLP data and four groups were obtained (see paragraph 3.4.2.1). The first group contains south and some individuals of northeast Syrian populations, the second group included Turkish individuals, while the third and the fourth groups are mainly with northeast and mid of Syria. On the other hand, the principle component analysis (PCA) confirmed clearly the distance between the Turkish *P. atlantica* and three main groups from south, mid and northeast of Syria. The results suggest that AFLP analysis could be used as efficient tools to detect biodiversity differentiation between the populations in *Pistacia atlantica* which is probable due the isolation by geographic distance (Chabane *et al*., 2005). On the other hand, the similarity between some individuals in northeast and mid or between the mid and south of Syria could be explained according to Zohary who reported (1952) that distribution of the *P. atlantica* is more or less continuous from the northern and western of Pakistan to palaestina through out Syria. But due to the degradation of the forest in Syria, which could be estimated 50 per cent in both Jordan and Syria (FAO 2001), over the past 30 years, natural forest areas have been fragmented and isolated; as a resut it turned into a mosaic with agricultural fields in Syria, and with urban dwellings in Lebanon and Syria (World Bank and UNDP 1998, GORS 1991). The *P. atlantica* populations were isolated in deferent ecologies. However, there are some evidences of genetic relatedness between them.

ISSR data clustered the genotypes into five groups according to their genetic relatedness (see paragraph 3.4.2.2). Also the principle component analysis (PCA) confirmed clearly the five main groups. The first group contains the Turkish individuals

and the other four groups included the Syrian ones which were discriminated geographically from Northeast, south and mid of Syria.

The genetic relatedness among the genotypes was investigated using SSR data and clustered into several groups (see paragraph 3.4.2.3), but always males from females in each group were separated. On other hand, the principle component analysis (PCA) confirmed clearly the three main groups:

IV. Group one: contains female individuals from all of Syria and Turkey;
V. Group two: contains almost all male individuals from all of Syria and Turkey;
VI. Group three: contains male individuals from south of Syria (Qanawat and Al-Kafer sites).

The genetic relatedness among the genotypes was investigated also using the data obtain from all the three techniques, in this case the clusters were six and one site (Maaria) did not cluster with any other (see paragraph 3.4.2.4). These results showed the high diversity of *P. atlantica* in Syria which can be considered as one of the centers of origin for this species (Post, 1932; Khalife, 1958; Mouterde, 1966). The AFLP and ISSR techniques and AFLP and SSR techniques have a highly significant correlation but the SSR and ISSR techniques have no significant correlation.

4.3.3. *Pistacia palaestina*

The genetic relatedness among the genotypes was investigated by using AFLP data which cluster them into five groups, but the principle component analysis (PCA) showed just three main groups and separates Wadi Baradah site in one group alone due to the geographic distance and isolation of this site in south of Syria while the other sites were located in north and northwest of Syria (see paragraph 3.4.3.1).

The results of genetic relatedness among the genotypes by using ISSR data showed three groups. As well as the principle component analysis (PCA) has got three main groups. This analysis separates the individuals from South of Syria (Wadi Baradah) alone in one group out of second group (see paragraph 3.4.3.2).

The result of genetic relatedness among the genotypes was investigated also using SSR data which clustered them mainly according to their gender into two groups (see paragraph 3.4.3.3), while the principle component analysis (PCA) grouped the individuals into six groups (4 for females and 2 for males).

The genetic relatedness among the genotypes was investigated also using the data obtain from all the three molecular techniques, which clustered them into six groups (see

paragraph 3.4.3.4). The correlations between the three different techniques were highly significant as well as in *Pistacia atlantica* and *P. vera*. Similar results of highly significant correlation between the AFLP and ISSR were obtained when these techniques applied on grapevine (Fossati *et al.*, 2001).

4.3.4. *Pistacia terebinthus*

The genetic relatedness among the *Pistacia terebinthus* genotypes was investigated using AFLP data, which clustered them into three groups (see paragraph 3.4.4.1). In the first group there were the female individuals from Turkey and Italy, the second group has the males, and the third group has Syrian male and female individuals together. The principle component analysis (PCA) confirmed clearly three main groups according to their country of origin which are Syria, Turkey and Italy.

On the other hand, the genetic relatedness for this species analyzed using ISSR and SSR data discriminates the individuals according to their country of origin which are Syria, Turkey and Italy (see paragraphs 3.4.4.2 – 3.4.4.3). As well as the principle component analysis (PCA) confirmed these results. The correlations between the three different techniques have either significant or high significant correlation.

4.3.5. *Pistacia khinjuk*

The genetic relatedness for this species by using data obtained from three different techniques (i.e. AFLP, ISSR and SSR) discriminates the individuals according to their gender one group for male and one for females, while the principle component analysis (PCA) obtained just one group for the males and the females found very dissimilar from each other (see paragraph 3.4.5). On the other hand, the correlations between the three different techniques were no significant.

4.3.6. *Pistacia lentiscus*

The genetic relatedness among the genotypes was investigated using AFLP data, which clustered them into three groups (see paragraph 3.4.6.1). The first group has female individuals from Turkey and Italy, the second group has the males and the third group has Syrian male and female individuals together. The principle component analysis (PCA) confirmed clearly three main groups according to their country of origin which are Syria, Turkey and Italy.

The genetic relatedness between *Pistacia lentiscus* genotypes, detected using ISSR and SSR data, discriminates the individuals according to their country of origin which are

Syria, Turkey and Italy (see paragraphs 3.4.7.2 – 3.4.7.3), as well as the principle component analysis (PCA). The correlations between the results obtained by the three different techniques were either significant or high significant. The results obtained by AFLP data divided the genotypes into groups according to their gender and geographic origin, while the results obtained with ISSR and SSR divided the genotypes just for the geographic origin, in agreement with the results of Barazani *et al.*, (2003) who studied Mediterranean *P. lentiscus* using RAPD and discriminate his accessions geographically.

4.3.7. *Pistacia* spp.

The genetic relatedness among the *Pistacia* species was investigated using AFLP data which clustered them into two groups (see paragraph 3.4.7.1). The first group contains *P. atlantica* and *P. vera* (wild and cultivated) and *P. khinjuk*, while the second group contains *P. palaestina, P. terebinthus* and *P. lentiscus.* The clusters obtained using ISSR data divided the *Pistacia* species into four groups (see paragraph 3.4.7.2): the first group contains *P. palaestina, P. terebinthus* and *P. lentiscus*, the second group contains wild and cultivated *P. vera*, while the third and the fourth have a single species which was respectively *P. khinjuk* and *P. atlantica*. The genetic relatedness using SSR data grouped the *Pistacia* species into four groups with *P. lentiscus* isolated in a cluster (see paragraph 3.4.7.3).

The principle component analysis (PCA) run utilizing data obtained by each technique, confirmed clearly four groups, the first group contains *P. atlantica* and *P. khinjuk*, then second group wild and cultivated *P. vera* and the third group contains *P. palaestina* and *P. terebinthus* while in the fourth there is only *P. lentiscus*. The genetic relatedness among the *Pistacia* species was also investigated using all the data obtained from the three techniques, in this case two clusters were obtained (see paragraph 3.4.7.4), one with *P. atlantica*, *P. vera* (wild and cultivated) and *P. khinjuk*, and the other with *P. palaestina, P. terebinthus* and *P. lentiscus*. On the other hand, this study found that wild *Pistacia vera* were much closer to *P. khinjuk* but the cultivated *P. vera* were closer to *Pistacia atlantica* due to the open pollination between the *Pistacia* species especially in Syria where the presence of *P. atlantica* in the pistachio orchard and may hybrids were found in previous study of the Syrian female varieties (Ibrahim Basha *et al*., 2006) .

This result explains the two opposite reports about the relationships among *P. vera*, *P. khinjuk* and *P. atlantica*. The one by Parfit & Badenes (1997) that found *P. khinjuk* and *P. vera* were close related species according to chloroplast genome analysis and the one of

Kafkas & Perl-Treves (2001b) that found *P. khinjuk* and *P. atlantica* were close related species according to RAPD analysis. The correlations between the results obtained by the three different techniques were highly significant.

This study confirms that *P. terebinthus* and *P. palaestina* had a close relationship with all Molecular techniques applied. Engler (1883) considered *P. palaestina* as a variety of *P. terebinthus*. On the other hand, Zohary (1952) considered *P. palaestina* as a distinct species. Then, Post (1932), Yaltirik (1967) and Shalabi (1986) described *P. palaestina* as a subspecies of *P. terebinthus*. Recently, Kafkas & Perl-Treves (2001b) supported Engler's and Yaltirik's classifications. More recently, Katsiotis *et al.* (2003) and Golan-Goldhirsh *et al.* (2004) had similar results by RAPD and AFLP analysis. Additionally Kafkas (2006) obtained similar result in his phylogenetic investigation of the genus *Pistacia* using AFLP technique.

Also this study agreed with the results of several studies (Kafkas & Perl-Treves, 2001a, b; Katsiotis *et al.*, 2003; Kafkas, 2006) which are suggested to separate *P. terebinthus* from *P. khinjuk*, *P. atlantica* and *P. vera* group. However, other authors (Zohary, 1952; Parfitt & Badenes, 1997; Golan-Goldhirsh *et al.,* 2004) grouped *P. terebinthus* together with *P. vera, P. khinjuk*.

4.4. Molecular marker versus ecogeographic and morphological

The results of this study showed the existence of significant correlations between the climate and the molecular marker data which are applied on *Pistacia* species. The correlation was highly significant in *P. vera* between the climate and all markers, while it was just significant in *P. atlantica*. On the other hand the correlation was highly significant in *P. palaestina* and between climate and AFLP and ISSR markers but not correlated was found between climatic characters and SSR marker. The opposite situation was found in *P. terebinthus* where the correlations were not significant between the climate and AFLP and ISSR markers, but was significant between clime characters and SSR marker. In *P. lentiscus* and *P. khinjuk* the correlations were not significant between the climates characters and the molecular markers.

This may reflect the rather small sample number or the limited number of studied populations in these species. Similar results due to the low number of the samples and populations which affected the correlations between AFLP molecular marker and the geographic, was reveled on Uruguayan weedy rice by Federic *et al*. (2001).

The quantitive morphological characters of leaves and nuts were also compared with the molecular markers data for male and female groups in each site. The results showed that there are no correlations between the leaves and leaflets dimensions and any of the used molecular marker techniques, except for SSR technique and the nut dimensions in *P. palaestina* and *P. terebinthus*, which were significantly correlated.

These results agreed with papers showed differences between molecular markers and morphological characteristics e.g., genotypes of *Fragaria virginiana* ssp. *gluaca* in northern USA (Harrison *et al*., 2000), and various varieties of *Hordeum vulgare* L. different in their resistant to barley mild mosaic virus (Bahrman *et al.*, 1999). On the other hand, Barazani *et al.* (2003) has reported that the significant correlation between the genetic and morphological traits matrices is indicative of the genetic basis for the observed difference between the populations. The correlation between morphological and molecular markers depends also by the study conditions and if all the plants under study are grown on the same plot under the same environmental conditions. In our study there was a wide range of environmental conditions.

4.5. Complementary conservation strategy

Several authors mentioned that no single conservation technique can adequately conserve the full range of genetic diversity of a target species or genepool (Hoyt, 1988; Maxted *et al*., 1997b; Dulloo *et al*., 1998). A combination of several conservation methods of both *in situ* and *ex situ* needed to be applied to have a successful conservation strategy for the target species. The selection of the conservation technique is depending on the nature of the target species and the objective of the activity. Many efforts in the Mediterranean basin, Central Asia and Iran had been applied for conserving the *Pistacia* species (see paragraph 1.2).

Based on the results of this study in assessing the genetic diversity of the *Pistacia* species in wild population and field gene bank for this region, and the literature review a complementary conservation strategy will be suggested and identify areas where more research work is required.

4.5.1. *Ex Situ* Conservation

4.5.1.1. Conventional seed storage

In terms of static conservation, the most convenient way of maintaining plant germplasm would by dried seed storage (at 3-4% moisture content) at low temperature, usually -20°C

for long term storage or 4°C for medium- and short-term storage, as recommended in the Genebank Standards published by FAO and IPGRI (1994).

Pistacia spp. show orthodox seed storage characteristics (Ayfer & Serr, 1961; Joley, 1960; Joley & Opitz 1971). Seeds of *Pistacia* spp. can show considerable dormancy (Joley, 1960). A year and half after-ripening is required to remove dormancy (Kravchenko, 1961). It is clear that *Pistacia* species are mostly dioecious trees this leading us that in this method only female genotypes will be conserved. On the other hand, the seed are a sexual propagation and Pistacia species are open pollinated species and they can be considered as primary genepool. Therefore the seedling produced may not reflect the traits of the mother tree or the traits we want to conserve. According to the literature reviewed there is no seed gene bank for *Pistacia* spp. Although in 1985 IBPGR has published a handbook of seed technology for genebanks with detailed in formation on *Pistacia* spp. seed germination and storage.

4.5.1.2. Field genebanks

Although the field gene banks hazard is to being damaged by natural calamities, infection, neglect or abuse, it is still necessary for many important varieties such as horticultural and forestry species (Ramanatha Rao & Riley, 1995; Ramanatha Rao *et al.*, 1996). This method is very common for conserving *Pistacia* spp. (Vargas *et al.*, 1993; Hadj Hassan, 1998; Ibrahim Basha *et al*., 2006).

According to our results the field genebanks in Syria represents most of the Syrian pistachio variety but not wild relatives and in Uzbekistan the field genebank is holding some of wild *P. vera* genotypes introduced from several countries in Central Asia but need to have a duplicate of this genebank in order to ovoid the hazard.

4.5.2. *In Situ* Conservation

In situ conservation is the most widely used strategy for conserving wild species, recalcitrant seed species and those species which depend on other organisms within the ecosystem (Ford-Lloyd & Jackson, 1986; Maxted *et al*., 1997b). The great advantage of this conservation strategy is the dynamic adaptive evolutionary processes. However, germplasm are often difficult to document and use by breeders, except for materials conserved on-farm (Dulloo, 1998).

4.5.2.1. Biosphere reserves or protected areas

Conservation of wild species crop relatives in genetic reserves involves the location, designation, management and monitoring of genetic diversity in a particular, natural location (Maxted *et al.*, 1997a).

In Syria, the government protected some areas for *in situ* conservation of the pistachio populations living there, this is the case for Jabal Al Bala'as (12000 ha) in Hama and Jabal Abdul-Aziz (84050 ha) in Deir el-Zour which are addressed for conserving the *Pistacia atlantica* Stand. Jabal Abou Rajman, desert Mountain, is also suggested to be a protected area for *Pistacia atlantica* (Barkoudah *et al.*, 2000). According to our results we found that these populations contain a wide range of variation both within and between the populations. Moreover, not only *Pistacia atlantica*, but also *Pistacia khinjuk* were found there.

On the other hand, in Syria *P. lentiscus* and *P. palaestina* are not target species for conservation, while they are a component of the Mediterranean maquis (Zohary, 1996) further more *P. lentiscus* was found to be one of the most drought tolerant plants among other evergreen species in the Mediterranean maquis (Gratani, 1995). Fortunately, they are co-dominant component in some protected areas such as Frolok protected area. In any event, these species need more attention to be conserved.

In Tajikistan a wide range of wild *Pistacia vera* diversity were found according to our molecular and morphological assessment, but unfortunately the deforestation has become really threatening. The area of valuable juniper (*Juniperus*), walnuts (*Juglans*), birch (*Betula*), and pistachio (*Pistacia*) forests has been reduced by 20-25% during the last decades (Safarov, 2003). Therefore it is highly recommended to give more attentions for conserving the wild *P. vera* in their center of origin.

4.5.2.2. On- Farm conservation

The on–Farm conservation is one method of *in situ* conservation of agro-biodiversity which maintains the traditional crop cultivars by farmers within traditional agricultural systems (Hodgkin *et al.*, 1993). In Syria the pistachio cultivation is one of the most important and tradition cultivation according to Ibrahim Basha *et al.* (2006) whom found that the variation between varieties within same orchard is about 86% which means that the farmer are holding a wide range of cultivated pistachio variation in their orchards. Unfortunately, this conservation method is not applied in Syria although the wide range of varieties and environments where pistachio is cultivated.

4.6. Future prospective of Pistachio's studies

The present study has helped to focus several questions about (i) the natural distribution of *Pistacia* in central and west Asia, (ii) the phylogenetic relationships among *Pistacia* populations and (iii) the assessment of diversity in *Pistacia* species at both the morphological and genetic level. These aspects are essential to carry out successful program on both germplasm conservation and utilization. Nevertheless, there is still a need to carry out a range of studies on different aspects of the biology of *Pistacia*. For examples the topics which would require particular attention include:

- Researches on complementary conservation strategy of the genus *Pistacia* in Central and West Asia, both in term of methodology effectiveness and costs;
- Research on *Pistacia ex situ* conservation by cyropreservation and *in vitro* propagation;
- Better knowledge of the floral biology including phenology, breeding system and pollination vectors. This is particularly important for the *Pistacia* species which are primary genepool and have the problem related to protandry.
- More attention should be paid for the genetic diversity of the wild *Pistacia vera* in Central Asia which is the center of origin, or center of diversity, for this species. In particular conservation programs should be run in order to protected areas for *in situ* -conservation.
- Jointly scientific studies between the countries interested in pistachio conservation and production in order to set up a definitive *Pistacia* taxonomy, especially to assess the whole cultivated pistachio varieties in the world which are about 100 verities;
- Establish international field gene banks to conserve this important genus for the dry areas, with large number of accessions in order to be assessed and utilized in breeding programs with collaboration between the scientific institutions and the national and international organizations including the NGOs which are interested in the plant genetic resources.

Summary

Pistachio (*Pistacia vera* L.) is one of the most promising nut trees in the Central and West Asia region due to its high nutritional and medicinal value. It is one of the major crops significantly contributing to the economy and nutrition of many poor communities in the region. The pistachio crop currently depends on a very narrow genetic base and this constitutes a serious threat to the sustainability of its production in this region. Moreover, traditional cultivars are increasingly being replaced by few improved types in areas of greatest diversity, while the destruction of natural habitats by deforestation, overgrazing, over cutting, and man–made fires contributes to further the loss of wild species. Syria is considered as a center of origin for some Pistacia species. Wild species such as *P. atlantica, P. palaestina, P. khinjuk*, and *P. terebinthus* constitute an important source of genetic diversity for the Pistachio crop. These wild relatives, together with local varieties of *Pistacia vera*, form the total *Pistacia* genetic resources in Syria, which should be maintained for sustainable pistachio cultivation.

Syria has about 25 cultivated varieties distinguished by morphological traits. The Pistachio species can be found growing in private farms, forests, national protected areas and national and international field gene banks. Although, Syria is classified as the fourth pistachio producing country in the world, it holds some unique diversity not found elsewhere. Pistachio is a major cash commodity in Iran, Turkey, Syria, Afghanistan and Central Asia on the other hand it could be considered as a neglected and under utilized genetic resources having high income potential. On the other hand, the pure stand of the *P. vera* in central Asia (center of origin for this specie) makes the area a valuable source of the genetic diversity, but unfortunately a severe forest degradation affected these population.

The purpose of this research is to assess the level of genetic diversity in *Pistacia* gene pool, conserved both in *ex-situ* and *in-situ*/on farm in Syria, Uzbekistan and Tajikistan, using molecular techniques in order to better understand the genetic structure, pattern and distribution of diversity within *ex-situ* collections and in the wild and to develop a complementary conservation and use strategy for pistachio. This research was carried out during 2004-2006.

A based ecogeographic survey was first undertaken to determine the distribution of the different *Pistacia* genus in Central and West Asia, principally in Syria, Tajikistan and Uzbekistan. Fifty four sites were chosen to represent the distribution of all *Pistacia*

species and to collect the plant material to be characterized and evaluated. Then several visits were paid to these sites. The results of present research showed that the *Pistacia* genus was found in different climatic areas ranging from dry up to humid areas. These results indicate that pistachio is a drought resistant tree and flourishing in arid and semi-arid zones. *Pistacia* genus was found in margin areas with wide range of soils, especially in that very shallow, moderately developed, non-acid with clay-enriched subsoil, and also on no significant soil profile development or poorly developed soils of semi-deserts.

All surveyed accessions were thoroughly studied to assess their morphological variability. Characters related to the tree growth, leaves, nuts, were among those considered during these evaluations. The *Descriptor Lists* produced by IPGRI (1997; 1998) were adopted in these activities. The results of this studied showed a highly significant variability between and within these species, due to there environmental conditions.

AFLP, ISSR, SSR molecular data analyzed by multivariate (Factor and Principal Component Analyses) and cluster analysis showed a large amount of variability both within and between species in the wild populations of *Pistacia* of this region. The correlations between the data of these three molecular markers techniques were either significant or highly significant. This study confirms that *P. terebinthus* and *P. palaestina* had a close relationship with all Molecular techniques applied this confirms the opinion that *P. palaestina* is subspecies of *P. terebinthus*. On the other hand, the principle component analysis showed that these species could be clustered in three main groups, first with *P. atlantica* and *P. khinjuk*, the second contained the wild and cultivated *P. vera* and the third groups contained *P. palaestina* and *P. terebinthus*. While *P. lentiscus* the only evergreen species never grouped with any of the pervious groups.

The data obtained wiht the ecogeogarphic survey were compared with those of each molecular marker technique, the results revealed the existence of significant correlations between the climate and the molecular marker data. The quantitative morphological characters of leaves and nuts were also compared with the molecular markers data for male and female groups in each site. The results showed that there are no correlations between leaves and leaflets dimensions and any of the used molecular markers, while some significant correlation was reveled between SSR markers and the nut dimensions in *P. palaestina* and *P. terebinthus*.

