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NUCUL - CONSTRÂNGERI ȘI AVANTAJE PENTRU O DEZVOLTARE DURABILĂ
THE WALNUT - CONSTRAINTS AND ADVANTAGES FOR A SUSTAINABLE DEVELOPMENT

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Abstract

The Persian walnut or English walnut (*Juglans regia* L.) is a commonly grown species for nut production and noble wood. The nut is one of the oldest food and traditional medicine sources. The native and commercial walnut genotypes present a large diversity that differ widely in nut productivity and quality. However, genetic erosion poses a serious threat to this tree. Several researches of walnut genetic diversity are being carried out utilizing morphological, biochemical, and molecular approaches in order to select superior walnut cultivars of different agroclimatic areas to increase nut production and quality. Genetic resource evaluation and agrodiversity conservation have a major role in ensuring food security for future generations through a continuous supply of new rootstocks and improved cultivars.

Cuvinte cheie: nuc, resurse genetice, program de ameliorare, eroziune genetică, genomică.
Key words: walnut, genetic resources, breeding program, genetic erosion, genomic.

1. Introduction

The *Juglandaceae* family includes 10 genera and 60 species. The *Juglans* genus, which is one of the most important genera, includes 20 species (Song et al., 2019). This genus is subdivided according to the structure of the fruit in four sections: *Trachycaryon*, *Cardiocaryon*, *Rhysocaryon* and *Dioscaryon*. In addition, they are classified according to the characteristics of their wood in three main groups: *Juglans nigra*, *Juglans cinerea* and *Juglans regia* (Manning, 1978). *Juglans regia* tree reaches a height of 40 to 60 feet and has a lifespan exceeding 60 years (Hill and Sharma, 1988). Their natural range extends from Eastern Europe's Carpathian Mountains to the Southern Caucasus, Northern Turkey, Iran, western China's Tian Shan Province, the Himalayan states of India, Sikkim, and Bhutan (Angmo et al., 2013). It is the most cultivated species in temperate regions for its economic value due to its excellent wood and its nourishing nut, allowing it to be considered a priority plant of the FAO (Gandev, 2007; Shamasbi et al., 2018). The world nut production was about 3.83 million tons on an area of 1.18 million hectares. China is the world's largest producer with 50.27% of the total world production, followed by the United States of America with 14.92%, Iran with 9.12% and Turkey with 5.48% (FAOSTAT, 2018). Over time, this food has provided multiple functions due of its energy value, proteins, essential acids, vitamins and minerals (Noor Shah et al., 2018). According to Reiter et al. (2005), the ingredients contained in the nuts are expected to decrease the incidence of cancer, delay or mitigate neurodegenerative diseases and reduce the severity of cardiovascular disease. As a result of these advantages, the conservation and improvement in the quality and quantity of this species are required. For these purposes, it is necessary to introduce new genotypes and to conserve the old ones in gene banks (Francesca et al., 2010). The first step in achieving this goal is to assess their genetic diversity, which is still concentrated in regions called "centers of diversity," located mostly in the developing world. Farmers in these regions, who still practice traditional agriculture, plant local varieties called "landraces" that have been selected over generations. (Ercisli, 2004; Tie et al., 2021). Currently, the diversity within walnut germplasm worldwide has yet to be fully deciphered (Shah et al., 2018). Thus, the great potential of walnut diversity needs to be discovered and exploited using recent and effective tools (Torokeldiev et al., 2019). In this regard, the present review focused on the identification of walnut genetic resources, the problem of genetic erosion and the methods of conservation and improvement of walnut genetic germplasm to guarantee the sustainability of the benefits of this generous tree, especially the food security of future generations of this nutritious fruit.

2. Results and discussions

2.1. Genetic resources

In general, the perennial nature of forest trees leads to the development of natural mechanisms to maintain high levels of genetic variability within species (FAO, 2014). Martínez et al. (2010) reported that walnut varieties present a great diversity regarding different characteristics such as silviculture, productivity, physical and chemical traits of the nut. In general, the walnut is a vigorous tree. The density of branching as well as the position of the flowering on the long or short shoots allows distinguishing 3 main types of fruiting. Varieties with terminal fruiting (e.g., 'Franquette') are the most abundant. They are characterized by a low density of branching: it only appears in sub-terminal position under the winter growth stop. The flowering is terminal on these branches so it is kept mainly on the periphery of the tree. Fruiting is slow and the production potential is low. The varieties with lateral fruiting (ex.: 'Lara', 'Fernor') are characterized by numerous and short lateral branches carrying the flowering. This one spread out in "manchon" along the main branches. If the interior of the tree is sufficiently lightened, the fruiting on these branches can be maintained for several years. The trees have an earlier start in production than the previous type. Finally, there is an intermediate type of fruiting (e.g., 'Hartley') combining morphological characteristics of the 2 previous types (Roose et al., 2010). Indeed, there are many cultivars or varieties of walnuts that are grown commercially, each with its own unique characteristics. Table 1 shows the main walnut cultivars in the leading producing countries in the world. Although the walnut is monoecious, most of the varieties present a discrepancy between the male and female flowering, hence the importance of the association of two or three varieties to ensure the pollination which is anemophilous (Serrar, 2006).

2.2. Genetic erosion

The propagation of new varieties from crop improvement programs is the primary source of the genetic erosion (Brush, 1999). Undoubtedly, the "green revolution" has contributed and continues to contribute to the loss of genetic diversity, as Wood and Lenne (1997) indicate in the equation "green revolution = loss of genetic diversity. In many areas of the world, farmers have had many socioeconomic reasons to replace local varieties with uniform and high-quality varieties that have been rapidly and widely distributed (Teklu and Hammer, 2006). In addition, population growth, urbanization, deforestation, pest and disease epidemics, lack of recognition of the current or future value of genetic resources, poor management and monitoring and lack of long-term breeding programs are all important causes of genetic erosion (Myers, 1994; Hammer and Teklu, 2008). In this context, for a multifunctional species like walnut, in addition to the genetic erosion caused by the propagation of improved cultivars, there is the direct dysgenic effect caused by the desire for good quality wood causing the extinction of the most valuable trees and the reproduction of inferior quality trees (Fornari et al., 1999). In fact, the outreach effort of Rana et al. (2007) demonstrates that natural walnut populations are declining at a rapid rate, with limited new plantings. In this study, the authors mentioned some causes leading to the genetic erosion of this species, such as the frequent uses of walnut trees to produce the wood and furniture, because the benefits from the sale of wood are more important than the earnings obtained from the collection and sale of nuts. In addition, the limited productivity, caused by lack of high-quality planting material, insufficient pollination, weak density of trees by unit area, predominance of terminal bearing, long juvenile period, big size of trees, poor filling, limited grafting success rate and climatic fluctuations, were considered responsible for the lack replanting initiatives of walnut trees. Similarly, poor regeneration was caused by some animals prematurely damaging the thin-shelled nuts and by farmers who are reticent to share the germplasm of good nut morphotypes with programs, even for a fee. As examples, the European walnut populations were undergoing genetic erosion, but showed a relevant ability to maintain a high level of genetic diversity (Fornari et al., 1999). This finding may indicate both the genetic plasticity and the response of this species to human selection (Fornari et al., 1999). Moreover, this problem appears in Central Asia, which presents an important center of walnut genetic diversity (Gaisberger et al., 2020). Regarding Latin America, it makes sense for smallholders to have good walnut planting material, this can lead to serious genetic erosion of the gene pool of native *Juglans* species (Williams and Haq, 2002).

2.3. Assessment of genetic diversity

Given the importance of biodiversity to breeders' programs, genetic resource management through exploration, collection, characterization, evaluation, and conservation must be a priority for the current and future human well-being (Arzani and Ashraf, 2017). In this context, the markers are crucial in the study of variability and diversity, the establishing of linkage maps and in the diagnosis of individuals or lines carrying certain linked genes (Kalendar et al., 2011). The morphological markers are the first markers to be observed, but their constraints rapidly emerged (Schulman, 2007). The Developments in biochemistry biology have allowed the strengthening of morphological markers, using isoenzymes.

(Tanksley, 1983). However, limitations of isoenzymes as markers led to the development of markers based on DNA polymorphisms (Schulman, 2007).