Finally, suggestions for complementary conservation strategy according to the results obtained from this study and the possibilities available in these countries were discussed. Four possible conservation methods could being recommended according to the conditions of the *Pistacia* genus. Two *ex-situ* conservation methods which are conventional seed storage and field gene banks are the most suitable ways to conserve the *Pistacia* spp. On the other hand, Biosphere reserves or protected areas and on farm conservation are the most convenient *in-situ* conservations for these species. The combination of these four methods would overpass the disadvantage of some of them such as the static conservation of the seed storage or the possible loss of the diversity in the cultivated pistachio if the on-farm conservation was involved.

This study was a joint cooperation between the Department of Agrobiology and Agrochemical, (University of Tuscia, Italy), the CGIAR scientists in Bioversity International (Italy), the International Center for Agricultural Research in the Dry Areas (ICARDA, Syria) and Bioversity International the regional office for Central, West Asia and North Africa (CWANA, Syria).

6. Chapter Six: References

Adams R. P., J. S. Miller, E. M. Goldenberg and J. E. Adams. 1994. Conservation of Plants Genes II. Monographs in Systematic Botany from the Missouri Botanical Garden, Vol. 48.
Aggarwal, R. K., D. S. Brar, S. Nandi, N. Huang and G. S. Khush, 1999. Phylogenetic Relationships among *Oryza* Species Revealed by AFLP Markers. Theoretical and Applied Genetics 98: 1320-1328.
Ahmad, R., L. Fergusin, S. M. Southwick. 2003. identification of pistachio *P. vera* L. nuts with Microsatellite Markers. J. Amer. Soc. Hort. Sci. 128(6): 898-903.
Ahn, S. and S.D. Tanksley. 1993. Comparative linkage maps of the rice and maize genomes. Proc. Natl Acad. Sci. U.S.A. 90(17):7980-7984.
Al-Husny, B. 1972. The Pistachio. Leaflet No. 22, Ministry of Agriculture, Syria (in Arabic).
Al-Qabani, S. 1994. Food No Drugs. Beirut Lebanon (in Arabic).
Al-Yafi J. 1978. New characters differentiating *Pistacia atlantica* subspecies. Candollea 33: 201–208.
Alyafi, J. 1979. Approches systematique et ecologique du genre *Pistacia* L. dans la region mediterraneenne. These pour obtenir le litre versite de droit D'economie et des Sciences D'Aix-Marseille, Faculte des Science et Techniques St Jerome.
Ammiraju, J. S. S., B. B. Dholakia, D.K. Santra, H. Singh, M. D. Lagu, S. A. Tamhankar, H. S. Dhaliwal, V. S. Rao, V. S. Gupta and P. K. Ranjekar. 2001. Identification of inter-simple sequence repeat (ISSR) markers associated with seed size in wheat. Theor Appl Genet 102:726–732.
Anwar, R. and M. A. Rabbani. 2001. Natural occurrence, distribution and uses of *Pistacia* species in Pakistan. In: Padulosi S. and A. Hadj-Hassan, (Eds). 2001. Project on Underutilized Mediterranean Species. *Pistacia*: towards a comprehensive documentation of distribution and use of its genetic diversity in Central and West Asia, North Africa and Mediterranean Europe. Report of the IPGRI Workshop, 14-17 December 1998, Irbid, Jordan.
Arcade, A., F. Anselin, P. Faivre Rampant, M.C. Lesage, L.E. Paques and D. Prat. 2000. Application of AFLP, RAPD and ISSR markers to genetic mapping of European and Japanese Larch. Theor Appl Genet 100: 299–307.
Arens, P., G. Bredemeijer, M. J. M. Smulders and B. Vosman. 1995. Identification of tomato cultivars using microsatellites. Acta Horticulturae 412, 49–57.
Atli, H. S., S. Arpaci, N. Kaska and H. Ayanoglu. 2001b. Wild *Pistacia* species in Turkey. In: Padulosi S. and A. Hadj-Hassan, (Eds). 2001. Project on Underutilized Mediterranean Species. *Pistacia*: towards a comprehensive documentation of distribution and use of its genetic diversity in Central and West Asia, North Africa and Mediterranean Europe. Report of the IPGRI Workshop, 14-17 December 1998, Irbid, Jordan.
Atli, H.S., S. Arpaci and H. Ayanoglu. 2001b. Comparison of seedling characteristics of some *Pistacia* species. In Ak B.E. (ed.). 11 GREMPA Seminar on pistachios and almonds = 11ème Colloque du GREMPA sur le pistachier et l'amandier. Zaragoza : CIHEAM-IAMZ, 2001. p. 215-218.
Ayfer, M. and Serr, E.F. 1961. Effects of gibberellin and other factors on seed germination and early growth in *Pistacia* species. Proceedings of the American Society for Horticultural Science, 77, 308-315.
Bahrman N., J. Le Gouis, D. Hariri, L. Guilbaud and L. Jestin. 1999. Genetic diversity of old French six-rowed winter barley varieties assessed with molecular, biochemical and morphological markers and its relation to BaMMV resistance. Heredity 83: 568–574.

Barazani, O., A. Atayev, B. Yakubov, V. Kostiukovsky, K. Popov and A. Golan-Goldhirsh. 2003. Genetic variability in Turkmen populations of *Pistacia vera* L. Genetic Resources and Crop Evolution 50: 383–389, 2003. 383
Barkoudah Y., A. I. Darwish and M. Abi Antoun, 2000. Biological Diversity Syrian National Report. pp. 34.
Barone, E., L. Di Marco, F.P. Marra, M. Sibari. 1996. Isoenzymes and canonical discriminate analysis to identify pistachio (*P. vera* L.) germplasm. HortSci. 31(1): 134-138.
Barone, E., T. Caruso. 1996. Genetic diversity within *P. vera* in Italy. In: S. Padulosi, T. Caruso and E. Barone (Eds.). Taxonomy, Distribution, conservation and uses of *Pistacia* genetic resources. Report of a workshop, 29-30 June 1995, Palermo, Italy. International Plant Genetic Resources Institute, Rome Italy pp. 20-28.
Batlle I., F. J. Vargas and M. A. Romero. 1996. Natural occurrence, conservation and uses of *Pistacia* species in Spain. In S. Padulosi, T. Caruso and E. Barone, (Eds.). Taxonomy, distribution, conservation and uses of *Pistacia* genetic resources. Report of a Workshop, June 1995, Palermo, Italy. IPGRI, Rome, Italy. 42-45p.
Batlle, I., M. A. Romero, M. Rovira and F.J. Vargas. 2001. *Pistacia* conservation, characterization and use at IRTA: current situation and prospects in Spain. In: Padulosi S. and A. Hadj-Hassan, (Eds). 2001. Project on Underutilized Mediterranean Species. *Pistacia*: towards a comprehensive documentation of distribution and use of its genetic diversity in Central and West Asia, North Africa and Mediterranean Europe. Report of the IPGRI Workshop, 14-17 December 1998, Irbid, Jordan.
Bean., W. 1981. Trees and Shrubs Hardy in Great Britain. Vol. 1 - 4 and Supplement. Murray.
Beismann, H., J. H. A. Barker, A. Karp and T. Speck,1997. AFLP Analysis Sheds Light on Distribution of Two Salix Species and Their Hybrid Along a Natural Gradient. Molecular Ecology 6: 989-993.
Bennett S. J. and Maxted N. 1997. An ecogeographic analysis of the Vicia narbonensis complex. Genetic Resources and Crop Evolution 44: 411-428.
Bennett, S. J. and S. Bullitta. 2003. Ecogeographical analysis of the distribution of six Trifolium species in Sardinia. Biodiversity and Conservation 12: 1455–1466.
Besse, P., G. Taylor, B. Carroll, N. Berding, D. Burner and C.L. Mcintyre, 1998. Assessing Genetic Diversity in a Sugarcane Germplasm Collection Using an Automated AFLP Analysis. Genetica 104, 143–153.
Boivin, K., M. Deu, J. F. Rami, G. Trouche and P. Hamon, 1999. Towards a Saturated Sorghum Map Using RFLP and AFLP Markers. Theoretical and Applied Genetics 98, 320–328.
Bown., D. 1995. Encyclopedia of Herbs and their Uses. Dorling Kindersley, London.
Bradshaw J. E., C. A. Hackett, R. C. Meyer, D. Milbourne, J. W. Mcnichol, M. S. Philips and R. Waugh,1998. Identification of AFLP and SSR Marker Associated With Quantitative Resistance to *Globodera pallida* (Stone) in Tetraploid Potato (*Solanum tuberosum* subsp. *tuberosum*) With A View to Marker-Assisted Selection. Theoretical and Applied Genetics 97: 202-210.
Browicz, K. 1988. Chorology of Trees and Shrubs in South-west Asia and Adjacent Regions. Vol. 6. Polish Scientific Publications, Warsawa, Poznan.
Brown, J.S., 1991. Principal component and cluster analyses of cotton cultivar variability across the U.S. Cotton Belt. Crop Sci. 31: 915–922.
Cabrita, L., P. Elisiário, J. Leitão and A. Guerreiro, 2001. Assessment of the Genetic Relationships among Citrus Species and Varieties by Isozyme and RAPD Markers. Acta Hort. (ISHS) 546:177-181.

Caetano-Anollés, G., B.J. Bassam and P.M. Gresshoff. 1992. DNA fingerprinting: Mapping out a RAPD redefinition? Bio/Technology 10 (9):937.
Caicedo, A. L., E. Caitan, M. C. Duque, O. Toro Chica, D. G. Debouck and J. Tohme, 1999. AFLP Fingerprinting of *Phaseolus lunatus* L. and Related Wild Species from South America. Crop Science 39:1497-1509.
Camussi, A., E. Ottaviano, T. Calinski and Z. Kaczmarek. 1985. Genetic distances based on quantitative traits. Genetics 111, 945–962.
Caruso, T., C. Lannini, F. Monastra, G. Zakynthinos, D. Rouskas, E. Barone, F. P. Marra, F. Sottile, I. Batlle, F. Vargas, M. Romero, S. Padulosi, CI. Greco, M. R. Sabina, G. Martelli, B.E. Ak, M. Laghezali. 1998. Genetic and Phenotypic Diversity in Pistachio (*P. vera* L.) Germplasm Collected in Mediterranean Countries. In: L. Ferguson and D. Kester (Eds.). Proceeding of The Second International Symposium on Pistachios And Almonds. Acta Horticulturae Number 470.
CBD. 1992. Convention on Biological Diversity. 5 June, Rio de Janeiro.
Cekic, C., N. H. Battey and M. J. Wilkinson. 2001. The potential of ISSR-PCR primer-pair combinations for genetic linkage analysis using the seasonal flowering locus in Fragaria as a model. Theor Appl Genet 103:540–546.
Chabane, K., G.A. Ablett, G.M. Cordeiro, J. Valkoun, and R.J. Henry. 2005. EST versus genomic derived microsatellites for genotyping wild and cultivated barley. Genet. Resources & Crop Evol. 52 (7): 907-913
Chabane, K., T.O.M. Bazun & A. Ibrahim Basha. 2005. Assessment of Genetic Diversity of *Pistacia* atlantica Desf. (*Anarcardiaceae*) from Syria by AFLP analysis. International Agrobiodiversity Symposium, ICARDA, April 2005.
Chandler, W.H. 1965. Deciduous Orchards. Lea and Febiger pub. Philadelphia, USA.
Chen, X., S. Temnykh, Y. Xu, Y. G. Cho and S. R. McCouch. 1997. Development of microsatellite framework map providing genome-wide co*vera*ge in rice (*Oryza sativa* L.). Theoretical and Applied Genetics 95, 553–567.
Chevallier., A. 1996. The Encyclopedia of Medicinal Plants. DK ADULT; 1st American Ed edition. 336 p.
Chiej, R. 1984. Encyclopedia of Medicinal Plants. MacDonald. London
Chin, E. C. L., M. L. Senior, H. Shu, and J. S. C. Smith.1996. Maize simple repetitive DNA sequences: abundance and allele variation. Genome 39, 866–873.
Chopra, R. N., S. L. Nayar and L. C. Chopra. 1986. Glossary of Indian Medicinal Plants. Council of Scientific and Industrial Research, New Delhi.
Cipriani, G., M. T. Marrazzo, R. Marconi, A. Cimato and R. Testolin. 2002. Microsatellite markers isolated in olive (*Olea europaea* L.) are suitable for individual fingerprinting and reveal polymorphism within ancient cultivars. Theor. Appl. Genet. 104:223-228.
Cowen, N. M. and K. J. Frey. 1987. Relationships between three measures of genetic distance and breeding methods in oat (*Avena sativa* L.). Genome 29: 97–106.
CRFG, California Rare Fruit Growers. 1997. Pistachio.
http://www.crfg.org/pubs/ff/pistachio.html
Cruz, C.D. and A..J. Regazzi 1994. Modelos biométricos aplicados ao melhoramento genético, Universidade Federal de Viçosa, Viçosa.
De Candolle, A. 1882. Origin of Cultivated Plants, second edition.-London.
De Vicente, M.C. and T. Fulton. Using molecular marker technology in studies on plant genetic diversity. Illus. Nelly Giraldo. IPGRI, Rome, Italy and Institute for Genetic Diversity, Ithaca, New York, USA.

De Vienne, D., S. Santoni and M. Falque. 2003. Principal Sources of Molecular Markers. In D. De Vienne (ed). Molecular Markers in Plant Genetics and Biotechnology. pp 1- 46.
Dean, R. E., J. A. Dahlberg, M. S. Hopkins, S. E. Mitchell and S. Kresovich. 1999. Genetic redundancy and diversity among 'Orange' accessions in the U.S. national sorghum collection as assessed with Simple Sequence Repeat (SSR) markers. Crop Sci. 39:1215-1221.
Dubreuil, P. and A. Charcosset. 1999. Relationships among maize inbred lines and populations from European and North American origins as estimated using RFLP markers. Theor. Appl. Genet. 99:473-480.
Duke, J. A. 1989. CRC Handbook of Nuts. CRC Press. pp. 240-243.
Duke. J. A. and E. S. Ayensu. 1985. Medicinal Plants of China. Reference Publications, Inc.
Dulloo, M.E., L. Guarino, F. Engelmann, N. Maxted, H.J. Newbury, F. Attere and B.V. Ford-Lloyd. 1998. Complementary conservation strategies for the genus Coffea: A case study of Mascarene Coffea species. Genetic Resources and Crop Evolution, Vol 45: 565-579.
Dulloo, M.E., N. Maxted, L. Guarino, D. Florens, H.J. Newbury and B. V. Ford Lloyd. 1999. Ecogeographic Survey of The Genus Coffea in The Mascarene Islands. Botanical Journal of the Linnean Society 131:263-284.
Edwards, K. J., J. H. A. Barker, A. Daly, C. Jones and A. Karp. 1996. Microsatellite libraries enriched for se*veral* microsatellite sequences in plants. BioTechniques 20, 759–760.
Ehrmann T. and P.S. Cocks. 1990. Ecogeography of annual legumes in Syria: distribution patterns. Journal of Applied Ecology 27: 578-591.
El – Ghawawi, H. Pistachio cultivation in Libya. In: Padulosi S. and A. Hadj-Hassan, (Eds). 2001. Project on Underutilized Mediterranean Species. *Pistacia*: towards a comprehensive documentation of distribution and use of its genetic diversity in Central and West Asia, North Africa and Mediterranean Europe. Report of the IPGRI Workshop, 14-17 December 1998, Irbid, Jordan.
El-Oqlah A.A. 1996. Biosystematic research on the genus *Pistacia*. in Jordan. In: Padulosi S., Caruso T. and Barone E. (Eds). Taxonomy, Distribution, Conservation and Uses of *Pistacia* Genetic Resources. Project on Underutilized Mediterranean Species pp. 12–19, report of a workshop 29–30 June 1995, Palermo, Italy, IPGRI.
Engelmann, F. 1997. In Vitro Conservation Methods. In: B. V. Ford-Lloyd, N. J.H. and J. A. Callow(Eds.). Biotechnology and Plant Genetic Resources: Conservation and Use. CABI, Wallingford. pp. 119-162.
Engler A. 1883. Burseraceae et Anacardiaceae. In: De Candolle A.C. (ed.), Monographiae Phanerogamarum Vol. 4. Paris., pp. 284–293.
Enjalbert, J., I. Goldringer, S. Paillard and P. Brabant. 1999. Molecular markers to study genetic drift and selection in wheat populations. J. Expl Bot. 50(332):283-290.
Esmail-Pour, A. 1998a. Evaluation and Comparison of Quality and Quantity Characters of 23 Female Pistachio Cultivars in Rafsanjan. Annual Report for 1998, Pistachio Research Institute, Rafsanjan, Iran.
Esmail-Pour, A. 1998b. Evaluation, Identification and Collection of Male Pistachio Cultivars. Annual Report for 1998, Pistachio Research Institute, Rafsanjan, Iran.
Eyzaguirre, P.B., S. Padulosi and T. Hodgkin. 1999. IPGRI's Strategy for Neglected and Underutilized Species and The Human Dimension of Agrobiodiversity. In: S. Padulosi (Eds.). Priority Setting for Underutilized and Neglected Plant Species of the

Mediterranean Region. Report of the IPGRI Conference, 9-11 February 1998, ICARDA, Aleppo, Syria. International Plant Genetic Resources Institute, Rome, Italy.
Fabbri A., Valenti C. 1997. The Sicilian Pistachio industry: an overview. In: L. Ferguson and D. Kester (Eds.). Proceeding of The Second International Symposium on Pistachios And Almonds. Acta Horticulturae Number 470.
Fang, D., R. R. Krueger and M. L. Roose. 1998. Phylogenetic relationships among selected Citrus germplasm accessions revealed by inter simple sequence repeat (ISSR) markers. J Am Soc Hortic Sc 123: 616–617.
FAO, 1995. Digital Soil Map of the World and Derived Properties version 3.5.
FAO. 2006. FAOSTAT database.
http://faostat.fao.org/site/567/DesktopDefault.aspx?PageID=567.
FAO.2001b. State of the world's forests 2001.Rome, Food and Agriculture Organization.
FAO/IPGRI. 1994. Genebank Standards. Food and Agriculture Organisation of the United Nations, Rome; International Plant Genetic Resources Institute, Rome.
Federici, M. T., D. Vaughan, N. Tomooka, A. Kaga, X. W. Wang, K. Doi, M. Francis, G. Zorrilla and N. Saldain. 2001. Analysis of Uruguayan Weedy Rice Genetic Diversity Using AFLP Molecular Markers. EJB Electronic Journal of Biotechnology. Vol.4 No.3.
Felsenstein, J. 1985. Phylogenies and the comparative method. American Naturalist 125: 1-12.
Ford-Lloyd B. V. 2001, Genotyping in Plant Genetic Resources. In: Henry R. J. (ed), Centre for Plant Conservation Genetics, Southern Cross University, Lismore, Australia. pp. 59-81.
Ford-Lloyd B.V. and Jackson M.T. 1986. Plant genetic resources: an introduction to their conservation and use. Edward Arnold, London.
Fossati T., M. Labra, S. Castiglione, O. Failla, A. Scienza, F. Sala. 2001.The use of AFLP and SSR molecular markers to decipher homonyms and synonyms in grapevine cultivars: the case of the varietal group known as ‘‘Schiave’’ Theor Appl Genet (2001) 102:200–205.
Frankel O.H., A. H. D. Brown and J.J. Burdon, 1998. Conservation of plant biodiversity. Cambridge university press. Pp. 179-180.
Galande, A. A., R. Tiwari, J. S. S. Ammiraju, D. K. Santra, M. D. Lagu, V. S. Rao, V. S. Gupta, B. K. Misra, S. Nagarajan and P. K. Ranjekar. 2001. Genetic analysis of kernel hardness in bread wheat using PCR-based markers. Theor Appl Genet 103:601–606.
Gašic, K., V. Ognjanov, R. C. Boškovi, K. R. Tobutt and C. James, 2001. Characterization of Vineyard Peach Biodiversity. Acta Hort. (ISHS) 546:119-125
Gebhardt, C., E. Ritter, A. Barone, T. Debener, B. Walkemeier, U. Schachtschabel, H. Kaufmann, R. D. Thompson, M. W. Bonierbale, M. W. Ganal, S. D. Tanksley, F. Salamini. 1991. RFLP maps of potato and their alignment with the homeologous tomato genome. Theor Appl Genet 83:49–57.
Ghislain, M., D. M. Spooner, F. Rodriguez, F. Villamon, J. Nunez, C. Vasquez, R. Waugh and M. Bonierbale. 2004. Selection of highly informative and user-friendly microsatellites (SSRs) for genotyping of cultivated potato. Theor. Appl. Genet. 108:881-890.
Ghorbel, A. and M.L. Kchouk. 1996. Genetic resources of horticultural crops in Tunisia. Second Meeting of the WANA Working Group on Horticultural Crops. 8-15 May 1996. International Plant Genetic Resources Institute, Aleppo, Syria.