2.4. Morphological analysis: The first step of the selection

Genetic variability allows the use of valuable selections in conservation programs that guarantee to avoid their loss due to genetic erosion (Botu et al., 2014). In addition, the phenotypic variation of fruit is helpful to provide the basis for forest improvement and ex-situ conservation (Garcia et al., 2018). Across the years, walnut native areas have shown increasing diversity in nut shell size, shape, thickness and color, kernel quality and color, and other morphological attributes, due to its high allelic diversity and seed propagation (Arzani et al., 2008). Commercially, walnut is graded based on nut size, shell thickness, percentage of kernels and kernel color. This later differs among cultivars according to their ability to produce extra-clear kernels and to orchard management factors. 'Chandler' which is the main walnut cultivar cultivated in California, has a high frequency of light-colored kernels (Zaini et al., 2020). Evaluation of germplasm collections is usually conducted using several morphological descriptors such as the IPGRI (International Plant Genetics Research Institute (now called Bioversity International). This descriptor gives ontologies for managing germplasm collections based on morphological measurements like length and diameter or thickness of fruit as well as visual assessment for traits that are difficult to quantify such as fruit shape or rugosity (Bernard et al., 2020). Moreover, the UPOV (International Union for the Protection of New Varieties of Plants) has established guidelines for determining differentiation, homogeneity and stability of new cultivars in most plants (Solar et al., 2002). Until date, the assessment of morphological variability carried out according to a traditional method with measurements using on caliper and micrometer instrument, as well as basic visual observation. Recently, Bernard et al. (2020) presented a better resolution nut phenotyping method based on X-ray tomography compared to conventional measurement methods.

2.5. Deepening of genetic diversity using molecular markers

Molecular markers are based on variation in DNA, which is found in the nucleus (nuclear genome) and organelles such as plastids and mitochondria in plant cells (Guney et al., 2018). They are divided into three groups: the first group includes hybridization markers such as restricted fragment length polymorphism (RFLP). The second group includes PCR based markers such as random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), simple sequence repeats or microsatellites (SSR), inter-simple sequence repeats (ISSR), sequence characterized amplified region (SCAR), sequence-related amplified polymorphism (SRAP). While the last group includes DNA sequencing based molecular markers such as single nucleotide polymorphism (SNP), diverse array technology (DArT) and next generation sequencing (NGS). Molecular markers are used to consistently assess diversity between plant populations as well as genotypes within the same population (Guney et al., 2018). Indeed, molecular markers are commonly employed to research walnut genetic diversity, and the following part includes several studies of walnut genetic diversity evaluation using various types of DNA molecular markers. For instance, the RFLP markers were applied by Fjellstrom et al. (1994) to study the genetic diversity of 48 cultivars of California walnut and from different countries of the world. The RAPD technique applied to assess the genetic diversity of eight genotypes of Turkish walnut trees (Erturk et al., 2011). In addition, Xu et al. (2012) assessed walnut varieties by AFLP in different environments in western China. In Morocco, the ISSR markers were used by Kabiri et al. (2019) to evaluate the genetic diversity of 66 trees from 11 accessions. Using SSR markers, 189 genotypes from 25 different regions in 14 countries belonging to three continents were analyzed to study their genetic relationships and diversity (Ebrahimi et al., 2016). Moreover, Ciarmiello et al. (2011) studied 18 walnut cultivars from Italy, Hungary, France, USA, Spain, Portugal and Greece. These authors characterized the first and second transcribed internal spacer (ITS1 and ITS2) as well as the intermediate 5.8S coding region of the RNAr gene. In this regard, Yaman et al. (2020), evaluated the genetic diversity among the walnut genotypes selected from Uşak province of Turkey with the use of SRAP molecular markers. The study of genetic fingerprinting of 20 Persian walnut populations in Iran, including 3 wild and 17 cultivated populations was conducted using SCoT markers (Tabasi et al., 2020). Although these types of markers are commonly used in plant breeding, but most of them are restricted in their applications due to their limited availability and high costs (Sonah et al., 2011). However, with next-generation sequencing technologies, the SNP markers became more valuable due to their abundance in a genome and are also suitable for analysis of a wide range of genomic scales (Zhu et al., 2003). In China, restriction-associated DNA (RAD) sequencing revealed 6357 SNPs divided the 41 walnut cultivars analyzed into two main groups (Wang et al., 2020).