Ghorbel, A. and M.L. Kchouk. 1998. Status and needs of genetic resources for horticultural crops in Tunisia. WANANET Meeting, 9-11 February 1998. International Plant Genetic Resources Institute, Aleppo, Syria.
Godwin, I. D., E. A. B. Aitken and L.W. Smith. 1997. Application of inter simple sequence repeat (ISSR) markers to plant genetics. Electrophoresis 18:1524–1528.
Golan-Goldhirsh, A., and V. Kostiukovsky. 1998. The Mediterranean *Pistacia* Genus Germplasm Collection at Sede, Boker. In: L. Ferguson and D. Kester (Eds.). Proceeding of The Second International Symposium on Pistachios And Almonds. Acta Horticulturae Number 470.
Golan-Goldhirsh, A., O. Barazani, Z. S. Wang, D. K. Khadka, J. A. Saunders, V. Kostiukovsky and L. J. Rowland. 2004. Genetic relationships among Mediterranean *Pistacia* species evaluated by RAPD and AFLP markers. Plant Syst. Evol. 246: 9–18.
GORS.1991. The Study of Soils and Forests of Coastal Area Using Remote Sensing Techniques (Lattakia Governorate). Damascus, General Organization of Remote Sensing (in Arabic)
GRATANI, L. 1995. Structural and ecophysiological plasticity of some evergreen species of the Mediterranean maquis in response to climate. Photosynthetica 31:335–343.
Grieve. A. 1984. Modern Herbal. Penguin.
Griffiths, A.J.F., J.H. Miller, D.T. Suzuki, R.C. Lewontin and W.M. Gelbart. 1996. The nature of the gene. Pp. 345-358 in An Introduction to Genetic Analysis (6th edn.). W.H. Freeman and Co., NY.
Gussone, J. 1884. Flora Siculae Synopsis. 2, Neapoli.
Haanstra, J. P. W., C. Wye, H. Verbakel, F. Meijer-Dekens, P. Van Den Berg, P. Odinot, A. W. Van Heusden, S. Tanksley, P. Lindhout, and J. Peleman, 1999. An Integrated High Density RFLP-AFLP Map of Tomato Based on Two Lycopersicon esculentum _ L. pennelii F-2 Populations. Theoretical and Applied Genetics 99, 254–271.
Hadj Hassan, A. 2003. Establishment of a fruit-tree field genebank. In CGIAR Programme facilitation Unit for Central Asia and the Caucasus. 2003. Conservation through sustainable use of fruit genetic resources in Central Asia. Training course 21-25 August 2000, Tashkent, Uzbekistan. IPGRI, Rome, Italy.
Hadj Ibrahim, I., M. Kardoush, R. Rais.1998. Pistachio Tree and Its Techniques. ACSAD, SN/N59/1998.
Hadj-Hassan, A. 1988. Characters of most important Syrian pistachio female varieties widely cultivated in Aleppo. ACSAD, Damascus, Syria. PS. P 25.
Hadj-Hassan, A. 1988. Characters of most important Syrian pistachio female varieties widely cultivated in Aleppo. ACSAD, Damascus, Syria. P. 25.
Hanetl, P. 20001. Mansfeld's Encyclopedia of Agriculture and Horticlutre Crop: (Except Ornamental). Springer –Verlag Berlin Heidelberg New York. pp. 1054-1057.
Hanson, J. 1985. Procedures for Handling Seeds in Genebanks. Practical Manuals for Genebanks: No. 1. International Board for Plant Genetic Resources, Rome, Italy.
Harrington, J.F. 1970. Seed and Pollen Storage for Conservation of Plant Gene Resources. In: O.H. Frankel and E. Sennett(Eds.). Genetic Resources in Plants - Their Exploration and Conservation. Blackwell Scientific, Oxford. pp. 501.
Harris, H. 1966. Enzyme polymorphism in man. Proc. R. Soc. Lond. (b) 164:289-310.
Harrison R.E., Luby J.J., Furnier G.R. and Hancock J.F. 2000. Differences in the apportionment of molecular and morphological variation in North American strawberry and the conesquences for genetic resource management. Gen. Res. Crop Evol. 47: 647–657.

Hartl, L., V. Mohler, F.J. Zeller, S.L.K. Hsam, and G. Schweizer, 1999. Identification of AFLP Markers Closely Linked to the Powdery Mildew Resistance Genes Pm1c and Pm4a in Common Wheat (Triticum aestivum L.). Genome 42, 322–329.
Hearne, C. M., S. Ghosh and J. A. Todd. 1992. Microsatellites for linkage analysis of genetic traits. Trends in Genetics 8:288–294.
Hedenäs, L., A.M. Kooijman. 1996. Phylogeny and habitat adaptations within a monophyletic group of wetland moss genera Amblystegiaceae. Plant Systematics and Evolution 199: 33–52.
Hendricks, L., and L. Ferguson, 1995. The Pistachio Tree. In Ferguson, L. (ed). Pistachio production pp. 7-10.
Herrán, A., L. Estioko, D. Becker, M. J. B. Rodríguez, W. Rohde and E. Ritter. 2000. Linkage mapping and QTL analysis in coconut (Cocos nucifera L.). Theor Appl Genet 101:292–300.
Herrera, E., 1997. Growing Pistachio in Mexico. http://www.cahe.nmsu.edu/pubs/_circulars/circ532.pdf.
Heun, M., R. Schäfer-Pregl, D. Klawan, R. Castagna, M. Accerbi, B. Borghi and F. Salamini. 1997, Site of Einkorn Wheat Domestication Identified by DNA Fingerprinting. Science 278: 1312-1314.
Heywood, V. (1991) Conservation of germplasm of wild plant species. In: Sandlund, O.T., Hindar, K. and Brown, A.H.D. (Eds.) Conservation of Biodiversity for Sustainable Development. Norwegian University Press and Cambridge, pp. 189–203.
Hill., A. F. 1952. Economic Botany. The Maple Press.
Hodgkin, T. H., V. Ramanatha Rao and K.W. Riley. 1993. Current Issues in Conserving Crop Landraces. Presented at the ÈAO-IBPGR On-Farm Conservation Workshop, 6-8 December 1993, Bogor, Indonesia.
Holton, T. A., 2001. Plant Genotyping by Analysis of Microsatellites in Edited by R J Henry. plant Genotyping: The DNA Fingerprinting of Plants. Centre for Plant Conservation Genetics, Southern Cross University, Lismore, Australia. Pp15-28.
Hormaza J. I., L. Dollo and V. S. Polito. 1994. Identification of a RAPD marker to sex determination in *Pistacia vera* using bulked segregant analysis. Theoretical and Applied Genetics 89: 9-13.
Howel, E. C., H. J. Newbury, R. L. Swennen, L. A. Withers and B. V. Ford-Lloyd, 1994. The Use of RAPD for Identifying and Classifying Musa germplasm. Genome 37:328-332.
Hoyt E. 1988. Conserving wild relatives of crops. IBPGR/IUCN/WWF, Gland, Switzerland
Hu J. and L. F. Quiros, 1991. Identification of Broccoli and Cauliflower Cultivars with RAPD Markers. Plant Cell Replication 10:505-511.
Huang, J. C. and M. Sun. 2000. Genetic diversity and relationships of sweet potato and its wild relatives in Ipomoea series Batatas (Convolvulaceae) as revealed by inter simple sequence repeat (ISSR) and restriction analysis of chloroplast DNA. Theor Appl Genet 100: 1050–1060.
Huxley., A. 1992. The New RHS Dictionary of Gardening. MacMillan Press. London.
IBPGR. 1985. Ecogeographic surveying and in situ conservation of crop relatives. Report of an IBPGR task force meeting held at Washington DC. IBPGRI, Rome, Italy.
Ibrahim Basha, A., S. Padulosi, A. Hadj Hassan, 2003. Eco-Geographic Survey and Genetic Diversity Assessment of Female Varieties of Pistachio Species (*Pistacia Vera* L.) in Syria. Aleppo –Syria. (Master thesis in Arabic).

Ibrahim. Basha, A., S. Padulosi, K. Chabane, A. Hadj-Hassan, E. Dulloo , M. A. Pagnotta, E. Porceddu . 2006. Genetic diversity of Syrian pistachio varieties evaluated by AFLP markers. Genetic Resources and Crop Evolution (in press).
IPGRI, 1997. Descriptors for Pistachio (*Pistacia vera* L.). International Plant Genetic Resources Institute, Rome, Italy.
IPGRI, 1998. Descriptors for *Pistacia* spp. (excluding *Pistacia vera* L.). International Plant Genetic Resources Institute, Rome, Italy.
Jacquy, P. 1973. La Culture du Pistachier en Tunisie. AGP.TUN/72/003.FAO, Rome, Italy.
Jarne, P. and P. J. L. Lagoda. 1996. Microsatellites, from molecules to populations and back. Trends Ecology and Evolution 11:424–429.
Javouhey, M., F. Daguin and R. Letouzé, 2000. Somatic Embryogenesis, an Efficient Tool for Date Palm (*Phoenix dactylifera* L.) Industrial Micropropagation. Characterization and Genetic Stability of Original Offshoots and Regenerated Plantlets By RAPD Markers. Acta Hort. (ISHS) 530:237-242.
Jin, H., L. L. Domier, X. J. Shen and F. L. Kolb, 2000. Combined AFLP and RFLP Mapping in Two Hexaploid Oat Recombinant Inbred Populations. Genome 43, 94–101.
Joley, L.E. 1960. Experiences with propagation of the genus *Pistacia*. Proceedings of the Plant Propagators' Society, 10, 287-292.
Joley, L.E. and Opitz, K.W. 1971. Further experiences with propagation of *Pistacia*. Combined Proceedings of the International Plant Propagators' Society, 21, 67-76.
Joshi, S. P., V. S. Gupta, R. K. Aggarwal, P. K. Ranjekar and D. S. Brar. 2000. Genetic diversity and phylogenetic relationship as revealed by inter simple sequence repeat (ISSR) polymorphism in the genus Oryza. Theor Appl Genet 100: 1311–1320.
Kafkas S. and R. Perl-Treves. 2001a. Inter-specific relationships in useful as descriptors for species classification. the genus *Pistacia* L. (Anacardiaceae) based on RAPD finger-printing. HortScience 36 (in press).
Kafkas, S. and R. Perl-Treves. 2001b.Morphological and molecular phylogeny of *Pistacia* species in Turkey. Theor Appl Genet 102:908–915
Kafkas, S., E. Kafkas and R. Perl-Treves. 2002. Morphological diversity and a germplasm survey of three wild *Pistacia* species in Turkey. Genetic Resources and Crop Evolution 49: 261–270.
Kafkas, S., N. Kaska1, A. N. Wassimi and S. Padulosi. 2006. Molecular characterisation of Afghan pistachio accessions by amplified fragment length polymorphisms (AFLPs). Journal of Horticultural Science & Biotechnology 81 (5) 864–868.
Kafkas, S., S. Centner and R. Perl-Treves. 2001. Development of Sex-Associated RAPD Markers in Wild *Pistacia*. Journal of Horticultural Science & biotechnology Vol:76, pp.242-246
Kardolus, J. P., H. J. Van Eck and R. G. Van Den Berg, 1998. The Potential of AFLPs in Biosystematics: a First Application in Solanum Taxonomy (Solanaceae). Plant Systematics and Evolution 210: 87-103.
Karp A, O. Seberg and M. Buiatti. 1996. Molecular techniques in the assessment of botanical diversity. Annals of Botany 78:143–149.
Karp, A. and K. J. Edwards.1997. Molecular techniques in the analysis of the extent and distribution of genetic diversity. In: W.G. Ayad, T. Hodgkin, A. Jaradat, and V.R. Rao (Eds) Molecular Genetic Techniques for Plant Genetic Resources. IPGRI, Rome, pp. 11–22
Karp, A., K. J. Edwards, M. Bruford, S. Funk, B. Vosman, M. Morgantem, O. Seberg, A. Kremer, P. Boursot, P. Arctander, D. Tautz and G. M. Hewitt. 1997a. Molecular

technologies for biodiversity evaluation: opportunities and challenges. Nature Biotechology 15:625–628.
Karp, A., S. Kresovich, K.V. Bhat, W. G. Ayad and T. Hodgkin. 1997b. Molecular tools in plant genetic resources conservation: a guide to the technologies IPGRI Technical Bulletin No. 2. International Plant Genetic Resources Institute, Rome, Italy.
Kaska, N., S. çaglar and S. Kafkas. 1996. Genetic diversity and germplasm conservation of *Pistacia* in Turkey. In: S. Padulosi, T. Caruso and E. Barone (Eds.). Taxonomy, Distribution, conservation and uses of *Pistacia* genetic resources. Report of a workshop, 29-30 June 1995, Palermo, Italy. International Plant Genetic Resources Institute, Rome Italy pp. 46-50.
Katsiotis, A., M. Hagidimitriou, A. Drossou, C. Pontikis and M. Loukas. 2003. Genetic relationships among species and cultivars of *Pistacia* using RAPDs and AFLPs. Euphytica 132: 279–286.
Kaushik, A., N. Saini, S. Jain, P. Rana, R. K. Singh and R. K. Jain. 2003. Genetic analysis of a CSR10 (indica) × Taraori Basmati F3 population segregating for salt tolerance using ISSR markers. Euphytica 134: 231–238.
Kayimov, A.K., R.A. Sultanov and G.M. Chernova. 2001. *Pistacia* in Central Asia. In: Padulosi S. and A. Hadj-Hassan, (Eds). 2001. Project on Underutilized Mediterranean Species. *Pistacia*: towards a comprehensive documentation of distribution and use of its genetic diversity in Central and West Asia, North Africa and Mediterranean Europe. Report of the IPGRI Workshop, 14-17 December 1998, Irbid, Jordan.
Kermali I. R. 1994. Morphometric diversity in short-season maize (Zea mays L.) germplasm. Ph.D thesis, University of Guelph. 168pp.
Khadari, B., and A. Bervillé, 2001. Genetic Diversity of Moroccan Cultivated Olive Using Rapd Markers. Acta Hort. (ISHS) 546:439-442
Khaldi, A. and M. K. Khouja. 1996. Atlas pistachio (*P. atlantica* Desf.) in North Africa: Taxonomy, geographical distribution, utilization and conservation. In: S. Padulosi, T. Caruso and E. Barone (ed.). Taxonomy, Distribution, conservation and uses of *Pistacia* genetic resources. Report of a workshop, 29-30 June 1995, Palermo, Italy. International Plant Genetic Resources Institute, Rome Italy pp. 46-50.
Khalife, T. 1958. Pistachio Region Maaref Agric. Directorate, Aleppo –Syria, 63 pp (in Arabic).
Kokwaro J.O. and Gillett J.B. 1980. Notes on the Anacardiaceae of Eastern Africa. Kew Bull. 34: 745–760.
Korzun, V., A. Borner, A. J. Worland, C. N. Law and M. S. Roder. 1997. Application of microsatellite markers to distinguish inter-varietal chromosome substitution lines of wheat (Triticum aestivum L.). Euphytica 95, 149–155.
Krauss, S. L. and R. Peakall. 1998. An Evaluation of The AFLP Fingerprinting Technique for The Analysis of Paternity in Natural Populations of *Persoonia mollis* (*Proteaceae*). Australian Journal of Botany 46:533-546.
Kravchenko, V.I. 1961. The effect of the duration of pistachio seed storage on their germinating power in the ground. Izvest. Akad. Nauk Turkmen SSR Ser. Biol. Nauk, 5, 83-87.
Lagercrantz, U. and D.J. Lydiate. 1996. Comparative genome mapping in Brassica. Genetics 144(4):1903-1910.
Lee, A., J. K. Suh, M. S. Roh and J. P. Slovin, 2001. Analysis of Genetic Relationships of Ardisia spp. Using RAPD Markers. Tektran, United State Department of Agriculture, Agricultural Research Service

Levi, A., C. E. Thomas, T. Joobeur, X. Zhang and A. Davis. 2002. A genetic linkage map for watermelon derived from a testcross population: (Citrullus lanatus var. citroides Ẋ C. lanatus var. lanatus) anḍ Citrullus colocynthis. Theor Appl Genet 105:555–563.
Lewontin, R. C. and J. L. Hubby. 1966. A molecular approach to study of genetic heterozygosity in natural population. II. Amount of variation in natural population of Drosophila pseudoobscura. Genetics 54:595-609.
Lin T.S., Crane J.C., Ryugo K., PolitoV.S. and Dejong T.M. 1984. Comparative study of leaf morphology, photosynthesis and leaf conductance in selected *Pistacia* species. J. Amer. Soc. Hort. Sci. 109: 325–330.
Liu, Z. W., R. M. Biyashev and M. A. Saghai Maroof. 1996. Development of simple sequence repeat DNA markers and their integration into a barley linkage map. Theoretical and Applied Genetics 93, 869–876.
Loh, J. P., R. Kiew, A. Hay, A. Ke, L. H. Gan, and Y. Y. Gan, 2000. Intergeneric and Interspecific Relationships in Araceae Tribe Caladieae and Development of Molecular Markers Using Amplified Fragment Length Polymorphism (AFLP). Annals of Botany 85, 371–378.
Lu, J., M.R. Knox, M.J. Ambrose, J.K.M. Brown and T.H.N. Ellis, 1996. Comparative Analysis of Genetic Diversity in Pea Assessed by RFLP- and PCR-Based Methods. Theoretical and Applied Genetics 93, 1103–1111.
Mace, E. S., C. G. Gebhardt, and R. N. Lester, 1999. AFLP Analysis of Genetic Relationships in the Tribe *Datureae* (*Solanaceae*). Theoretical and Applied Genetics 99: 634-641
Maggs, D.H. 1973. Genetic Resources of Pistachio FAO Genetic Resources Newsletter, No. 29, 7-15 pp
Mantel, N. A. 1967. The detection of disease clustering and a generalized regression approach. Cancer Res 27:209–220.
Mardia, K.V., J. T. Kent and J. M. Bibby. 1979. Multivariate analysis. Academic Press, London.
Maxted N., B. V. Ford-Lloyd and J.G. Hawkes. 1997b. Complementary Conservation Strategies. In: Maxted N., Ford-Lloyd B.V. and J.G. Hawkes (Eds.) Plant Genetic Conservation: The In-Situ Approach. Chapman and Hall. Pp.15-39.
Maxted N., J. G. Hawkes, L. Guarino, and M. Sawkins. 1997a. Towards The Selection Of Taxa For Plant Genetic Conservation. Genetic Resources and Crop Evolution 44: 337-348.
Maxted N., M.W. Van Slageren and J. R. Rihan. 1995. Ecogeographic surveys. In: L. Guarino, V. Ramanatha Rao and R. Reid (Eds.). Collecting Plant Genetic Diversity. CABI. pp. 255-285.
Maxted, N. and S. Kell. 1998. Ecogeographic techniques and in situ conservation: a case study for the legume genus Vicia L. in Turkey. Proceedings of Conference in Turkey.
Mazzola, P., F.M. Raimondo and G. Venturella.1996.Natural occurrence and distribution of *Pistacia* in Italy. In: S. Padulosi, T. Caruso and E. Barone (Eds.). Taxonomy, Distribution, conservation and uses of *Pistacia* genetic resources. Report of a workshop, 29-30 June 1995, Palermo, Italy. International Plant Genetic Resources Institute, Rome Italy pp. 29-32.
Mielke, E. A. and F. True, 1979 Pistachio Production in Arizona, cooperative Extension Service, College of Agriculture, University of Arizona Tucson, Arizona.
Minà Palumbo, F. 1882. Monografia botanica ed agraria sulla coltivazione dei
Mlika, M. 1980. Contribution à l'étude du pistachier en Tunisie. Mémoire de fin d'études, INA Tunis, Tunisia 75pp.

Morgante, M. and A. M. Olivieri. 1993. PCR-amplified microsatellites as markers in plant genetics. Plant Journal 3:175–182.
Morgante, M., H. Hanafey and W. Powell. 2002. Microsatellites are preferentially associated with nonrepetitive DNA in plant genome. Nature Genetics 30:194–200.
Mouterde, S. J. 1966. Nouvelle Flore du Liban et de la Syrie. Tome premier. Ed. del'Imprimerie Catholique. Beyrouth, Liban.
Mueller, U. G. and L. L. Wolfenbarger, 1999. AFLP Genotyping and Fingerprinting. Trends in Ecology and Evolution 14, 389–394.
Muluvi, G.M., J.I. Sprent, N. Soranzo, J. Provan, D. Odee, G. Folkard, J.W. Mcnicol and W. Powell, 1999. Amplified Fragment Length Polymorphism (AFLP) Analysis of Genetic Variation in Moringa oleifera Lam. Molecular Ecology 8, 463–470.
Nachit, M. M., I. Elouafi, M. A. Pagnotta, A. El Saleh, E. Iacono, M. Labhilili, A. Asbati, M. Azrak, H. Hazzam, D. Benscher, M. Khairallah, J. M. Ribaut, O. A. Tanzarella, E. Porceddu, and M. E. Sorrells. 2001. Molecular linkage map for an intraspecific recombinant inbred population of durum wheat (*Triticum turgidum* L. var durum). Theor. Appl. Genet. 102:177–186.
Nahal, I, A. Rahme, and M. N. Shalabi. 1995. Forestry and forestry nurseries University of Aleppo. pp 224-230.
Nahal, I. 1981. The Mediterranean climate from a biological viewpoint. In Mediterranean-type shrublands. (Eds) F.d. Castro, D.W. Goodall & R.L. Specht), pp. 63-85. Elsevier Scientific Publishing Company, Amsterdam.
Nahal, I. 1995a. Study on sustainable forest resources development in Syria. University of Aleppo Agricultural Science Series, 23, 29-67.l
Nahal, I. 1996a. Contribution a L'Etude des Changements et de L'Histoire de la Vegetation Forestiere Naturelle en Syrie. Research Journal of Aleppo University. No.25 – 1996, 61-75.
Nahal, I. 1996b. Deforestation et Desertification en Syrie et dand les Pays Voisins. Première Parie. Historique des Changements Climatiques et de la Couverture Forestiere Naturelle. Research Journal of Aleppo University. No. 26-1996, 57-74.
Nahal, I. 1996c. Deforestation et Desertification en Syrie et dand les Pays Voisins. Deuxième Parie. Exploitation des Forets, Deforestation et Desertification. Research Journal of Aleppo University. No. 26-1996, 75-90.
Nahlawi, N., M. A. Kotob, A. Hadj-Hassan, M. Nahlawi and I. Haj-Ibrahim. 1985. Effect of modern techniques in growing pistachio trees under arid zone conditions, ACSAD, Damascus, Syria. PS.P 17. (in Arabic with English summary).
Nei, M. 1972. Genetic distance between populations. American Naturalist 106: 283-292.
Olufowote J. O., Y. Xu, X. Chen, W. D. Park, H. M. Beachell, R. H. Dilday, M. Goto and S. R. McCouch. 1997. Comparative evaluation of within-cultivar variation of rice (*Oryza sativa* L.) using microsatellite and RFLP markers. Genome 40:370–378.
Padulosi, S., T. Caruso, E. Barone, P. Van Mele and N. Kaska. 1998. IPGRI's Initiatives for the Promotion of Better Conservation and Use of *Pistacia* spp. Genetic Resources. In: L. Ferguson and D. Kester (Eds.). Proceeding of The Second International Symposium on Pistachios And Almonds. Acta Horticulturae Number 470.
Parfitt, D. E. 1995. Pistachio Cultivars. In: Pistachio production, University of California, Davis, pp.43-46.
Parfitt, D. E. and M. L. Badenes. 1997. Phylogeny of the genus *Pistacia* as determined from analysis of the chloroplast genome. Proc. Natl. Acad. Sci. USA. Vol. 94, pp. 7987–7992, July 1997

Parker, P.G., A. A. Snow, M. D. Schug, G. C. Booton and P. A. Fuerst. 1998. What molecules can tell us about populations: choosing and using a molecular marker. Ecology 79:361–382.
Pasqualone, A., F. Caponio, A. Blanco. 2001. Inter-simple sequence repeat DNA markers for identification of drupes from different Olea europaea L. cultivars. Eur Food Res Technol 213:240–243.
Peacock W.J., 1989. Molecular Biology and Genetic Resources. In: A. H. D. Brown, O. H. Frankel, D. R. Marshall and J.T. Williams(Eds.). The Use of Plant Genetic Resources. Cambridge university press. pp. 363-76.
Peakall, R., P. E. Smouse, D. R. Huff. 1995. Evolutionary implications of allozyme and RAPD variation in diploid populations of Buffalograss. (Buchloë dactyloides Nutt. Engelm.). Mol Ecol 4:135–147.
Peeters, J.P. and J.A. Martinelli. 1989. Hierarchical cluster analysis as a tool to manage variation in germplasm collections. Theoretical and Applied Genetics 78, 42–48.
Perry, M.C. and M.S. McIntosh, 1991. Geographical patterns of variation in the USDA soybean germplasm collection. I. Morphological traits. Crop Sci. 31: 1350–1355.
pistacchi in Sicilia. Lorsnaider Giovanni Tipografo, Palermo.
Post, G. E. 1932. Flora of Syria, Palestine and Sinai. Vol. 1. Faculty of Arts and Sciences. American University of Beirut, Lebanon. 658p.
Powell, W., G. C. Machray and J. Provan. 1996b. Polymorphism revealed by simple sequence repeats. Trends in Plant Science 1, 215–222.
Powell, W., M. Morgante, C. Andre, M. Hanafey, M. J. Vogel, S.V. Tingey and A. Rafalski, 1996. The Comparison of RFLP, RAPD, AFLP and SSR (Microsatellites) Markers for Germplasm Analysis. Molecular Breeding 2: 225-235.
Prevost, A. and M. J. Wilkinson. 1999. A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. Theor Appl Genet 98: 107–112.
Quarta, R., M. T. Dettori, I. Verde, U. Marchesi and M. A. Palombi, 2001. Characterization and Evaluation of Genetic Diversity in Peach Germplasm Using Rapd and Rflp Markers. Acta Hort. (ISHS) 546:489-496.
Queller, D. C., J. E. Strassmann and C. R. Hughes. 1993. Microsatellites and kinship. Trends in Ecology and Evolution 8:285–288.
Ramanatha Rao, V. and K.W. Riley. 1995. Towards a coconut conservation strategy. Paper presented at the COGENT-ADB Project and Steering Committee Meeting. 1-15 September. CCRI, Kasargod, India (Mimeographed).
Ramanatha Rao, V., K.W. Riley, J.M.M. Engels, F. Engelmann and M. Diekmann 1998. Towards a coconut conservation strategy. In Proceedings of Regional Coconut Genebank Planning Workshop, 26-28 February 1996 (V. Ramanatha Rao and Pons Batugal, eds.). Pekanbaru, Indonesia.
Ratnaparkhe, M. B., M. Tekeoglu, F. J. Muehlbauer,1998. Inter-simple-sequence-repeat (ISSR) polymorphisms are useful for finding markers associated with disease resistance gene clusters. Theor Appl Genet (1998) 97: 515-519.
Ribaut, J. M., M. Bänziger, J. Betran, C. Jiang, G. O. Edmeades, K. Dreher and D. Hoisington. 2002. Use of Molecular Markers in Plant Breeding: Drought Tolerance Improvement in Tropical Maize. In Edited by M S Kang,. Quantitative Genetics, Genomics and Plant Breeding. Louisiana State University, USA pp85-99
Rieger, M., 2002. Pistachio- *Pistacia vera* L. http://www.uga.edu/fruit/pistacio.htm
Rieseberg, L. H., M. J. Kim and G. J. Seiler, 1999. Introgression between the Cultivated Sunflower and a Sympatric Wild Relative, *Helianthus petiolaris* (*Asteraceae*). International Journal of Plant Science 160: 102-108.

Roberts, E.H. 1975. Problems of Long-Term Storage of Seed and pollen of Genetic Resources Conservation. In: O.H. Frankel and J.G. Hawkes (Eds.). Crop Genetic Resources for Today and Tomorrow. Cambridge University Press, Cambridge. pp. 269-296.
Robinson, A. J., C. G. Love, J. Batley, G. Barker and D. Edwards.2004. Simple sequence repeat marker loci discovery using SSR primer. BIOINFORMATICS Vol. 20 no. 9 2004. pages 1475–1476
Rohlf, F. J. 2000. NTSYS-pc: numerical taxonomy and multivariate analysis system, version 2.1. Exeter Software: Setauket, NY.
Rossetto, M., A. McLauchlan, F. Harriss, R. Henry, P. Baverstock, L. S. Lee, T. Maguire and K. Edwards. 1999a. Abundance and polymorphism of microsatellite markers in tea tree (*Melaleuca alternifolia – Myrtaceae*). Theoretical and Applied Genetics 98, 1091–1098.
Rossetto, M., R. W. Slade, P. R. Baverstock, R. J. Henry and L. S. Lee. 1999b. Microsatellite variation and assessment of genetic structure in tea tree (*Melaleuca alternifolia – Myrtaceae*). Molecular Ecology 8, 633–643.
Rottsieper., E.H.W. 1946. Vegetable Tannins. The Forestal Land, Timber and Railways Co. Ltd.
Rouskas, D. 1996. Conservation strategies of *Pistacia* genetic resources in Greece. In: S. Padulosi, T. Caruso and E. Barone (Eds.). Taxonomy, Distribution, conservation and uses of *Pistacia* genetic resources. Report of a workshop, 29-30 June 1995, Palermo, Italy. International Plant Genetic Resources Institute, Rome Italy pp.37-41.
Rovira, M., I. Batlle, M. Romero and F. J. Vargas. 1994. Isoenzymic identification of *Pistacia* species. Pistachio cultivar improvement at IRTA- Mas Bové. First International Symposium on Pistachio Nut. ISHS-FAO, Adana (Turkey). Acta Horticulturea.
Rus-Kortekaas, W., M. J. M. Smulders, P. Arens, and B. Vosman. 1994. Direct comparison of levels of genetic variation in tomato detected by a GACA-containing microsatellite probe and by random amplified polymorphic DNA. Genome 37, 375–381.
Russell J. R., J. D. Fuller, G. Young, B. Thomas, G. Taramino, M. Macaulay, R. Waugh and W. Powell. 1997. Discriminating between barley genotypes using microsatellite markers. Genome 40:442–450.
Russell, J. R., J. C. Weber, A. Booth, W. Powell, C. Sotelo-Montes and I.K. Dawson, 1999. Genetic Variation of Calycophyllum spruceanum in The Peruvian Amazon Basin, Revealed By Amplified Fragment Length Polymorphism (AFLP) Analysis. Molecular Ecology 8: 199-204.
S. Kafkas. 2006. Phylogenetic analysis of the genus *Pistacia* by AFLP markers. Plant Systematic Evolution. 262: 113–124.
Safarov, N. 2003. First National Report On Biodiversity Conservation. 95p.
Salhi-Hannachi, A., M. Trifi, S. Zehdi, J. Hedfi, M. Mars, A. Rhouma and M. Marrakchi. 2004. Inter-Simple Sequence Repeat fingerprints to assess genetic diversity in Tunisian fig (*Ficus carica* L.) germplasm. Genetic Resources and *Crop Evolution* 51: 269–275.
Sankar, A. A., and G. A. Moore. 2001. Evaluation of inter-simple sequence repeat analysis for mapping in Citrus and extension of the genetic linkage map. Theor Appl Genet 102:206–214.
Sankary. 1981. Ecology, plants and range of the Arid and very Arid Syrian areas its protect and development University of Aleppo. pp435-441
Sasanuma, T., K. Chabane, T. R. Endo, J. Valkoun. 2002. Genetic diversity of wild wheat and its relatives in the Near East detected by AFLP. Euphytica. 127: 81-93.

Scarascia-Mugnozza G.T. and P. Perrino, 2002. The history of Ex Situ Conservation and Use of Plant Genetic Resources. In: J. M. M. Engels V. Ramanatha Rao, A. H. D. Brown and M. T. Jackson (Eds.). Managing plant genetic resources. pp.1-22.
Schlötterer C. 2004. The evolution of molecular markers—just a matter of fashion?. Nature Reviews Genetics 5:63–69.
Schondelmaier, J., G. Steinrucken and C. Jung, 1996. Integration of AFLP Markers into a Linkage Map of Sugar Beet (*Beta vulgaris* L.). Plant Breeding 115, 231–237.
Sensi, E., R. Vignani, W. Rhode and S. Biricolti, 1996. Characterization of Genetic Biodiversity with Vitis vinifera L. Sangiovese and Colorino Genotypes by AFLP and ISTR DNA Marker Technology. Vitis 35, 183–188.
Shalabi, M. N. 1986. the most important wild relatives of the xerophytes fruit trees in Arab world. ACAD pp.1-25.
Sinclair, W.T., J.D. Morman and R.A. Ennos. 1999. The postglacial history of Scots pine (*Pinus sylvestris* L.) in western Europe: evidence from mitochondrial DNA variation. Mol. Ecol. 8:83-88.
Smith, J. S. C., E. C. L. Chin, H. Shu, O. S. Smith, S. J. Wall, M. L. Senior, S. E. Mitchell, S. Kresovich and J. Ziegle. 1997 An evaluation of the utility of SSR loci as molecular markers in maize (*Zea mays* L.): comparisons with data from RFLPs and pedigree. Theoretical and Applied Genetics 95, 163–173.
Smouse, P. E., J. C. Long and R. R. Sokal. 1986. Multiple regression and correlation extensions of the Mantel test of matrix correspondence. Systematic Zool 35:627–632.
Smulders, M. J. M., G. Bredemeijer, W. Rus-Kortekaas, P. Arens, and B. Vosman. 1997. Use of short microsatellites from database sequences to generate polymorphisms among Lycopersicon esculentum cultivars and accessions of other Lycopersicon species. Theoretical and Applied Genetics 97, 264–272.
Sokal, R. R. and Rohlf, F. J. 1981. Biometry. Second Edition. W.H. Freeman & Co.
Souza, E. and M. E. Sorrells, 1991. Relationships among 70 American oat germplasm. I. Cluster analysis using quantitative characters. Crop Sci. 31: 599–605.
Spooner D., R. van Treuren and M.C. de Vicente, 2005. Molecular markers for genebank management. IPGRI Technical Bulletin No. 10. International Plant Genetic Resources Institute, Rome, Italy.
Stephenson, P., G. Bryan, J. Kirby, A. Collins, K. Devos, C. Busso and M. Gale.1998. Fifty new microsatellite loci for the wheat genetic map. Theoretical and Applied Genetics 97, 946–949.
Sudupak, M. A. 2004. Inter and intra-species Inter Simple Sequence Repeat (ISSR) variations in the genus Cicer. Euphytica 135: 229–238, 2004.
Sun, C.Q., X.K. Wang, Z.C. Li, A. Yoshimura and N. Iwata. 2001. Comparison of the genetic diversity of common wild rice (*Oryza rufipogon* Griff.) and cultivated rice (*O. sativa* L.) using RFLP markers. Theor. Appl. Genet. 102:157-162.
Talhouk, S. N., G. A. Nehme, R. Baalbaki, R. Zurayk and Y. Adham. 2001. Ecogeographic characterization of *Pistacia* spp. in Lebanon. In: Padulosi S. and A. Hadj-Hassan, (Eds). 2001. Project on Underutilized Mediterranean Species. *Pistacia*: towards a comprehensive documentation of distribution and use of its genetic diversity in Central and West Asia, North Africa and Mediterranean Europe. Report of the IPGRI Workshop, 14-17 December 1998, Irbid, Jordan.
Talhouk, S.N., G.A. Nehme, R. Baalbaki, R. Zurayk and Y. Adham. 1998. Ecogeographic characterization of *Pistacia* spp. in Lebanon. In: Padulosi S. and A. Hadj-Hassan, (Eds). 2001. Project on Underutilized Mediterranean Species. *Pistacia*: towards a comprehensive documentation of distribution and use of its genetic diversity

in Central and West Asia, North Africa and Mediterranean Europe. Report of the IPGRI Workshop, 14-17 December 1998, Irbid, Jordan.
Tavaud, M., A. Zanetto, F. Santi and E. Dirlewanger, 2001. Structuration of Genetic Diversity in Cultivated and Wild Cherry Trees Using Aflp Markers. Acta Hort. (ISHS) 546:263-269.
Taylor, M.B. 1996. Tissue Culture as a Conservation strategy for South Pacific Root and Tuber Crops. Journal of South Pacific Agriculture 3, 10-20.
Tekin, H. and F. Akkök, 1995. Selection of Pistachio Nut and Their Comparison to Turkish Standard Varieties. First International Symposium on Pistachio Nut. ACTA Horticulturae, 419: 287-292. Vargas, F. J. and M. A. Romero. 1996. Vigor and juvenile stage in Pistachio progenies. In Proceedings of the X GREMPA meeting, organized by IRAM in collaboration with the FAO-CIHEAM Network on Nuts, Meknes, Morocco.
Temnykh, S., G. DeClerck, A. Lukashova, L. Lipovich, S. Cartinhour, and S. R. McCouch. 2001. Computational and experimental analysis of microsatellites in rice (*Oryza sativa* L.): frequency, length variation, transposon associations, and genetic marker potential. Genome Research 11, 1441–1452.
Temnykh, S., W. D. Park, N. Ayres, S. Cartinhour, N. Hauck, L. Lipovich, Y. G. Cho, T. Ishii, and S. R. McCouch. 2000. Mapping and genome organization of microsatellite sequences in rice (*Oryza sativa* L.). Theoretical and Applied Genetics 100, 697–712.
Thomas, C. M., P. Vos, M. Zabeau, D. A. Jones, K. A. Norcott, B. P. Chadwick and J. D. G. Jones, 1995. Identification of Amplified Restriction Fragment Polymorphism (AFLP) Markers Tightly Linked to The Tomato Cf-9 Gene for Resistance to Cladosporium fulvum. Plant Journal 8, 785–794.
Tikunov,Yu. M., L. I. Khrustaleva and G. I. Karlov. 2003. Application of ISSR markers in the genus Lycopersicon. Euphytica 131: 71–80.
Tohme, J., D.O. Gonzalez, S. Beebe and M.C. Duque, 1996. AFLP Analysis of Gene Pools of a Wild Bean Core Collection. Crop Science 36,1375–1384.
Tohme, J., P. Jones, S. Beebe and M. Iwanaga. 1995. The combined use of agroecological and characterization data to establish the CIAT Phaseolus vulgaris core collection. in T. Hodgkin, A.H.D. Brown, Th.J.L. van Hintum and E.A.V. Morales, (Eds.). Core collections genetic resources. John Wiley and Sons, Chichester, UK.. pp. 95-107
Tous, J. and L. Ferguson, 1996. Mediterranean fruits. In: J. JANICK (Eds.), Progress in new crops. ASHS press, Arlington, VA.
Towill, L.E. and C. Walters. 2000. Cryopreservation of Pollen. In: F. Engelmann and H. Takagi (Eds.). Cryopreservation of Tropical Plant Germplasm - Current Research Progress and Applications. Rome, Italy, Japan International Centre for Agricultural Sciences/international Plant Genetic Resources Institutes. pp. 115-129.
UNEP. 1995. Global Biodiversity Assessment. United Nations Environment Programme, Cambridge University Press, Cambridge, UK.
Uphof. J. C. Th. 1959. Dictionary of Economic Plants. Weinheim H.R. Engelmann.
USDA Nutrient Data Laboratory, 2006. USDA Nutrient Database for Standard Reference, Release 19. http://www.ars.usda.gov/nutrientdata.
USDA, NRCS. 2006. The PLANTS Database (http://plants.usda.gov, 1 October 2006). National Plant Data Center, Baton Rouge, LA 70874-4490 USA.
Usher. G. 1974. A Dictionary of Plants Used by Man: Constable.
Vargas, F. J., M. Romero, J. Plana, M. Rovira and I. Batlle. 1994. Characterization and behavior of cultivars in cattalonia (Spain). I International Symposium on Pistachio Nut. ISHS-FAO, Adana (Turkey). Acta Horticulturea.

Vargas, F. J., M. Romero, M. Rovira and I. Batlle. 1993. Pistachio cultivar improvement at IRTA- Mas Bové. IX GREMPA Meeting Pistachio, May 1993. Sciacca (Agrigento), Italy.
Vavilov, N. I., 1926. Tzentry Proiskhozhdeniya Kulturnyky Rastenii. The Centers of Origin of Cultivated Plants. Works of applied botany and plant breeding 16(2) 248P. (Russian, English).
Vavilov, N. I., 1960. Izbrannye Trudy. Problemy Selektzi, Rol Evrazii I Novogo Sveta v Proiskhozhdenii Kulturnyky Rastenii. Selected Works. The Problems of Breeding, The Role pf EurAsia and New World in Origin of Cultivated Plants. Vol. 2. USSR Academy of Science Press, M.-L. 520p.
Vijayan, K., A. Tikader, P. K. Kar, P. P. Srivastava, A. K. Awasthi, K. Thangavelu and B. Saratchandra. 2006. Assessment of genetic relationships between wild and cultivated mulberry (*Morus*) species using PCR based markers. Genetic Resources and Crop Evolution 53: 873–882.
Vos, P., R. Hogers, M. Bleeker, M. Reijans, T. Van De Lee, M. Hornes, A. Frijters, J. Pot, J. Peleman, M. Kuiper, M. Zabeau, 1995. AFLP: a New technique for DNA Fingerprinting. Nucleic Acids Research 23: 4407-4414.
Vosman, B., P. Arens, W. Rus-Kortekaas and M. J. M. Smulders. 1992. Identification of highly polymorphic DNA regions in tomato. Theoretical and Applied Genetics 85, 239–244.
Wang, Y. H., C. E. Thomas, and R. A. Dean. 1997. A Genetic Map of Melon (*Cucumis melo* L.) Based on Amplified Fragment Length Polymorphism (AFLP) Markers. Theoretical and Applied Genetics Vol:95, pp.791-798
WCMC. 1992. Global Biodiversity: Status of the Earth's Living Resources. World Conservation Monitoring Center, Chapman and Hall, London, UK.
Weising, K., H. Nybom, K. Wolff and G. Kahl. 2005. DNA Fingerprinting in plants, Principles, Methods, and Applications 2ed. Pp21-73.
Westman, A. L. and S. Kresovich. 1999. Simple sequence repeats (SSR)-based markervariation in Brassica nigra genebank accessions and weed populations. Euphytica 109:85-92.
Whitkus, R., J. Doebley and J. F. Wendel. 1994. Nuclear DNA markers in systematics and evolution. In R.L. Phillips and I.K. Vasil, (Eds.). DNA-based markers in plants (Advances in cellular and molecular biology of plants, vol. 1.). Kluwer Academic Publishers, Dordrecht, The Netherlands. pp. 116–141
Whittaker, R. H. 1967. Gradient analysis of vegetation. Biol. Review 42:207-264.
Williams, J. G. K., A. R. Kubelik, K. J. Livak, J. A. Rafalski, S. V. Tingey. 1990. DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. Nucleic Acids Res 18:6531–6535.
Winfield M. O., G. M. Arnold, F. Cooper, M. Le Ray, J. White, A. Karp and K. J. Edwards, 1998. A Study of Genetic Diversity in Populus nigra subsp. betulifolia in The Upper Severn Area of The UK using AFLP markers. Molecular Ecology 7: 3-10.
Winter, P., A. M. Benko-Iseppon, B. Hüttel, M. Ratnaparkhe, A. Tullu, G. Sonnante, T. Pfaff, M. Tekeoglu, D. Santra, V. J. Sant, P. N. Rajesh, G. Kahl, F. J. Muehlbauer. 2000. A linkage map of the chickpea (Cicer arietinum L.) genome based on recombinant inbred lines from a C. arietinum X C. reticulatum cross: localization of resistance genes for fusarium wilt races 4 and 5. Theor Appl Genet 101:1155–11630.
Withers, L. A. and J. M. M. Engels. 1990. The test tube genebank a safe alternative to field conservation. IBPGR NL for Asia and the Pacific 3: 1-2.
World Bank and UNDP. 1998. The State of the Environment in Syria. London, Environmental Resource Management.