2.6. Marker-assisted selection

As a result of the rapid development of high-through put genotyping tools such as Genotyping by Sequencing (GBS; Davey et al., 2011), the association studies can be extended to the entire genome (Genome- wide association studies; GWAS; Atwell et al., 2010). However, new methodologies could also be developed, such as genomic selection (GS; Meuwissen et al., 2001), which predicts the genetic value (Genetic-Estimated Breeding Value; GEBV) of genotyped individuals.

For walnut, the publication of its genome sequence (Martínez-García et al., 2016) and the creation of AxiomTM *J.regia* 700K SNP array in 2018 by Marrano et al. (2019) have facilitated advanced genetic and genomic studies. The first GWAS publication using the Axiom® *J. regia* 700K chip is very recent and shows 55 loci on 11 chromosomes, which were shown to be strongly, correlated with six nut and kernel characteristics. For nut weight, three SNPs on chromosome 7 were identified, while Kernel percentage was shown to be controlled by six SNPs on chromosome 3. One common SNP on chromosome 1 was revealed for nut width and thickness. For form index, two SNPs on chromosome 10 and one each on chromosomes 3, 4, 7, and 13 were detected (Arab et al., 2019). In this context, more than 60 marker-trait associations (MTAs) were discovered by Bernard et al., 2020, including a highly significant SNP associated with nut diameter, nut volume and kernel volume on chromosome 14, and 5 additional associations for walnut weight. They also recorded associations on chromosomes 5 and 11 with nut suture strength, which were recently recorded by the University of California, Davis. Regarding the roundness index, nine SNPs were found, three on chromosome 10 and one each on chromosomes 1, 3, 4, 6, 8, and 13. In addition, GWAS method indicates 27 genomic loci responsible for 18 essential agronomic variables, including JrFAD2 and JrANR, that are genes with major effects on linoleic acid concentration and nut endo pleural color, respectively (Ji et al., 2021).

2.7. Biochemical characterization

Walnut has a high level of genetic diversity developed through evolution under difficult environmental conditions resulting a large differentiation in walnut germplasm and significantly influencing fruit chemical composition (Wan et al., 2017). In this context, the identification of the biochemical potential of each plant species is necessary before proceeding with the selection (Akhiani et al., 2017). The phytochemical components and their nutritive effects in common walnuts had been investigated by many scientists. Effectively, several investigations illustrated that, depending on the variety, 40-60% of walnut fruits are composed of kernels with high levels of oil content (52-70%) (Labuckas et al., 2008). A study on the biochemical compounds of walnut varieties in Argentina showed a large difference among varieties for all fatty acid compounds, including palmitic (6.38-8.15%), stearic (0.93-2.16%), oleic (16.1-25.4%), linoleic (52.5-58.9%) and linolenic (11.4-16.5%) acid (Martínez and Maestri, 2008). Moreover, walnut fruits revealed a high amount of protein (16-24%), carbohydrates (12-21%), fiber (1.5-2%) (Chatrabnous et al., 2018), melatonin, minerals (1.7-2%), folic acid, vitamin E (Mao and Hua 2012), phytosterols (Pereira et al., 2008), flavonoids (Martínez et al., 2010), tannins and polyphenols (Li et al., 2006; Khodadadi et al., 2016; 2020). Indeed, the variation of phytochemical components between cultivars have been recorded for the most important commercial nuts (Rabadán et al., 2019). The basic criteria considered in the nut selection approach included tasty kernel, and good chemical composition of the kernel (Jaćimović et al., 2020). The results of Rabadán et al. 2019), show that by using different cultivars, some of the main nutritional parameters of nuts, such as oil content or linoleic concentration, can be controlled. The content of fatty acids and other metabolites in walnut kernels depends largely on genotype, geolocation, developmental stage, and post-harvest handling practices (Amaral et al., 2005; Kodad et al., 2016).