Xu M. L., A. E. Melchinger, X. C. Xia and T. Lübberstedt, 1999. High-Resolution Mapping of Loci Conferring Resistance to Sugarcane Mosaic Virus in Maize Using RFLP, SSR and AFLP Markers. Molecular and General Genetics 261: 574-581.
Xu, R.Q., N. Tomooka, and D. A. Vaughan, 2000. AFLP Markers for Characterizing the Azuki Bean Complex. Crop Science 40:808-815.
Yaltirik F. 1967. Anacardiaceae. In: Davis P.H. (ed.), Flora of Turkey Vol. 2., pp. 544–519.
Yang, G. P., M. A. Maroof, C. G. Xu, Q. Zhang and R. M. Biyashev. 1994. Comparative analysis of microsatellite DNA polymorphism in landraces and cultivars of rice. *Molecular and General Genetics* 245, 187–194.
Yawen, Z., S. Shiquan, L. Zichao, Y. Zhongyi, W. Xiangkun, Z. Hongliang and W. Guosong. 2003. Ecogeographic and genetic diversity based on morphological characters of indigenous rice (*Oryza sativa* L.) in Yunnan, China Genetic Resources and Crop Evolution 50: 567–577.
Yoon, M. S., K. Doi, A. Kaga, N. Tomooka and D. A. Vaughan. 2000. Analysis of The Genetic Diversity in the Vigna minima Complex and Related Species in East Asia. Journal of Plant Research 113:375-386.
Youssef, R., S. Padulosi, A. Hadj Hassan, 2003. Assessment of distribution, diversity and use of pomegranate in Syria. (Master thesis in Arabic)
Zabeau, M., P. Vos. 1993. Selective restriction fragment amplification: a general method for DNA fingerprinting. European Patent Application 92402629.7. Publication # EP 0534858A1.
Zakynthinos G. and D. Rouskas. 2001. Wild and cultivated *Pistacia* species in Greece. In: Padulosi S. and A. Hadj-Hassan, (Eds). 2001. Project on Underutilized Mediterranean Species. *Pistacia*: towards a comprehensive documentation of distribution and use of its genetic diversity in Central and West Asia, North Africa and Mediterranean Europe. Report of the IPGRI Workshop, 14-17 December 1998, Irbid, Jordan.
Zhang, L. X., W. C. Chang, Y.J. Wei, L. Liu and Y.P. Wang. 1993. Cryopreservation of Ginseng Pollen. Hortscience 28(7): 742-743
Zhu J., M.D. Gale, S. Quarrie, M. T. Jackson and G.J. Bryan.1998. AFLP Markers for The Study of Rice Biodiversity. Theoretical and Applied Genetics 96: 602-611.
Zietkiewicz, E., A. Rafalski and D. Labuda. 1994. Genome fingerprinting by simple sequence repeat (SSR)-anchored polymerase chain reaction amplification. Genomics 20:176-183.
Zohary M. 1972. *Pistacia* L. Flora Palestine. Israel Academy of Sciences and Humanities, Jerusalem 2: 297–300.
Zohary, D. 1996. The Genus *Pistacia* L. In: S. Padulosi, T. Caruso and E. Barone (Eds.). Taxonomy, Distribution, Conservation and Uses of *Pistacia* genetic resources. Report of a workshop, 29-30 June 1995, Palermo, Italy. International Plant Genetic Resources Institute, Rome Italy pp.1-11.
Zohary, M. 1952. A Monographic Study of Genus *Pistacia*. Palestine P J. Bot., Series 5 (4): 187-228.
Zohary, M. 1973. Geobotanical Foundations of the Middle East. Gustav Fischer Verlag. Stuttgart Swets and Zeitlinger. Amsterdam.

Annexes

Annex 1

Key to the FAO Soil Units in the FAO/UNESCO soil map of the world which is extracted from "Legend of the Soil Map of the World", 1974, UNESCO, Paris. This Annex is part of website downloaded form the FAO website http://www.fao.org/AG/agl/agll/key2soil.stm.

LITHOSOLS (I)

Soils which are limited in depth by continuous coherent and hard rock within 10 cm of the surface.

VERTISOLS (V)

Soils which, after the upper 20 cm are mixed, have 30 percent or more clay in all horizons to at least 50 cm from the surface; at some period in most years have cracks at least 1 cm wide at a depth of 50 cm, unless irrigated, and have one or more of the following characteristics: gilgai microrelief, intersecting slickensides or wedge-shaped or parallelepiped structural aggregates at some depth between 25 and 100 cm from the surface.

Pellic Vertisols (Vp):	Vertisols having moist chromas of less than 1.5 dominant in the soil matrix throughout the upper 30 cm
Chromic Vertisols (Vc):	Other Vertisols

FLUVISOLS (J)

These soils developed from recent alluvial deposits, having no diagnostic horizons other than (unless buried by 50 cm or more new material) an ochric or an umbric A horizon, an H horizon, or a sulfuric horizon.

Thionic Fluvisols (Jt):	Fluvisols having a sulfuric horizon or sulfidic material, or both, at less than 125 cm from the surface
Calcaric Fluvisols (Jc):	Other Fluvisols which are calcareous, at least between 20 and 50 cm from the surface
Dystric Fluvisols	Other Fluvisols having a base saturation (by NH4OAc) of less

(Jd):	than 50 percent, at least in some part of the soil between 20 and 50 cm from the surface
Eutric Fluvisols (Je)	Other Fluvisols

REGOSOLS (R)

Other soils having no diagnostic horizons or none other than (unless buried by 50 cm or more new material) an ochric A horizon.

Gelic Regosols (Rx)	Regosols having permafrost within 200 cm of the surface
Calcaric Regosols (Rc)	Other Regosols which are calcareous at least between 20 and 50 cm from the surface
Dystric Regosols (Rd)	Other Regosols having a base saturation (by NH4OAc) of less than 50 percent, at least in some part of the soil between 20 and 50 cm from the surface
Eutric Regosols (Re)	Other Regosols

RENDZINAS (E)

Soils having a mollic A horizon which contains or immediately overlies calcareous material with a calcium carbonate equivalent of more than 40 percent (when the A horizon contains a high amount of finely divided calcium carbonate the colour requirements of the mollic A horizon may be waived).

PODZOLS (P)

Soils having a spodic B horizon.

Placic Podzols (Pp):	Podzols having a thin iron pan in or over the spodic B horizon
Gleyic Podzols (Pg):	Other Podzols showing hydromorphic properties within 50 cm of the surface
Humic Podzols (Ph):	Other Podzols having a B horizon in which a subhorizon contains dispersed organic matter and lacks sufficient free iron to turn redder on ignition
Ferric PodzoIs	Other Podzols in which the ratio of percentage of free iron to

(Pf):	percentage of carbon is 6 or more in all subhorizons of the B horizon
Leptic Podzols (PI):	Other Podzols lacking or having only a thin (2 cm or less) and discontinuous albic E horizon; lacking a subhorizon within the B horizon which is visibly more enriched with carbon
Orthic Podzols (Po):	Other Podzols

XEROSOLS (X)

Soils having a weak ochric A horizon and an aridic moisture regime; lacking permafrost within 200 cm of the surface.

Luvic Xerosols (Xl):	Xerosols having an argillic B horizon; a calcic or gypsic horizon may underlie the B horizon
Gypsic Xerosols (Xy):	Other Xerosols having a gypsic horizon within 125 cm of the surface
Calcic Xerosols (Xk):	Other Xerosols having a calcic horizon within 125 cm of the surface1
Haplic Xerosols (Xh):	Other Xerosols

YERMOSOLS (Y)

Soils having a very weak ochric A horizon and an aridic moisture regime; lacking permafrost within 200 cm of the surface.

Takyric Yermosols (Yt):	Yermosols showing takyric features
Luvic Yermosols (Yl):	Other Yermosols having an argillic B horizon; a calcic or gypsic horizon may underlie the B horizon
Gypsic Yermosols (Yy):	Other Yermosols having a gypsic horizon within 125 cm of the surface
Calcic Yermosols (Yk):	Other Yermosols having a calcic horizon within 125 cm of the surface1

Haplic Yermosols (Yh):	Other Yermosols

LUVISOLS (L)

Soils having an argillic B horizon.

Plinthic Luvisols (Lp):	Luvisols having plinthite within 125 cm of the surface
Gleyic Luvisols (Lg):	Other Luvisols showing hydromorphic properties within 50 cm of the surface
Albic Luvisols (La):	Other Luvisols having an albic E horizon
Vertic Luvisols (Lv):	Other Luvisols showing vertic properties
Calcic Luvisols (Lk):	Other Luvisols having a calcic horizon or concentrations of soft powdery lime within 125 cm of the surface when the weighted average textural class is coarse, within 90 cm for medium textures, within 75 cm for fine textures
Ferric Luvisols (Lf):	Other Luvisols showing ferric properties
Chromic Luvisols (Lc):	Other Luvisols having a strong brown to red B horizon (rubbed soil has a hue of 7.5YR and a chroma of more than 4, or a hue redder than 7.5YR)
Orthic Luvisols (Lo):	Other Luvisols

CAMBISOLS (B)

Soils having a cambic B horizon or an umbric A horizon which is more than 25 cm thick.

Gelic Cambisols (Bx)	Cambisols having permafrost within 200 cm of the surface
Gleyic Cambisols (Bg)	Other Cambisols showing hydromorphic properties within 100 cm of the surface
Vertic Cambisols (Bv)	Other Cambisols showing vertic properties
Calcic Cambisols (Bk)	Other Cambisols showing one or more of the following: a calcic horizon or a gypsic horizon or concentrations of soft

	powdery lime within 125 cm of the surface when the weighted average textural class is coarse, within 90 cm for medium textures, within 75 cm for fine textures; calcareous at least between 20 and 50 cm from the surface
Humic Cambisols (Bh)	Other Cambisols having an umbric A horizon which is thicker than 25 cm when a cambic B horizon is lacking
Ferralic Cambisols (Bf)	Other Cambisols having a cambic B horizon with ferralic properties
Dystric Cambisols (Bd)	Other Cambisols having a base saturation of less than 50 percent (by NH4OAc) at least in some part of the B horizon
Chromic Cambisols (Bc)	Other Cambisols which have a strong brown to red B horizon (rubbed soil has a hue of 7.5YR and a chroma of more than 4, or a hue redder than 7.5YR)
Eutric Cambisols (Be)	Other Cambisols

Annex 2

Table 33. ANOVA table for leaf and leaflet dimensions in *P. vera*'s populations.

			Sum of Squares	df	Mean Square	F	Sig.
Leaf_length * Population	Between Groups	(Combined)	124.895	7	17.842	2.481	0.019
	Within Groups		1,078.685	150	7.191		
	Total		1,203.580	157			
Leaf_width * Population	Between Groups	(Combined)	283.236	7	40.462	4.019	0.000
	Within Groups		1,510.060	150	10.067		
	Total		1,793.296	157			
Leaflet_length * Population	Between Groups	(Combined)	30.194	7	4.313	1.647	0.126
	Within Groups		392.822	150	2.619		
	Total		423.017	157			
Leaflet_width * Population	Between Groups	(Combined)	33.261	7	4.752	3.255	0.003
	Within Groups		218.969	150	1.460		
	Total		252.230	157			
Leaflet length /width Ratio * Population	Between Groups	(Combined)	2.139	7	0.306	3.784	0.001
	Within Groups		12.113	150	0.081		
	Total		14.252	157			

Table 34. ANOVA table for leaf and leaflet dimensions in *P. vera*'s individuals.

			Sum of Squares	df	Mean Square	F	Sig.
Leaf_length * samples	Between Groups	(Combined)	930.404	69	13.484	4.344	0.000
	Within Groups		273.177	88	3.104		
	Total		1,203.580	157			
Leaf_width * samples	Between Groups	(Combined)	1,325.481	69	19.210	3.614	0.000
	Within Groups		467.815	88	5.316		
	Total		1,793.296	157			
Leaflet_length * samples	Between Groups	(Combined)	265.730	69	3.851	2.155	0.000
	Within Groups		157.287	88	1.787		
	Total		423.017	157			
Leaflet_width * samples	Between Groups	(Combined)	173.028	69	2.508	2.786	0.000
	Within Groups		79.202	88	0.900		
	Total		252.230	157			
Leaflet length /width Ratio * samples	Between Groups	(Combined)	9.312	69	0.135	2.404	0.000
	Within Groups		4.941	88	0.056		
	Total		14.252	157			

Table 35. ANOVA table for leaf and leaflet dimensions in *P. atlantica*'s populations.

			Sum of Squares	df	Mean Square	F	Sig.
Leaf_length * Population	Between Groups	(Combined)	368.457	18	20.470	3.258	0.000
	Within Groups		1,577.195	251	6.284		
	Total		1,945.653	269			
Leaf_width * Population	Between Groups	(Combined)	371.330	18	20.629	3.803	0.000
	Within Groups		1,361.549	251	5.424		
	Total		1,732.879	269			
Leaflet_length * Population	Between Groups	(Combined)	134.648	18	7.480	3.824	0.000
	Within Groups		490.969	251	1.956		
	Total		625.617	269			
Leaflet_width * Population	Between Groups	(Combined)	37.652	18	2.092	5.230	0.000
	Within Groups		100.385	251	0.400		
	Total		138.038	269			
Leaflet length /width Ratio * Population	Between Groups	(Combined)	21.087	18	1.172	3.179	0.000
	Within Groups		92.484	251	0.368		
	Total		113.571	269			

Table 36. ANOVA table for leaf and leaflet dimensions in *P. atlantica*'s individuals.

			Sum of Squares	df	Mean Square	F	Sig.
Leaf_length * samples	Between Groups	(Combined)	1,232.033	89	13.843	3.492	0.000
	Within Groups		713.620	180	3.965		
	Total		1,945.653	269			
Leaf_width * samples	Between Groups	(Combined)	1,028.032	89	11.551	2.950	0.000
	Within Groups		704.847	180	3.916		
	Total		1,732.879	269			
Leaflet_length * samples	Between Groups	(Combined)	367.277	89	4.127	2.875	0.000
	Within Groups		258.340	180	1.435		
	Total		625.617	269			
Leaflet_width * samples	Between Groups	(Combined)	77.851	89	0.875	2.616	0.000
	Within Groups		60.187	180	0.334		
	Total		138.038	269			
Leaflet length /width Ratio * samples	Between Groups	(Combined)	54.355	89	0.611	1.856	0.000
	Within Groups		59.216	180	0.329		
	Total		113.571	269			

Table 37. ANOVA table for leaf and dimensions in *P. palaestina*'s populations.

			Sum of Squares	df	Mean Square	F	Sig.
Leaf_length * Population	Between Groups	(Combined)	213.379	14	15.241	1.974	0.022
	Within Groups		1,366.420	177	7.720		
	Total		1,579.799	191			
Leaf_width * Population	Between Groups	(Combined)	212.940	14	15.210	2.588	0.002
	Within Groups		1,040.239	177	5.877		
	Total		1,253.179	191			

Table 38. ANOVA table for leaf dimensions in *P. palaestina*'s individuals.

			Sum of Squares	df	Mean Square	F	Sig.
Leaf_length * samples	Between Groups	(Combined)	1,065.976	64	16.656	4.117	0.000
	Within Groups		513.823	127	4.046		
	Total		1,579.799	191			
Leaf_width * samples	Between Groups	(Combined)	852.333	64	13.318	4.219	0.000
	Within Groups		400.847	127	3.156		
	Total		1,253.179	191			

Table 39. ANOVA table for leaf and leaflet dimensions in *P. terebinthus*'s populations.

			Sum of Squares	df	Mean Square	F	Sig.
Leaf_length * Population	Between Groups	(Combined)	112.753	3	37.584	7.446	0.001
	Within Groups		146.371	29	5.047		
	Total		259.124	32			
Leaf_width * Population	Between Groups	(Combined)	29.209	3	9.736	3.013	0.046
	Within Groups		93.713	29	3.231		
	Total		122.922	32			
Leaflet_length * Population	Between Groups	(Combined)	5.852	3	1.951	1.092	0.368
	Within Groups		51.824	29	1.787		
	Total		57.676	32			
Leaflet_width * Population	Between Groups	(Combined)	1.501	3	0.500	1.270	0.303
	Within Groups		11.422	29	0.394		
	Total		12.922	32			
Leaflet length /width Ratio * Population	Between Groups	(Combined)	4.155	3	1.385	2.385	0.090
	Within Groups		16.837	29	0.581		
	Total		20.991	32			

Table 40. ANOVA table for leaf and leaflet dimensions in *P. terebinthus*'s individuals

			Sum of Squares	df	Mean Square	F	Sig.
Leaf_length * samples	Between Groups	(Combined)	215.714	10	21.571	10.932	0.000
	Within Groups		43.410	22	1.973		
	Total		259.124	32			
Leaf_width * samples	Between Groups	(Combined)	89.954	10	8.995	6.003	0.000
	Within Groups		32.968	22	1.499		
	Total		122.922	32			
Leaflet_length * samples	Between Groups	(Combined)	47.947	10	4.795	10.843	0.000
	Within Groups		9.728	22	0.442		
	Total		57.676	32			
Leaflet_width * samples	Between Groups	(Combined)	10.996	10	1.100	12.556	0.000
	Within Groups		1.927	22	0.088		
	Total		12.922	32			
Leaflet length /width Ratio * samples	Between Groups	(Combined)	10.152	10	1.015	2.060	0.076
	Within Groups		10.840	22	0.493		
	Total		20.991	32			

Table 41. ANOVA table for leaf and leaflet dimensions in *P. khinjuk*'s populations

			Sum of Squares	df	Mean Square	F	Sig.
Leaf_length * Population	Between Groups	(Combined)	2.288	1	2.288	0.463	0.512
	Within Groups		49.449	10	4.945		
	Total		51.737	11			
Leaf_width * Population	Between Groups	(Combined)	0.042	1	0.042	0.087	0.774
	Within Groups		4.808	10	0.481		
	Total		4.850	11			
Leaflet_length * Population	Between Groups	(Combined)	0.202	1	0.202	0.134	0.722
	Within Groups		15.065	10	1.507		
	Total		15.267	11			
Leaflet_width * Population	Between Groups	(Combined)	0.354	1	0.354	1.080	0.323
	Within Groups		3.282	10	0.328		
	Total		3.637	11			
Leaflet length /width Ratio * Population	Between Groups	(Combined)	0.098	1	0.098	2.549	0.141
	Within Groups		0.385	10	0.039		
	Total		0.484	11			

Table 42. ANOVA table leaf and leaflet dimensions in *P. khinjuk*'s individuals

			Sum of Squares	df	Mean Square	F	Sig.
Leaf_length * samples	Between Groups	(Combined)	29.158	4	7.290	2.260	0.163
	Within Groups		22.578	7	3.225		
	Total		51.737	11			
Leaf_width * samples	Between Groups	(Combined)	3.767	4	0.942	6.085	0.020
	Within Groups		1.083	7	0.155		
	Total		4.850	11			
Leaflet_length * samples	Between Groups	(Combined)	2.875	4	0.719	0.406	0.799
	Within Groups		12.392	7	1.770		
	Total		15.267	11			
Leaflet_width * samples	Between Groups	(Combined)	2.038	4	0.510	2.232	0.167
	Within Groups		1.598	7	0.228		
	Total		3.637	11			
Leaflet length /width Ratio * samples	Between Groups	(Combined)	0.159	4	0.040	0.859	0.532
	Within Groups		0.324	7	0.046		
	Total		0.484	11			

Table 43. ANOVA table for leaf and leaflet dimensions in *P. lentiscus*'s populations

			Sum of Squares	df	Mean Square	F	Sig.
Leaf_length * Population	Between Groups	(Combined)	13.458	2	6.729	1.991	0.145
	Within Groups		212.940	63	3.380		
	Total		226.398	65			
Leaf_width * Population	Between Groups	(Combined)	0.030	2	0.015	0.027	0.974
	Within Groups		36.143	63	0.574		
	Total		36.173	65			

Table 44. ANOVA table for leaf and leaflet dimensions in *P. lentiscus*'s individuals

			Sum of Squares	df	Mean Square	F	Sig.
Leaf_length * samples	Between Groups	(Combined)	197.158	21	9.388	14.128	0.000
	Within Groups		29.240	44	0.665		
	Total		226.398	65			
Leaf_width * samples	Between Groups	(Combined)	27.379	21	1.304	6.524	0.000
	Within Groups		8.794	44	0.200		
	Total		36.173	65			

Annex 3

Table 45. Genetic distance matrix among populations of *P. vera* using Nei (1972) coefficient based on AFLP data.

	FV02	FV08	FV22	FV23	FV38	FV39	FV40	FV41	FV42	FV43	FV50	FV52	FV54	FV58	MV08	MV22	MV40	MV42	MV43	MV44	MV52	MV54	MV58
FV02	0.00																						
FV08	0.23	0.00																					
FV22	0.21	0.28	0.00																				
FV23	0.19	0.23	0.09	0.00																			
FV38	0.22	0.22	0.19	0.15	0.00																		
FV39	0.20	0.22	0.15	0.14	0.08	0.00																	
FV40	0.18	0.20	0.14	0.11	0.07	0.05	0.00																
FV41	0.18	0.20	0.14	0.11	0.07	0.05	0.02	0.00															
FV42	0.18	0.20	0.14	0.12	0.08	0.05	0.03	0.03	0.00														
FV43	0.17	0.22	0.14	0.12	0.12	0.09	0.05	0.05	0.06	0.00													
FV50	0.20	0.23	0.13	0.12	0.12	0.08	0.09	0.08	0.08	0.11	0.00												
FV52	0.27	0.30	0.21	0.22	0.20	0.19	0.21	0.19	0.19	0.23	0.12	0.00											
FV54	0.22	0.19	0.13	0.15	0.14	0.13	0.12	0.12	0.12	0.13	0.10	0.12	0.00										
FV58	0.16	0.21	0.12	0.12	0.12	0.12	0.12	0.10	0.11	0.11	0.07	0.09	0.07	0.00									
MV08	0.13	0.12	0.20	0.18	0.16	0.16	0.14	0.14	0.15	0.16	0.19	0.28	0.20	0.16	0.00								
MV22	0.29	0.32	0.07	0.22	0.24	0.20	0.19	0.19	0.20	0.20	0.19	0.29	0.20	0.20	0.24	0.00							
MV40	0.22	0.24	0.18	0.14	0.11	0.09	0.07	0.05	0.08	0.12	0.12	0.21	0.15	0.13	0.17	0.24	0.00						
MV42	0.17	0.20	0.15	0.11	0.08	0.05	0.03	0.03	0.02	0.06	0.07	0.19	0.12	0.11	0.15	0.20	0.08	0.00					
MV43	0.17	0.20	0.14	0.10	0.07	0.05	0.03	0.03	0.02	0.04	0.08	0.19	0.12	0.10	0.15	0.20	0.08	0.00	0.00				
MV44	0.17	0.21	0.12	0.10	0.08	0.05	0.03	0.03	0.03	0.05	0.05	0.17	0.10	0.09	0.15	0.19	0.07	0.03	0.03	0.00			
MV52	0.36	0.34	0.22	0.27	0.23	0.23	0.23	0.22	0.23	0.24	0.20	0.16	0.13	0.14	0.34	0.29	0.27	0.23	0.22	0.21	0.00		
MV54	0.23	0.29	0.18	0.19	0.20	0.18	0.16	0.15	0.16	0.17	0.13	0.15	0.10	0.11	0.25	0.26	0.18	0.16	0.16	0.14	0.17	0.00	
MV58	0.19	0.23	0.17	0.14	0.13	0.12	0.11	0.09	0.11	0.11	0.12	0.16	0.12	0.09	0.18	0.24	0.12	0.11	0.10	0.11	0.25	0.21	0.00

For the populations code see section 3.3.1

Table 46. Genetic distance matrix among populations of *P. vera* using Nei (1972) coefficient based on ISSR data.

	FV02	FV08	FV22	FV23	FV38	FV39	FV40	FV41	FV42	FV43	FV50	FV52	FV54	FV58	MV22	MV40	MV42	MV43	MV44	MV52	MV54	MV58	MV08
FV02	0.00																						
FV08	0.45	0.00																					
FV22	0.46	0.49	0.00																				
FV23	0.42	0.46	0.07	0.00																			
FV38	0.75	0.70	0.62	0.58	0.00																		
FV39	0.73	0.64	0.60	0.51	0.15	0.00																	
FV40	0.70	0.65	0.56	0.48	0.15	0.20	0.00																
FV41	0.67	0.50	0.42	0.39	0.46	0.46	0.37	0.00															
FV42	0.63	0.55	0.36	0.34	0.43	0.46	0.34	0.04	0.00														
FV43	0.67	0.56	0.39	0.37	0.44	0.45	0.35	0.05	0.05	0.00													
FV50	0.65	0.51	0.42	0.36	0.43	0.44	0.36	0.22	0.21	0.20	0.00												
FV52	0.91	0.82	0.65	0.59	0.98	0.97	0.79	0.65	0.63	0.70	0.69	0.00											
FV54	0.89	0.80	0.60	0.51	0.99	0.86	0.77	0.65	0.64	0.66	0.63	0.19	0.00										
FV58	0.79	0.75	0.62	0.55	0.79	0.72	0.60	0.60	0.59	0.62	0.59	0.16	0.14	0.00									
MV22	0.35	0.41	0.15	0.12	0.63	0.59	0.55	0.42	0.38	0.41	0.44	0.62	0.54	0.54	0.00								
MV40	0.81	0.78	0.61	0.56	0.25	0.35	0.17	0.47	0.43	0.42	0.52	0.81	0.98	0.80	0.65	0.00							
MV42	0.65	0.58	0.41	0.39	0.42	0.45	0.36	0.05	0.04	0.06	0.22	0.70	0.68	0.59	0.41	0.47	0.00						
MV43	0.71	0.58	0.45	0.40	0.58	0.56	0.44	0.14	0.12	0.15	0.31	0.67	0.70	0.66	0.42	0.52	0.18	0.00					
MV44	0.62	0.50	0.39	0.35	0.45	0.46	0.37	0.19	0.18	0.19	0.06	0.64	0.59	0.54	0.40	0.52	0.19	0.28	0.00				
MV52	1.36	1.13	1.05	0.92	1.08	1.03	0.86	0.69	0.73	0.71	0.69	0.42	0.22	0.36	0.91	1.21	0.73	0.84	0.65	0.00			
MV54	0.98	0.84	0.77	0.67	0.91	0.81	0.63	0.67	0.68	0.68	0.73	0.31	0.21	0.22	0.73	0.90	0.73	0.74	0.69	0.38	0.00		
MV58	0.68	0.78	0.56	0.48	0.67	0.68	0.54	0.59	0.58	0.61	0.51	0.14	0.25	0.09	0.49	0.67	0.58	0.60	0.49	0.46	0.32	0.00	
MV08	0.27	0.13	0.37	0.32	0.62	0.57	0.57	0.47	0.47	0.49	0.48	0.72	0.69	0.68	0.28	0.69	0.49	0.53	0.46	1.02	0.84	0.64	0.00

For the populations code see section 3.3.1

Table 47. Genetic distance matrix among populations of *P. vera* using Nei (1972) coefficient based on SSR data.

	FV02	FV08	FV22	FV23	FV38	FV39	FV40	FV41	FV42	FV43	FV50	FV52	FV54	FV58	MV08	MV22	MV40	MV42	MV43	MV44	Mv52	MV54	MV58
FV02	0.00																						
FV08	2.01	0.00																					
FV22	1.37	1.71	0.00																				
FV23	0.51	1.23	0.64	0.00																			
FV38	0.46	2.47	0.89	0.19	0.00																		
FV39	0.54	2.42	0.83	0.31	0.17	0.00																	
FV40	0.59	1.08	0.59	0.06	0.25	0.42	0.00																
FV41	1.19	0.67	1.17	0.78	0.92	0.87	0.99	0.00															
FV42	1.78	0.93	1.62	1.41	1.55	1.49	1.71	0.28	0.00														
FV43	2.11	0.84	1.56	1.56	1.72	1.67	1.88	0.17	0.30	0.00													
FV50	1.24	0.52	1.40	0.99	1.12	1.07	1.19	0.23	0.21	0.32	0.00												
FV52	1.09	1.43	0.97	0.80	0.86	0.80	0.94	0.65	0.61	0.68	0.47	0.00											
FV54	1.67	0.68	1.36	1.41	2.12	2.07	1.31	0.64	0.58	0.72	0.51	0.52	0.00										
FV58	1.43	0.76	0.90	0.95	1.49	1.43	0.91	0.63	0.68	0.72	0.47	0.39	0.29	0.00									
MV08	0.72	1.84	0.46	0.34	0.29	0.27	0.35	0.74	1.05	1.11	0.90	0.67	1.14	0.96	0.00								
MV22	0.74	2.55	0.41	0.38	0.40	0.31	0.49	0.84	1.36	1.39	1.06	0.65	1.64	1.19	0.17	0.00							
MV40	1.24	0.00	0.78	0.48	0.45	0.40	0.78	0.98	1.64	1.68	1.35	0.95	2.22	1.69	0.41	0.27	0.00						
MV42	1.00	2.32	0.54	0.57	0.45	0.39	0.76	0.75	1.17	1.12	0.84	0.71	1.97	1.45	0.26	0.13	0.30	0.00					
MV43	1.15	1.78	0.69	0.88	0.69	0.64	1.05	0.89	1.21	1.18	0.80	0.86	2.12	1.60	0.40	0.36	0.60	0.14	0.00				
MV44	1.60	1.90	0.63	0.71	0.73	0.68	0.74	0.91	1.30	1.14	1.07	0.98	1.74	1.55	0.26	0.28	0.44	0.21	0.32	0.00			
Mv52	0.00	1.67	1.43	2.67	2.19	2.14	2.88	0.92	0.85	0.79	0.85	1.15	0.63	0.93	0.80	1.35	1.59	1.12	0.80	0.99	0.00		
MV54	1.24	0.00	0.78	0.93	0.78	0.73	1.01	1.20	1.64	1.68	1.35	0.95	1.52	1.47	0.49	0.33	0.69	0.30	0.60	0.38	0.90	0.00	
MV58	1.04	0.00	0.58	0.40	0.25	0.19	0.58	0.84	1.43	1.48	1.15	0.75	2.01	1.49	0.21	0.19	0.20	0.17	0.40	0.39	1.39	0.49	0.00

For the populations code see section 3.3.1

Table 48. Genetic distance matrix among populations of *P. vera* using Nei (1972) coefficient based on the data obtained with all three molecular markers typologies.

	FV02	FV08	FV22	FV23	FV38	FV39	FV40	FV41	FV42	FV43	FV50	FV52	FV54	FV58	MV08	MV22	MV40	MV42	MV43	MV44	MV52	MV54	MV58
FV02	0.00																						
FV08	0.11	0.00																					
FV22	0.26	0.28	0.00																				
FV23	0.12	0.14	0.15	0.00																			
FV38	0.17	0.17	0.31	0.16	0.00																		
FV39	0.17	0.17	0.30	0.16	0.04	0.00																	
FV40	0.16	0.17	0.30	0.15	0.03	0.05	0.00																
FV41	0.15	0.14	0.27	0.13	0.09	0.09	0.07	0.00															
FV42	0.15	0.15	0.26	0.13	0.09	0.09	0.07	0.01	0.00														
FV43	0.16	0.16	0.26	0.13	0.09	0.09	0.07	0.02	0.01	0.00													
FV50	0.15	0.14	0.27	0.13	0.09	0.09	0.07	0.05	0.05	0.05	0.00												
FV52	0.18	0.19	0.32	0.17	0.13	0.14	0.13	0.12	0.14	0.14	0.13	0.00											
FV54	0.17	0.17	0.28	0.14	0.14	0.13	0.12	0.10	0.10	0.11	0.10	0.10	0.00										
FV58	0.15	0.16	0.28	0.14	0.11	0.11	0.09	0.09	0.09	0.10	0.09	0.08	0.02	0.00									
MV08	0.07	0.04	0.25	0.10	0.14	0.14	0.14	0.12	0.12	0.13	0.12	0.16	0.14	0.13	0.00								
MV22	0.11	0.13	0.21	0.09	0.11	0.11	0.10	0.08	0.08	0.08	0.08	0.10	0.08	0.08	0.09	0.00							
MV40	0.18	0.18	0.30	0.16	0.05	0.07	0.04	0.09	0.09	0.09	0.10	0.14	0.13	0.11	0.15	0.11	0.00						
MV42	0.15	0.16	0.27	0.13	0.08	0.09	0.07	0.01	0.01	0.01	0.05	0.13	0.11	0.09	0.12	0.08	0.09	0.00					
MV43	0.17	0.16	0.28	0.14	0.11	0.11	0.09	0.03	0.03	0.04	0.07	0.15	0.12	0.11	0.14	0.09	0.10	0.04	0.00				
MV44	0.14	0.14	0.26	0.12	0.09	0.09	0.07	0.04	0.04	0.04	0.01	0.12	0.09	0.08	0.12	0.08	0.10	0.04	0.06	0.00			
MV52	0.18	0.19	0.32	0.17	0.13	0.14	0.13	0.12	0.14	0.14	0.13	0.00	0.10	0.08	0.16	0.10	0.14	0.13	0.15	0.12	0.00		
MV54	0.18	0.19	0.32	0.17	0.13	0.14	0.13	0.12	0.14	0.14	0.13	0.00	0.10	0.08	0.16	0.10	0.14	0.13	0.15	0.12	0.00	0.00	
MV58	0.15	0.18	0.29	0.14	0.12	0.13	0.11	0.11	0.11	0.12	0.11	0.06	0.08	0.05	0.14	0.08	0.11	0.12	0.12	0.11	0.06	0.06	0.00

For the populations code see section 3.3.1

Table 49. Genetic distance matrix among countries of *P. vera* using Nei (1972) coefficient based on AFLP data.

	f-Syria	f-Turkey	f-IRAN	f-Central Asia	f-Italy	m-Syria	m-Central Asia	m-Italy
f-Syria	0.00							
f-Turkey	0.13	0.00						
f-IRAN	0.11	0.08	0.00					
f-Central Asia	0.07	0.07	0.04	0.00				
f-Italy	0.09	0.12	0.11	0.08	0.00			
m-Syria	0.07	0.15	0.13	0.11	0.15	0.00		
m-Central Asia	0.08	0.07	0.04	0.01	0.09	0.12	0.00	
m-Italy	0.10	0.11	0.11	0.07	0.03	0.16	0.08	0.00

Table 50. Genetic distance matrix among countries of *P. vera* using Nei (1972) coefficient based on ISSR data.

	f-Syria	f-Turkey	f-IRAN	f-Central Asia	f-Italy	m-Syria	m-Central Asia	m-Italy
f-Syria	0.00							
f-Turkey	0.56	0.00						
f-IRAN	0.50	0.15	0.00					
f-Central Asia	0.29	0.32	0.34	0.00				
f-Italy	0.49	0.83	0.75	0.50	0.00			
m-Syria	0.16	0.57	0.52	0.33	0.54	0.00		
m-Central Asia	0.30	0.38	0.40	0.03	0.49	0.34	0.00	
m-Italy	0.56	0.76	0.75	0.50	0.10	0.60	0.50	0.00

Table 51. Genetic distance matrix among countries of *P. vera* using Nei (1972) coefficient based on SSR data.

	f-Syria	f-Turkey	f-IRAN	f-Central Asia	f-Italy	m-Syria	m-Central Asia	m-Italy
f-Syria	0.00							
f-Turkey	0.21	0.00						
f-IRAN	0.31	0.17	0.00					
f-Central Asia	0.64	0.85	0.85	0.00				
f-Italy	0.80	1.33	1.27	0.36	0.00			
m-Syria	0.26	0.29	0.25	0.68	0.86	0.00		
m-Central Asia	0.53	0.57	0.52	0.77	1.26	0.16	0.00	
m-Italy	0.65	0.56	0.51	0.73	0.86	0.21	0.22	0.00

Table 52. Genetic distance matrix among countries of *P. vera* using Nei (1972) coefficient based on all three molecular markers typologies data.

	f-Syria	f-Turkey	f-IRAN	f-Central Asia	f-Italy	m-Syria	m-Central Asia	m-Italy
f-Syria	0.00							
f-Turkey	0.43	0.00						
f-IRAN	0.42	0.04	0.00					
f-Central Asia	0.37	0.06	0.07	0.00				
f-Italy	0.39	0.11	0.11	0.07	0.00			
m-Syria	0.26	0.16	0.16	0.12	0.14	0.00		
m-Central Asia	0.37	0.07	0.08	0.01	0.07	0.12	0.00	
m-Italy	0.41	0.11	0.12	0.08	0.02	0.15	0.08	0.00

Table 53. Genetic distance matrix among populations of *P. atlantica* using Nei (1972) coefficient based on AFLP data.

	FA1	FA10	FA12	FA13	FA14	FA15	FA16	FA17	FA18	FA2	FA20	FA3	FA37	FA5	FA6	FA7	FA9	MA1	MA10	MA11	MA12	MA13	MA14	MA15	MA16	MA17	MA18	MA19	MA2	MA3	MA37	MA5	MA6	MA7
FA1	0.00																																	
FA10	0.10	0.00																																
FA12	0.08	0.08	0.00																															
FA13	0.20	0.20	0.17	0.00																														
FA14	0.17	0.17	0.15	0.09	0.00																													
FA15	0.13	0.16	0.13	0.10	0.09	0.00																												
FA16	0.13	0.14	0.13	0.11	0.10	0.06	0.00																											
FA17	0.16	0.16	0.15	0.10	0.11	0.09	0.09	0.00																										
FA18	0.13	0.17	0.14	0.11	0.12	0.09	0.07	0.10	0.00																									
FA2	0.11	0.17	0.16	0.26	0.22	0.17	0.17	0.22	0.19	0.00																								
FA20	0.17	0.20	0.16	0.17	0.18	0.13	0.13	0.15	0.13	0.21	0.00																							
FA3	0.07	0.12	0.09	0.22	0.22	0.17	0.18	0.19	0.17	0.14	0.18	0.00																						
FA37	0.16	0.19	0.17	0.26	0.21	0.16	0.18	0.21	0.17	0.19	0.19	0.20	0.00																					
FA5	0.11	0.11	0.11	0.18	0.19	0.17	0.17	0.18	0.18	0.20	0.21	0.10	0.22	0.00																				
FA6	0.12	0.12	0.11	0.21	0.19	0.19	0.17	0.18	0.17	0.21	0.19	0.11	0.22	0.09	0.00																			
FA7	0.09	0.10	0.11	0.22	0.20	0.16	0.16	0.18	0.14	0.17	0.19	0.10	0.19	0.10	0.10	0.00																		
FA9	0.18	0.17	0.18	0.31	0.27	0.24	0.25	0.27	0.27	0.19	0.26	0.18	0.27	0.18	0.24	0.16	0.00																	
MA1	0.03	0.11	0.08	0.20	0.19	0.16	0.17	0.16	0.16	0.15	0.20	0.08	0.21	0.11	0.12	0.10	0.18	0.00																
MA10	0.10	0.08	0.11	0.20	0.17	0.17	0.15	0.18	0.18	0.18	0.21	0.11	0.20	0.10	0.13	0.10	0.12	0.12	0.00															
MA11	0.13	0.09	0.12	0.22	0.20	0.19	0.16	0.19	0.19	0.23	0.22	0.16	0.24	0.13	0.14	0.14	0.20	0.14	0.12	0.00														
MA12	0.14	0.14	0.12	0.25	0.21	0.18	0.16	0.19	0.19	0.20	0.18	0.17	0.24	0.19	0.22	0.16	0.20	0.16	0.17	0.13	0.00													
MA13	0.14	0.17	0.14	0.09	0.12	0.11	0.10	0.10	0.09	0.19	0.18	0.18	0.23	0.17	0.17	0.15	0.31	0.17	0.17	0.20	0.22	0.00												
MA14	0.15	0.16	0.14	0.13	0.10	0.10	0.10	0.12	0.13	0.20	0.19	0.18	0.20	0.18	0.18	0.17	0.24	0.16	0.16	0.19	0.20	0.14	0.00											
MA15	0.17	0.19	0.16	0.10	0.06	0.08	0.10	0.09	0.10	0.26	0.19	0.22	0.23	0.20	0.19	0.19	0.30	0.18	0.20	0.20	0.22	0.12	0.12	0.00										
MA16	0.16	0.15	0.14	0.10	0.11	0.07	0.07	0.10	0.11	0.20	0.16	0.19	0.21	0.18	0.18	0.18	0.25	0.16	0.17	0.21	0.20	0.12	0.13	0.10	0.00									
MA17	0.15	0.16	0.15	0.13	0.11	0.11	0.08	0.11	0.10	0.19	0.17	0.19	0.20	0.16	0.19	0.16	0.27	0.18	0.14	0.19	0.20	0.11	0.12	0.12	0.13	0.00								
MA18	0.14	0.18	0.14	0.10	0.11	0.10	0.09	0.08	0.06	0.21	0.14	0.17	0.18	0.19	0.17	0.16	0.28	0.17	0.18	0.21	0.22	0.08	0.13	0.09	0.10	0.11	0.00							
MA19	0.16	0.22	0.20	0.22	0.23	0.14	0.11	0.18	0.14	0.18	0.14	0.20	0.21	0.23	0.23	0.20	0.26	0.19	0.21	0.26	0.23	0.22	0.20	0.23	0.18	0.17	0.19	0.00						
MA2	0.10	0.17	0.15	0.27	0.23	0.16	0.18	0.23	0.20	0.04	0.21	0.13	0.18	0.21	0.21	0.16	0.19	0.13	0.17	0.23	0.19	0.21	0.18	0.26	0.20	0.19	0.20	0.18	0.00					
MA3	0.09	0.14	0.11	0.24	0.22	0.18	0.19	0.20	0.19	0.14	0.20	0.05	0.24	0.11	0.13	0.11	0.20	0.08	0.14	0.18	0.18	0.20	0.19	0.22	0.20	0.20	0.21	0.22	0.13	0.00				
MA37	0.22	0.21	0.20	0.29	0.26	0.19	0.21	0.23	0.20	0.26	0.22	0.23	0.11	0.26	0.25	0.21	0.31	0.25	0.24	0.27	0.28	0.24	0.25	0.28	0.24	0.21	0.24	0.29	0.27	0.25	0.00			
MA5	0.10	0.12	0.10	0.20	0.22	0.17	0.16	0.18	0.17	0.18	0.20	0.11	0.23	0.06	0.08	0.12	0.20	0.10	0.13	0.13	0.18	0.18	0.17	0.20	0.18	0.17	0.19	0.21	0.19	0.12	0.27	0.00		
MA6	0.09	0.11	0.09	0.20	0.18	0.15	0.15	0.17	0.15	0.16	0.16	0.08	0.17	0.08	0.06	0.07	0.18	0.10	0.10	0.13	0.17	0.15	0.16	0.18	0.17	0.16	0.14	0.19	0.15	0.10	0.23	0.08	0.00	
MA7	0.11	0.10	0.12	0.21	0.20	0.17	0.17	0.18	0.17	0.18	0.19	0.11	0.20	0.09	0.08	0.06	0.19	0.10	0.13	0.15	0.19	0.17	0.18	0.20	0.18	0.18	0.18	0.21	0.18	0.10	0.21	0.11	0.08	0.00

For the populations code see section 3.3.2

Table 54. Genetic distance matrix among populations of *P. atlantica* using Nei (1972) coefficient based on ISSR data.

	FA10	FA12	FA1	FA13	FA14	FA15	FA16	FA17	FA18	FA20	FA2	FA3	FA37	FA5	FA6	FA7	FA9	MA10	MA11	MA1	MA12	MA13	MA14	MA15	MA16	MA17	MA18	MA19	MA2	MA3	MA37	MA5	MA6	MA7
FA10	0.00																																	
FA12	0.65	0.00																																
FA1	0.41	0.56	0.00																															
FA13	0.59	0.16	0.48	0.00																														
FA14	0.62	0.29	0.51	0.19	0.00																													
FA15	0.53	0.20	0.47	0.18	0.23	0.00																												
FA16	0.53	0.14	0.45	0.15	0.16	0.16	0.00																											
FA17	0.51	0.26	0.43	0.17	0.24	0.19	0.15	0.00																										
FA18	0.50	0.55	0.58	0.51	0.53	0.47	0.54	0.57	0.00																									
FA20	0.48	0.45	0.51	0.39	0.53	0.42	0.45	0.44	0.20	0.00																								
FA2	0.50	0.64	0.38	0.53	0.59	0.55	0.48	0.51	0.60	0.56	0.00																							
FA3	0.38	0.55	0.19	0.45	0.47	0.43	0.43	0.39	0.52	0.46	0.29	0.00																						
FA37	0.77	0.64	0.69	0.67	0.69	0.71	0.67	0.70	0.68	0.67	0.69	0.69	0.00																					
FA5	0.41	0.57	0.22	0.48	0.54	0.50	0.48	0.48	0.61	0.53	0.35	0.16	0.64	0.00																				
FA6	0.45	0.58	0.24	0.54	0.57	0.52	0.50	0.48	0.60	0.57	0.43	0.23	0.65	0.17	0.00																			
FA7	0.28	0.52	0.33	0.45	0.47	0.46	0.44	0.45	0.51	0.45	0.53	0.35	0.61	0.33	0.40	0.00																		
FA9	0.36	0.80	0.52	0.69	0.67	0.67	0.70	0.69	0.71	0.69	0.66	0.55	0.77	0.49	0.55	0.36	0.00																	
MA10	0.13	0.60	0.39	0.53	0.59	0.53	0.51	0.47	0.54	0.48	0.45	0.34	0.67	0.33	0.45	0.24	0.28	0.00																
MA11	0.12	0.55	0.35	0.48	0.51	0.45	0.45	0.43	0.45	0.41	0.41	0.29	0.68	0.31	0.36	0.21	0.32	0.13	0.00															
MA1	0.49	0.53	0.17	0.46	0.49	0.51	0.46	0.41	0.66	0.51	0.42	0.24	0.64	0.20	0.23	0.37	0.66	0.47	0.42	0.00														
MA12	0.25	0.58	0.42	0.51	0.59	0.54	0.48	0.51	0.60	0.52	0.37	0.44	0.75	0.38	0.48	0.34	0.40	0.23	0.15	0.46	0.00													
MA13	0.64	0.18	0.50	0.13	0.21	0.21	0.13	0.20	0.55	0.45	0.54	0.48	0.70	0.52	0.57	0.51	0.79	0.54	0.51	0.49	0.54	0.00												
MA14	0.56	0.18	0.49	0.12	0.18	0.20	0.17	0.23	0.50	0.45	0.56	0.48	0.69	0.52	0.55	0.48	0.67	0.54	0.45	0.50	0.51	0.13	0.00											
MA15	0.54	0.22	0.47	0.18	0.19	0.14	0.13	0.20	0.54	0.45	0.52	0.43	0.73	0.46	0.51	0.40	0.59	0.47	0.42	0.47	0.51	0.18	0.19	0.00										
MA16	0.55	0.25	0.46	0.21	0.27	0.13	0.16	0.24	0.57	0.53	0.50	0.43	0.69	0.46	0.51	0.46	0.67	0.54	0.47	0.48	0.53	0.20	0.19	0.16	0.00									
MA17	0.58	0.26	0.49	0.19	0.21	0.25	0.18	0.18	0.55	0.47	0.48	0.44	0.69	0.49	0.54	0.47	0.69	0.54	0.51	0.50	0.55	0.23	0.22	0.20	0.27	0.00								
MA18	0.56	0.46	0.56	0.42	0.51	0.46	0.49	0.49	0.19	0.17	0.59	0.51	0.66	0.51	0.58	0.49	0.67	0.56	0.47	0.57	0.54	0.47	0.46	0.46	0.56	0.49	0.00							
MA19	0.53	0.61	0.60	0.50	0.69	0.56	0.55	0.62	0.28	0.28	0.63	0.55	0.74	0.57	0.62	0.53	0.83	0.55	0.47	0.71	0.59	0.57	0.60	0.61	0.63	0.66	0.36	0.00						
MA2	0.50	0.69	0.37	0.61	0.73	0.63	0.57	0.63	0.68	0.58	0.15	0.35	0.70	0.34	0.42	0.46	0.66	0.48	0.43	0.45	0.42	0.59	0.62	0.63	0.57	0.62	0.65	0.69	0.00					
MA3	0.51	0.72	0.24	0.62	0.64	0.55	0.56	0.55	0.60	0.55	0.34	0.10	0.82	0.29	0.34	0.46	0.72	0.49	0.42	0.34	0.57	0.61	0.62	0.55	0.53	0.57	0.70	0.68	0.38	0.00				
MA37	0.71	0.59	0.67	0.57	0.65	0.57	0.63	0.62	0.74	0.64	0.72	0.67	0.25	0.68	0.65	0.63	0.78	0.64	0.64	0.67	0.79	0.69	0.58	0.62	0.59	0.60	0.70	0.78	0.77	0.78	0.00			
MA5	0.44	0.56	0.21	0.49	0.55	0.51	0.50	0.47	0.67	0.56	0.36	0.23	0.68	0.14	0.23	0.30	0.57	0.37	0.34	0.21	0.36	0.53	0.57	0.52	0.50	0.52	0.58	0.64	0.36	0.37	0.70	0.00		
MA6	0.42	0.54	0.19	0.47	0.50	0.53	0.46	0.47	0.61	0.51	0.38	0.17	0.67	0.13	0.17	0.34	0.52	0.39	0.32	0.18	0.45	0.50	0.49	0.46	0.47	0.49	0.57	0.55	0.41	0.26	0.70	0.24	0.00	
MA7	0.27	0.54	0.32	0.45	0.47	0.45	0.41	0.40	0.50	0.42	0.41	0.27	0.65	0.30	0.40	0.11	0.39	0.21	0.16	0.38	0.30	0.50	0.47	0.37	0.44	0.43	0.49	0.50	0.42	0.37	0.66	0.29	0.30	0.00

For the populations code see section 3.3.2

Table 55. Genetic distance matrix among populations of *P. atlantica* using Nei (1972) coefficient based on SSR data.

	FA1	FA2	FA3	FA10	FA12	FA13	FA14	FA15	FA16	FA17	FA18	FA20	FA37	FA5	FA6	FA7	FA9	MA1	MA2	MA3	MA10	MA11	MA12	MA13	MA14	MA15	MA16	MA17	MA18	MA19	MA37	MA5	MA6	MA7
FA1	0.00																																	
FA2	1.33	0.00																																
FA3	0.66	0.72	0.00																															
FA10	1.11	0.74	0.72	0.00																														
FA12	0.90	0.95	1.02	0.39	0.00																													
FA13	0.48	0.96	0.42	0.63	1.01	0.00																												
FA14	1.35	1.08	0.74	0.56	0.38	0.72	0.00																											
FA15	0.78	0.82	0.54	0.35	0.58	0.41	0.86	0.00																										
FA16	0.75	1.77	1.25	1.26	1.84	0.65	2.20	0.60	0.00																									
FA17	0.99	0.63	0.70	0.30	0.89	0.51	1.09	0.42	0.95	0.00																								
FA18	0.65	1.14	0.45	0.74	1.26	0.58	0.99	0.79	1.21	0.44	0.00																							
FA20	0.99	0.43	0.65	0.84	1.01	1.02	1.09	1.11	1.65	0.98	1.13	0.00																						
FA37	1.49	1.10	0.79	0.85	0.52	0.65	0.41	1.05	2.08	0.84	1.27	0.84	0.00																					
FA5	1.26	1.21	0.65	0.76	0.37	0.70	0.23	0.67	1.41	1.15	1.41	0.86	0.25	0.00																				
FA6	0.70	0.80	0.68	0.57	0.29	0.65	0.45	0.51	1.40	0.76	0.93	0.67	0.41	0.28	0.00																			
FA7	1.01	0.73	0.80	0.35	0.65	0.66	1.29	0.33	1.04	0.44	0.75	0.98	1.13	1.35	0.47	0.00																		
FA9	2.51	0.66	1.71	0.91	0.92	1.33	1.56	1.42	2.25	1.01	1.96	1.01	1.15	1.47	1.27	0.99	0.00																	
MA1	1.07	1.77	1.25	1.26	2.25	0.65	2.20	0.76	0.49	0.95	1.21	2.34	2.08	2.11	1.63	1.04	1.56	0.00																
MA2	0.49	1.50	1.75	2.55	1.75	1.07	0.00	1.28	0.40	1.84	1.81	1.56	0.00	2.71	1.82	2.05	2.16	0.85	0.00															
MA3	0.86	1.21	1.16	0.76	1.24	0.78	1.70	0.87	0.85	0.38	0.90	1.33	1.14	1.61	0.98	0.75	1.06	0.60	0.92	0.00														
MA10	1.14	1.53	1.60	1.20	1.50	0.66	1.45	1.02	1.04	1.59	0.00	1.59	1.17	1.35	1.57	1.39	1.50	1.04	1.13	2.05	0.00													
MA11	1.52	1.34	1.64	1.24	1.31	0.85	1.26	0.94	0.85	1.22	0.00	1.40	1.14	1.07	1.38	1.42	1.54	0.62	1.07	1.17	0.28	0.00												
MA12	1.43	2.13	2.42	0.00	3.30	1.52	0.00	2.14	0.85	3.39	0.00	0.00	0.00	3.16	0.00	0.00	1.92	0.69	0.67	1.77	1.40	1.03	0.00											
MA13	0.98	2.60	1.57	1.86	0.00	0.78	0.00	0.99	0.72	1.15	1.12	0.00	0.00	0.00	2.23	1.35	2.16	0.40	0.76	1.32	1.13	1.17	0.59	0.00										
MA14	1.44	1.27	0.93	0.53	1.52	0.69	1.07	0.59	0.70	0.64	1.18	1.21	1.35	1.38	1.19	0.72	1.52	0.87	1.38	0.87	0.72	0.80	2.01	0.87	0.00									
MA15	1.84	1.39	1.45	0.83	0.95	0.96	0.90	0.88	0.61	1.22	0.00	1.04	0.78	0.65	1.02	1.24	1.35	1.08	1.21	1.21	0.55	0.59	1.26	1.50	0.66	0.00								
MA16	1.88	1.83	2.19	1.38	0.70	2.10	0.78	1.90	2.03	1.26	2.43	1.77	0.45	0.84	0.90	1.98	1.39	2.03	1.94	1.25	1.98	1.61	2.39	2.64	1.71	1.14	0.00							
MA17	1.23	2.56	0.00	1.83	1.43	0.00	2.07	0.00	2.07	1.52	1.78	1.81	1.67	0.00	2.19	0.00	0.00	0.00	1.29	1.29	0.00	3.44	0.00	0.00	0.00	0.00	0.52	0.00						
MA18	1.24	2.39	2.06	1.66	0.57	2.37	0.65	2.18	1.90	1.64	1.61	2.05	0.69	0.71	0.77	0.00	0.00	1.90	1.81	1.81	0.00	2.17	1.57	1.81	0.00	1.70	0.35	0.68	0.00					
MA19	1.44	1.05	2.59	1.27	1.24	1.11	1.74	1.79	1.34	1.19	1.74	0.97	1.22	1.65	1.31	1.28	1.10	1.05	1.25	1.65	0.99	1.03	0.92	0.96	1.31	1.32	1.87	0.00	1.23	0.00				
MA37	1.69	2.06	1.37	0.97	1.27	1.59	1.12	1.30	1.91	1.36	1.84	1.36	1.86	1.12	1.34	2.76	2.88	2.13	0.00	1.82	2.76	2.80	1.48	1.63	1.81	1.52	3.35	0.00	1.28	1.81	0.00			
MA5	1.04	1.56	0.78	1.01	1.12	0.62	0.78	0.83	1.48	0.93	1.18	1.62	1.20	0.69	0.79	1.42	2.22	1.25	2.77	0.98	2.11	1.45	1.28	1.38	1.44	1.97	2.70	2.74	1.18	1.71	0.92	0.00		
MA6	1.74	1.10	1.35	1.06	1.35	0.92	1.30	1.29	2.40	1.04	2.11	1.16	0.90	1.21	1.14	1.14	1.07	2.40	3.00	1.06	1.24	1.46	0.00	0.00	1.67	1.28	1.54	2.27	2.80	1.03	1.93	0.99	0.00	
MA7	1.41	1.04	0.79	0.62	1.20	0.85	1.56	0.91	1.56	0.60	0.86	0.69	0.75	1.06	0.87	0.72	0.92	1.33	2.85	0.77	1.50	1.54	0.00	2.16	1.01	1.13	2.09	2.82	0.00	1.10	1.37	1.31	0.66	0.00

For the populations code see section 3.3.2

Table 56. Genetic distance matrix among populations of *P. atlantica* using Nei (1972) coefficient based on all three molecular markers typologies' data.

	FA1	FA10	FA12	FA13	FA14	FA15	FA16	FA17	FA18	FA2	FA20	FA3	FA37	FA4	FA5	FA6	FA7	FA9	MA1	MA10	MA11	MA12	MA13	MA14	MA15	MA16	MA17	MA18	MA19	MA2	MA3	MA37	MA5	MA6	MA7
FA1	0.00																																		
FA10	0.01	0.00																																	
FA12	0.00	0.01	0.00																																
FA13	0.03	0.02	0.03	0.00																															
FA14	0.03	0.02	0.03	0.00	0.00																														
FA15	0.02	0.02	0.02	0.00	0.00	0.00																													
FA16	0.03	0.02	0.02	0.00	0.00	0.00	0.00																												
FA17	0.03	0.02	0.02	0.00	0.00	0.00	0.00	0.00																											
FA18	0.02	0.02	0.02	0.01	0.01	0.00	0.00	0.01	0.00																										
FA2	0.01	0.01	0.01	0.03	0.03	0.03	0.03	0.03	0.03	0.00																									
FA20	0.03	0.02	0.02	0.01	0.01	0.01	0.00	0.01	0.00	0.03	0.00																								
FA3	0.00	0.01	0.00	0.03	0.03	0.02	0.02	0.03	0.02	0.01	0.03	0.00																							
FA37	0.09	0.09	0.09	0.11	0.10	0.10	0.10	0.10	0.10	0.09	0.10	0.09	0.00																						
FA4	0.01	0.01	0.01	0.03	0.03	0.03	0.03	0.03	0.03	0.01	0.03	0.01	0.10	0.00																					
FA5	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.02	0.01	0.09	0.01	0.00																				
FA6	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.02	0.01	0.09	0.01	0.00	0.00																			
FA7	0.00	0.01	0.01	0.03	0.03	0.02	0.03	0.03	0.02	0.00	0.03	0.00	0.09	0.01	0.01	0.01	0.00																		
FA9	0.01	0.01	0.01	0.03	0.03	0.03	0.02	0.03	0.03	0.01	0.03	0.01	0.10	0.01	0.01	0.01	0.01	0.00																	
MA1	0.00	0.01	0.00	0.03	0.03	0.02	0.03	0.03	0.03	0.01	0.03	0.01	0.09	0.01	0.01	0.00	0.01	0.01	0.00																
MA10	0.01	0.00	0.00	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.02	0.01	0.09	0.01	0.01	0.01	0.01	0.01	0.01	0.00															
MA11	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.01	0.02	0.01	0.01	0.01	0.10	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00														
MA12	0.01	0.01	0.01	0.02	0.02	0.01	0.01	0.02	0.01	0.01	0.02	0.01	0.09	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00													
MA13	0.03	0.02	0.03	0.00	0.01	0.00	0.01	0.00	0.01	0.03	0.01	0.03	0.11	0.03	0.02	0.02	0.03	0.03	0.03	0.02	0.02	0.02	0.00												
MA14	0.03	0.02	0.03	0.00	0.00	0.00	0.00	0.00	0.01	0.03	0.01	0.03	0.10	0.03	0.02	0.02	0.03	0.03	0.03	0.02	0.01	0.02	0.01	0.00											
MA15	0.03	0.03	0.03	0.00	0.00	0.00	0.01	0.01	0.01	0.04	0.01	0.03	0.11	0.03	0.02	0.02	0.03	0.03	0.03	0.02	0.02	0.02	0.01	0.00	0.00										
MA16	0.02	0.02	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.02	0.10	0.03	0.02	0.02	0.02	0.03	0.02	0.02	0.02	0.01	0.01	0.00	0.01	0.00									
MA17	0.03	0.02	0.02	0.01	0.01	0.01	0.00	0.00	0.00	0.03	0.00	0.02	0.10	0.03	0.02	0.02	0.03	0.02	0.03	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.00								
MA18	0.02	0.02	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.02	0.10	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.00	0.01	0.01	0.00	0.00	0.00							
MA19	0.02	0.02	0.02	0.01	0.01	0.01	0.00	0.01	0.00	0.02	0.01	0.02	0.10	0.03	0.02	0.02	0.02	0.02	0.03	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.00						
MA2	0.00	0.01	0.00	0.03	0.03	0.03	0.03	0.03	0.02	0.00	0.03	0.00	0.09	0.01	0.01	0.01	0.00	0.01	0.01	0.01	0.02	0.01	0.03	0.03	0.03	0.03	0.03	0.03	0.02	0.00					
MA3	0.01	0.01	0.00	0.03	0.03	0.02	0.02	0.02	0.02	0.01	0.02	0.00	0.09	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.03	0.03	0.03	0.02	0.02	0.02	0.02	0.01	0.00				
MA37	0.09	0.08	0.08	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.08	0.02	0.09	0.08	0.08	0.09	0.09	0.09	0.08	0.09	0.09	0.09	0.09	0.10	0.09	0.09	0.09	0.09	0.09	0.08	0.00			
MA5	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.02	0.01	0.09	0.01	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.03	0.02	0.03	0.02	0.02	0.02	0.02	0.01	0.01	0.09	0.00		
MA6	0.00	0.01	0.00	0.03	0.03	0.02	0.02	0.03	0.02	0.00	0.03	0.00	0.09	0.01	0.01	0.00	0.00	0.01	0.00	0.01	0.01	0.01	0.03	0.03	0.03	0.02	0.02	0.02	0.02	0.00	0.01	0.08	0.01	0.00	
MA7	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.02	0.01	0.09	0.01	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.02	0.02	0.03	0.02	0.02	0.02	0.02	0.01	0.01	0.08	0.01	0.01	0.00

For the populations code see section 3.3.2

Table 57. Genetic distance matrix among populations of *P. palaestina* using Nei (1972) coefficient based on AFLP data.

	FP24	FP25	FP26	FP27	FP28	FP29	FP31	FP32	FP33	FP34	FP35	FP36	FP4	MP24	MP25	MP26	MP27	MP28	MP29	MP31	MP32	MP33	MP34	MP35	MP36	MP4
FP24	0.00																									
FP25	0.09	0.00																								
FP26	0.11	0.07	0.00																							
FP27	0.12	0.07	0.06	0.00																						
FP28	0.12	0.09	0.08	0.07	0.00																					
FP29	0.20	0.15	0.14	0.14	0.08	0.00																				
FP31	0.20	0.16	0.15	0.15	0.12	0.08	0.00																			
FP32	0.20	0.18	0.16	0.15	0.10	0.09	0.08	0.00																		
FP33	0.20	0.15	0.15	0.14	0.11	0.09	0.08	0.08	0.00																	
FP34	0.23	0.17	0.16	0.15	0.12	0.11	0.11	0.09	0.08	0.00																
FP35	0.21	0.16	0.16	0.13	0.10	0.08	0.07	0.07	0.06	0.09	0.00															
FP36	0.20	0.16	0.16	0.16	0.10	0.08	0.08	0.08	0.07	0.11	0.06	0.00														
FP4	0.29	0.24	0.26	0.23	0.20	0.20	0.23	0.21	0.21	0.26	0.26	0.21	0.00													
MP24	0.09	0.05	0.07	0.07	0.09	0.14	0.15	0.15	0.14	0.15	0.14	0.15	0.22	0.00												
MP25	0.12	0.09	0.09	0.10	0.10	0.15	0.18	0.17	0.15	0.19	0.16	0.17	0.25	0.10	0.00											
MP26	0.13	0.07	0.06	0.07	0.10	0.17	0.19	0.16	0.14	0.14	0.16	0.17	0.25	0.07	0.11	0.00										
MP27	0.11	0.06	0.06	0.07	0.10	0.16	0.17	0.19	0.17	0.18	0.18	0.18	0.25	0.07	0.10	0.09	0.00									
MP28	0.18	0.13	0.11	0.08	0.12	0.20	0.18	0.21	0.19	0.21	0.20	0.23	0.30	0.13	0.15	0.11	0.12	0.00								
MP29	0.22	0.16	0.15	0.14	0.07	0.07	0.12	0.12	0.11	0.13	0.11	0.09	0.24	0.16	0.18	0.18	0.17	0.21	0.00							
MP31	0.20	0.16	0.16	0.15	0.11	0.09	0.06	0.09	0.09	0.11	0.09	0.09	0.25	0.15	0.20	0.17	0.18	0.21	0.10	0.00						
MP32	0.21	0.19	0.18	0.17	0.12	0.10	0.07	0.09	0.11	0.12	0.10	0.10	0.24	0.18	0.21	0.21	0.20	0.22	0.13	0.10	0.00					
MP33	0.24	0.21	0.17	0.17	0.14	0.14	0.12	0.10	0.09	0.12	0.10	0.08	0.27	0.18	0.19	0.18	0.21	0.23	0.18	0.14	0.13	0.00				
MP34	0.25	0.21	0.18	0.20	0.16	0.16	0.15	0.13	0.09	0.06	0.13	0.14	0.29	0.20	0.21	0.18	0.23	0.27	0.18	0.14	0.16	0.14	0.00			
MP35	0.26	0.20	0.18	0.18	0.13	0.11	0.10	0.10	0.08	0.07	0.07	0.08	0.24	0.18	0.20	0.17	0.21	0.24	0.15	0.11	0.13	0.12	0.10	0.00		
MP36	0.25	0.21	0.21	0.20	0.15	0.14	0.16	0.14	0.14	0.16	0.15	0.13	0.25	0.18	0.21	0.22	0.21	0.25	0.17	0.16	0.14	0.16	0.19	0.17	0.00	
MP4	0.28	0.24	0.24	0.24	0.20	0.21	0.22	0.20	0.20	0.25	0.24	0.20	0.12	0.23	0.25	0.24	0.25	0.28	0.24	0.23	0.22	0.24	0.28	0.24	0.22	0.00

For the populations code see section 3.3.3

Table 58. Genetic distance matrix among populations of *P. palaestina* using Nei (1972) coefficient based on ISSR data.

	FP24	FP25	FP26	FP27	FP28	FP29	FP31	FP32	FP33	FP34	FP35	FP36	FP4	MP24	MP25	MP26	MP27	MP28	MP29	MP31	MP32	MP33	MP34	MP35	MP36	MP4
FP24	0.00																									
FP25	0.36	0.00																								
FP26	0.99	0.82	0.00																							
FP27	0.89	0.76	0.12	0.00																						
FP28	0.78	0.70	0.12	0.11	0.00																					
FP29	0.85	0.65	0.22	0.22	0.24	0.00																				
FP31	0.85	0.69	0.47	0.39	0.38	0.47	0.00																			
FP32	0.98	0.68	0.54	0.52	0.49	0.47	0.17	0.00																		
FP33	0.91	0.73	0.53	0.43	0.42	0.50	0.16	0.15	0.00																	
FP34	0.80	0.70	0.50	0.44	0.42	0.47	0.19	0.22	0.20	0.00																
FP35	0.83	0.62	0.55	0.49	0.45	0.50	0.14	0.18	0.14	0.15	0.00															
FP36	0.83	0.70	0.51	0.45	0.43	0.49	0.17	0.20	0.15	0.17	0.13	0.00														
FP4	0.81	0.68	0.80	0.75	0.79	0.74	0.63	0.68	0.64	0.58	0.67	0.51	0.00													
MP24	0.34	0.12	0.79	0.76	0.69	0.67	0.74	0.73	0.75	0.69	0.65	0.70	0.63	0.00												
MP25	0.41	0.18	0.73	0.71	0.68	0.62	0.66	0.73	0.71	0.63	0.59	0.66	0.67	0.19	0.00											
MP26	0.58	0.31	0.22	0.22	0.19	0.32	0.46	0.52	0.49	0.50	0.52	0.50	0.70	0.39	0.42	0.00										
MP27	0.99	0.82	0.13	0.11	0.15	0.24	0.48	0.60	0.51	0.52	0.55	0.52	0.82	0.78	0.76	0.26	0.00									
MP28	0.80	0.70	0.41	0.30	0.35	0.39	0.55	0.67	0.62	0.64	0.63	0.71	0.90	0.71	0.70	0.35	0.39	0.00								
MP29	0.86	0.72	0.27	0.21	0.25	0.15	0.53	0.50	0.52	0.53	0.57	0.53	0.85	0.75	0.70	0.30	0.29	0.44	0.00							
MP31	0.85	0.70	0.53	0.46	0.43	0.46	0.16	0.23	0.18	0.19	0.17	0.23	0.62	0.73	0.66	0.50	0.52	0.61	0.49	0.00						
MP32	0.74	0.66	0.51	0.46	0.42	0.53	0.12	0.17	0.16	0.23	0.16	0.23	0.68	0.64	0.64	0.50	0.56	0.59	0.55	0.18	0.00					
MP33	0.85	0.68	0.57	0.47	0.48	0.57	0.16	0.17	0.10	0.18	0.15	0.20	0.64	0.72	0.73	0.52	0.54	0.66	0.55	0.19	0.21	0.00				
MP34	0.78	0.72	0.65	0.60	0.50	0.64	0.19	0.25	0.19	0.23	0.20	0.28	0.77	0.73	0.69	0.55	0.69	0.68	0.72	0.24	0.16	0.23	0.00			
MP35	0.76	0.68	0.52	0.44	0.42	0.50	0.14	0.20	0.18	0.15	0.11	0.17	0.65	0.66	0.63	0.50	0.53	0.64	0.59	0.17	0.15	0.19	0.17	0.00		
MP36	0.84	0.61	0.69	0.72	0.66	0.69	0.67	0.66	0.71	0.80	0.70	0.65	0.60	0.61	0.64	0.63	0.72	1.12	0.73	0.80	0.74	0.65	0.91	0.77	0.00	
MP4	0.72	0.68	0.71	0.72	0.77	0.69	0.56	0.70	0.68	0.57	0.64	0.58	0.22	0.64	0.75	0.65	0.74	0.81	0.78	0.62	0.65	0.65	0.70	0.66	0.65	0.00

For the populations code see section 3.3.3

Table 59. Genetic distance matrix among populations of *P. palaestina* using Nei (1972) coefficient based on SSR data.

	FP24	FP25	FP26	FP27	FP28	FP29	FP31	FP32	FP35	FP34	FP35	FP36	FP4	MP24	MP25	MP26	MP27	MP28	MP29	MP31	MP32	MP33	MP34	MP35	MP36	MP4
FP24	0.00																									
FP25	0.38	0.00																								
FP26	1.63	0.69	0.00																							
FP27	0.99	0.45	0.61	0.00																						
FP28	1.70	0.58	0.55	0.59	0.00																					
FP29	0.73	0.23	0.94	0.65	1.00	0.00																				
FP31	0.56	0.21	0.99	0.63	1.06	0.37	0.00																			
FP32	1.68	0.68	0.79	0.43	0.52	0.80	1.03	0.00																		
FP35	0.76	0.30	0.97	0.27	0.94	0.42	0.20	0.61	0.00																	
FP34	1.78	0.71	0.99	0.46	0.95	0.68	0.65	0.67	0.47	0.00																
FP35	0.94	0.57	1.25	1.01	2.01	0.29	0.67	1.48	0.63	1.11	0.00															
FP36	1.26	0.59	1.06	0.77	1.64	0.43	0.62	1.33	0.55	0.57	0.37	0.00														
FP4	1.70	1.17	2.42	1.08	2.48	0.53	1.34	1.77	1.26	0.62	0.34	0.54	0.00													
MP24	0.82	0.51	1.09	1.14	1.40	0.71	0.62	1.38	0.82	0.88	1.09	0.65	1.16	0.00												
MP25	0.75	0.52	1.18	1.22	1.94	0.45	0.79	1.51	1.00	1.32	0.77	0.80	1.24	0.85	0.00											
MP26	0.61	0.66	1.55	1.19	1.62	0.94	0.76	1.37	0.77	1.00	0.86	1.18	1.21	0.53	0.66	0.00										
MP27	0.62	0.66	1.75	1.79	1.81	1.02	0.76	1.79	1.06	1.89	1.34	1.26	1.81	0.21	1.26	0.72	0.00									
MP28	1.08	0.77	1.40	1.44	1.87	1.08	0.73	1.44	0.78	1.54	1.11	1.72	1.87	0.41	0.91	0.60	0.50	0.00								
MP29	0.72	0.76	1.44	1.30	1.72	1.04	0.87	1.48	0.87	1.11	0.97	1.42	1.32	0.44	0.77	0.17	0.65	0.19	0.00							
MP31	0.76	0.88	1.70	1.53	1.77	1.21	1.03	1.75	1.12	1.29	1.30	1.62	1.37	0.73	0.82	0.35	0.61	0.75	0.45	0.00						
MP32	1.20	0.67	1.41	1.27	1.70	0.82	0.74	1.46	1.05	0.86	1.63	0.70	1.30	0.34	0.46	0.72	0.62	1.08	1.07	0.99	0.00					
MP33	1.06	0.84	1.49	1.31	1.84	1.13	0.70	1.31	0.91	1.07	1.27	1.41	1.15	0.57	1.01	0.37	0.57	0.54	0.39	0.28	0.77	0.00				
MP34	0.68	0.77	2.50	1.85	2.56	0.90	0.73	1.85	1.11	1.95	1.11	1.43	1.87	1.10	0.40	0.60	1.20	0.85	0.70	0.75	0.68	0.94	0.00			
MP35	1.76	1.23	2.07	1.42	2.54	1.29	1.40	2.52	2.01	1.23	1.38	1.41	0.75	0.68	1.08	0.87	0.77	1.52	1.09	1.14	0.51	0.92	1.01	0.00		
MP36	1.01	0.70	1.72	1.77	2.48	1.00	0.65	1.77	1.03	1.87	1.32	1.35	1.79	0.47	1.24	0.70	0.31	0.77	0.81	0.85	0.60	0.64	0.77	0.35	0.00	
MP4	1.61	1.59	0.00	1.68	2.39	1.83	1.66	1.68	1.86	1.08	2.33	1.55	1.01	0.82	1.15	0.84	1.03	1.08	0.94	1.27	0.51	0.77	1.08	0.66	1.01	0.00

For the populations code see section 3.3.3

Table 60. Genetic distance matrix among populations of *P. palaestina* using Nei (1972) coefficient based on all the three molecular marker typologies' data.

	FP24	FP25	FP26	FP27	FP28	FP29	FP31	FP32	FP33	FP34	FP35	FP36	FP4	MP24	MP25	MP26	MP27	MP28	MP29	MP31	MP32	MP33	MP34	MP35	MP36	MP4
FP24	0.00																									
FP25	0.07	0.00																								
FP26	0.16	0.12	0.00																							
FP27	0.16	0.13	0.03	0.00																						
FP28	0.33	0.30	0.20	0.20	0.00																					
FP29	0.27	0.22	0.15	0.15	0.18	0.00																				
FP31	0.23	0.20	0.17	0.16	0.21	0.13	0.00																			
FP32	0.23	0.18	0.18	0.17	0.22	0.13	0.06	0.00																		
FP33	0.24	0.20	0.18	0.17	0.21	0.14	0.06	0.05	0.00																	
FP34	0.23	0.19	0.17	0.16	0.22	0.14	0.07	0.08	0.07	0.00																
FP35	0.22	0.17	0.17	0.17	0.21	0.13	0.05	0.05	0.05	0.06	0.00															
FP36	0.22	0.19	0.18	0.18	0.20	0.12	0.06	0.06	0.05	0.07	0.04	0.00														
FP4	0.19	0.15	0.18	0.17	0.38	0.29	0.23	0.22	0.23	0.21	0.23	0.21	0.00													
MP24	0.07	0.03	0.13	0.13	0.31	0.23	0.20	0.19	0.21	0.19	0.18	0.19	0.15	0.00												
MP25	0.10	0.06	0.15	0.16	0.33	0.24	0.22	0.22	0.22	0.21	0.19	0.21	0.19	0.06	0.00											
MP26	0.11	0.06	0.05	0.05	0.22	0.18	0.17	0.16	0.16	0.16	0.16	0.16	0.16	0.07	0.10	0.00										
MP27	0.17	0.13	0.04	0.03	0.20	0.15	0.18	0.19	0.18	0.17	0.18	0.18	0.19	0.12	0.15	0.06	0.00									
MP28	0.16	0.13	0.10	0.08	0.27	0.20	0.20	0.21	0.21	0.21	0.20	0.23	0.21	0.14	0.16	0.09	0.10	0.00								
MP29	0.25	0.21	0.15	0.14	0.16	0.06	0.15	0.14	0.14	0.15	0.13	0.12	0.30	0.22	0.24	0.15	0.15	0.19	0.00							
MP31	0.25	0.21	0.19	0.19	0.22	0.13	0.05	0.07	0.06	0.08	0.06	0.07	0.25	0.22	0.23	0.19	0.20	0.22	0.13	0.00						
MP32	0.22	0.20	0.19	0.18	0.23	0.15	0.05	0.06	0.07	0.08	0.07	0.08	0.24	0.20	0.22	0.18	0.19	0.21	0.15	0.07	0.00					
MP33	0.23	0.19	0.19	0.17	0.24	0.17	0.07	0.06	0.05	0.07	0.06	0.06	0.21	0.20	0.22	0.17	0.18	0.22	0.16	0.08	0.08	0.00				
MP34	0.25	0.22	0.22	0.22	0.25	0.19	0.09	0.10	0.07	0.07	0.08	0.11	0.28	0.23	0.24	0.19	0.22	0.24	0.20	0.10	0.08	0.10	0.00			
MP35	0.24	0.21	0.19	0.18	0.23	0.16	0.06	0.08	0.07	0.05	0.05	0.07	0.24	0.20	0.22	0.18	0.20	0.23	0.17	0.08	0.07	0.07	0.07	0.00		
MP36	0.20	0.15	0.18	0.18	0.39	0.33	0.26	0.23	0.27	0.25	0.23	0.23	0.17	0.17	0.23	0.16	0.19	0.20	0.31	0.28	0.27	0.24	0.30	0.27	0.00	
MP4	0.19	0.16	0.19	0.18	0.40	0.30	0.23	0.24	0.25	0.23	0.24	0.24	0.06	0.17	0.22	0.17	0.19	0.22	0.30	0.26	0.25	0.23	0.29	0.26	0.20	0.00

For the populations code see section 3.3.3

Table 61. Genetic distance matrix among populations of *P. terebinthus* using Nei (1972) coefficient based on AFLP data.

	FT29	FT37	MT29	MT37	MT59	FT60
FT29	0.00					
FT37	0.12	0.00				
MT29	0.04	0.13	0.00			
MT37	0.10	0.11	0.10	0.00		
MT59	0.19	0.22	0.20	0.19	0.00	
FT60	0.13	0.11	0.14	0.10	0.11	0.00

For the populations code see section 3.3.4

Table 62. Genetic distance matrix among populations of *P. terebinthus* using Nei (1972) coefficient based on ISSR data.

	FT29	FT37	MT29	MT37	MT59	FT60
FT29	0.00					
FT37	0.75	0.00				
MT29	0.18	0.81	0.00			
MT37	0.77	0.28	0.79	0.00		
MT59	1.10	1.10	1.11	1.19	0.00	
FT60	0.98	0.87	0.88	0.91	0.35	0.00

For the populations code see section 3.3.4

Table 63. Genetic distance matrix among populations of *P. terebinthus* using Nei (1972) coefficient based on SSR data.

	FT29	FT37	MT29	MT37	MT59	FT60
FT29	0.00					
FT37	1.37	0.00				
MT29	0.10	1.27	0.00			
MT37	0.76	0.43	0.49	0.00		
MT59	1.03	0.52	1.04	0.60	0.00	
FT60	0.94	1.12	0.95	1.07	0.31	0.00

For the populations code see section 3.3.4

Table 64. Genetic distance matrix among populations of *P. terebinthus* using Nei (1972) coefficient based on all the three molecular marker typologies' data.

	FT29	FT37	MT29	MT37	MT59	FT60
FT29	0.00					
FT37	0.19	0.00				
MT29	0.06	0.21	0.00			
MT37	0.17	0.09	0.18	0.00		
MT59	0.33	0.27	0.36	0.29	0.00	
FT60	0.34	0.26	0.36	0.28	0.04	0.00

For the populations code see section 3.3.4

Table 65. Genetic distance matrix among populations of *P. khinjuk* using Nei (1972) coefficient based on AFLP data.

	MK16-1	MK18-4	FK16-4	FK18-5	FK18-3
MK16-1	0.00				
MK18-4	0.08	0.00			
FK16-4	0.19	0.25	0.00		
FK18-5	0.22	0.19	0.28	0.00	
FK18-3	0.18	0.17	0.23	0.14	0.00

For the populations code see section 3.3.5

Table 66. Genetic distance matrix among populations of *P. khinjuk* using Nei (1972) coefficient based on ISSR data.

	MK16-1	MK18-4	FK16-4	FK18-3	FK18-5
MK16-1	0.00				
MK18-4	0.23	0.00			
FK16-4	0.54	0.51	0.00		
FK18-3	0.58	0.50	0.32	0.00	
FK18-5	0.55	0.51	0.25	0.31	0.00

For the populations code see section 3.3.5

Table 67. Genetic distance matrix among populations of *P. khinjuk* using Nei (1972) coefficient based on SSR data.

	FK18-5	FK18-3	FK16-4	MK18-4	MK16-1
FK18-5	0.00				
FK18-3	0.97	0.00			
FK16-4	0.68	1.50	0.00		
MK18-4	0.00	0.00	0.00	0.00	
MK16-1	1.78	0.00	1.61	0.92	0.00

For the populations code see section 3.3.5

Table 68. Genetic distance matrix among populations of *P. khinjuk* using Nei (1972) coefficient based on all three molecular marker typologies' data.

	MK16-1	FK18-5	FK18-3	FK16-4	MK18-4
MK16-1	0.000				
FK18-5	0.003	0.000			
FK18-3	0.002	0.005	0.000		
FK16-4	0.012	0.009	0.010	0.000	
MK18-4	0.000	0.003	0.002	0.012	0.000

For the populations code see section 3.3.5

Table 69. Genetic distance matrix among populations of *P. lentiscus* using Nei (1972) coefficient based on AFLP data.

	FL21	FL40	FL54	ML21	ML40	ML54
FL21	0.00					
FL40	0.26	0.00				
FL54	0.26	0.20	0.00			
ML21	0.04	0.28	0.28	0.00		
ML40	0.32	0.17	0.21	0.33	0.00	
ML54	0.22	0.19	0.05	0.25	0.22	0.00

For the populations code see section 3.3.6

Table 70. Genetic distance matrix among populations of *P. lentiscus* using Nei (1972) coefficient based on ISSR data.

	FL21	FL40	FL54	ML21	ML40	ML54
FL21	0.00					
FL40	0.66	0.00				
FL54	0.76	0.66	0.00			
ML21	0.09	0.61	0.74	0.00		
ML40	0.74	0.09	0.71	0.71	0.00	
ML54	0.73	0.73	0.15	0.73	0.82	0.00

For the populations code see section 3.3.6

Table 71. Genetic distance matrix among populations of *P. lentiscus* using Nei (1972) coefficient based on SSR data.

	FL21	FL40	FL54	ML21	ML40	ML54
FL21	0.00					
FL40	0.58	0.00				
FL54	2.20	2.11	0.00			
ML21	0.12	0.34	2.16	0.00		
ML40	1.13	0.53	1.85	0.80	0.00	
ML54	1.05	1.28	0.48	1.04	1.42	0.00

For the populations code see section 3.3.6

Table 72. Genetic distance matrix among populations of *P. lentiscus* using Nei (1972) coefficient based on all the three molecular marker typologies' data.

	FL21	FL40	FL54	ML21	ML40	ML54
FL21	0.00					
FL40	0.01	0.00				
FL54	0.12	0.12	0.00			
ML21	0.00	0.01	0.12	0.00		
ML40	0.12	0.11	0.03	0.12	0.00	
ML54	0.13	0.13	0.01	0.13	0.04	0.00

For the populations code see section 3.3.6

Table 73. Genetic distance matrix among of *Pistacia* using Nei (1972) coefficient based on AFLP data.

	P. atlantica	*P. khinjuk*	*P. palaestina*	*P. terebinthus*	*P. vera*	Cultivated *P. vera*	Wild *P. vera*	*P. lentiscus*
P. atlantica	0.00							
P. khinjuk	0.07	0.00						
P. palaestina	0.09	0.13	0.00					
P. terebinthus	0.09	0.13	0.04	0.00				
P. vera	0.06	0.11	0.07	0.06	0.00			
Cultivated *P. vera*	0.06	0.11	0.09	0.09	0.01	0.00		
Wild *P. vera*	0.07	0.13	0.08	0.06	0.01	0.05	0.00	
P. lentiscus	0.08	0.10	0.07	0.06	0.06	0.08	0.06	0.00

Table 74. Genetic distance matrix among populations of *Pistacia* using Nei (1972) coefficient based on ISSR data.

	P. atlantica	*P. khinjuk*	*P. palaestina*	*P. terebinthus*	*P. vera*	*P. lentiscus*	Cultivated *P. vera*	Wild *P. vera*
P. atlantica	0.00							
P. khinjuk	0.22	0.00						
P. palaestina	0.28	0.42	0.00					
P. terebinthus	0.29	0.42	0.14	0.00				
P. vera	0.18	0.33	0.25	0.25	0.00			
P. lentiscus	0.22	0.25	0.20	0.19	0.23	0.00		
Cultivated *P. vera*	0.17	0.28	0.27	0.31	0.06	0.23	0.00	
Wild *P. vera*	0.30	0.48	0.34	0.30	0.05	0.33	0.23	0.00

Table 75. Genetic distance matrix among populations of *Pistacia* using Nei (1972) coefficient based on SSR data.

	P. atlantica	*P. khinjuk*	*P. palaestina*	*P. terebinthus*	*P. vera*	Cultivated *P. vera*	Wild *P. vera*	*P. lentiscus*
P. atlantica	0.00							
P. khinjuk	0.45	0.00						
P. palaestina	0.77	0.69	0.00					
P. terebinthus	0.55	0.74	0.18	0.00				
P. vera	0.56	0.63	1.11	0.92	0.00			
Cultivated *P. vera*	0.52	0.76	1.30	0.90	0.06	0.00		
Wild *P. vera*	0.73	0.63	1.05	1.05	0.06	0.26	0.00	
P. lentiscus	0.56	0.41	0.57	0.71	0.47	0.67	0.40	0.00

Table 76. Genetic distance matrix among populations of *Pistacia* using Nei (1972) coefficient based on all the three molecular marker typologies' data

	P. atlantica	Cultivated *P. vera*	*P. khinjuk*	*P. lentiscus*	*P. palaestina*	*P. terebinthus*	*P. vera*	Wild *P. vera*
P. atlantica	0.00							
Cultivated *P. vera*	0.07	0.00						
P. khinjuk	0.25	0.32	0.00					
P. lentiscus	0.08	0.09	0.25	0.00				
P. palaestina	0.09	0.10	0.29	0.07	0.00			
P. terebinthus	0.10	0.10	0.30	0.07	0.05	0.00		
P. vera	0.06	0.02	0.31	0.07	0.09	0.08	0.00	
Wild *P. vera*	0.32	0.39	0.08	0.30	0.35	0.37	0.38	0.00