2.8. Climate change impact on walnut tree

The impact of climate change on plants has been observed for decades. Therefore, global climate change points to the need for further research to assess the possible consequences on various ecosystems and changes in the distribution of certain species (Paź-Dyderska et al., 2021). For this purpose, an increasing number of studies have been published on the physiological responses of walnuts to environmental parameters such as water, temperature and nutrients (Gauthier and Jacobs, 2011). Many of these investigations have been carried out in France, the western United States and Southwest Asia, to deal with the problems associated with climate change, including the understanding of reduced growth or survival as a result of the reduction of winter cold accumulation and an increase in freeze-thaw phenomena for walnut production (Baldocchi and Wong, 2008; Luedeling et al., 2009). Indeed, in walnut climate change has revealed a change in the budbreak date of a variety with a rather late budbreak date 'Franquette' and a variety with an intermediate bud break date 'Geisenheim 139'. During the period 1984 to 1990, the average temperature between January and April was 3.7°C and the average budbreak dates were April 23 and May 5 for 'Franquette' and 'Geisenheim 139' respectively. During the period from 2000 to 2006, the average temperature between January and April was 0.9°C higher, or about 4.6°C, and the average budbreak dates advanced by 7 days for 'Franquette' and 3 days for 'Geisenheim 139' (Črepinšek et al., 2009). Moreover, the same phenomenon is observed in France over the period from 1989 to 2017. An advance in bud break date of 5 days on average is observed for 'Franquette' and 'Lara' (Bernard et al., 2018). Furthermore, the climate change in planting areas has a direct impact on phytochemical components (Shutian et al., 2020). Specific climatic elements play an important role in the formation and accumulation of phytochemical components during the growth stage of the nut (Shutian et al., 2020). In fact, Rabadán et al. (2019) revealed that minerals (Fe) and protein in walnuts were determined by the change of weather conditions. Moreover, lower minimum temperatures may promote the synthesis of unsaturated fatty acids (Fuentealba et al., 2017), while precipitation directly influences the phenolic content during the growing seasons of the kernels (Lynch et al., 2016). Dryness and low rainfall have also led to an increase in the tocopherols content of High Atlas walnuts. (Kodad et al., 2016).

2.9. Conservation and improvement approaches

Genetic diversity is the basic material for evolutionary change in populations (Frankel and Soule, 1981). However, many species and varieties are in danger of extinction and many more are threatened and endangered (Hammer and Teklu, 2008). As a result, genetic diversity conservation is a major priority in conservation and evolutionary biology. Maxted et al. (1997) suggested a plant genetic conservation model that encompasses the entire process of plant genetic conservation, from selection of a target crop gene pool to its exploitation (Figure 1). In walnuts, significant genetic diversity was found across its range. However, this species continues to decline across their natural range (Mapelli et al., 2014). For this reason, the conservation of the walnut forests has become an obligation, in particular from human activities (Orozumbekov et al., 2015). Indeed, the strategies for *in-situ* and *ex-situ* conservation can be implemented to conserve its genetic resources (Torokeldiev et al., 2019), but the *in-situ* conservation strategy is regarded as the most suitable for most broadleaved species (including *Juglans regia*) (Heuertz et al., 2001). The walnut germplasm collection at the University of California, Davis, provides a source of material for breeders in the Walnut Improvement Program through its wild accessions, established cultivars, and advanced selections, as well as genotypes from other countries (e.g., France, China, Afghanistan, and Japan) (Tulecke and McGranahan, 1994). In addition, in each European country interested in walnut plantations and genetic improvement, clonal archives of trees or clones selected for nut production and seed orchards are maintained (Fernández López et al., 2001). In fact, large collections are currently located in France, Italy, Spain and Hungary (Fernández López et al., 2001). Regarding central Asia, which is an important center of walnut diversity, the walnut conservation based an approach that encompasses (i) *ex-situ* conservation in areas with a "severe threat level" as a result to climate change and (ii) *in-situ* conservation in areas with a "minor threat level" due to climate change. In addition, we suggest (iii) assisted natural regeneration in areas where "minor threat levels" caused by climate change coincide with "severe threat levels" due to one or more short-term threats (Gaisberger et al., 2020).

Concerning the genetic improvement of walnut, it was started only in the 20th century, and today the most important walnut breeding programs in the world are established in California, France, and China (McGranahan and Leslie, 2012; Bernard et al., 2018). In general, the breeding programs of walnut, the late leafing, both terminal and lateral bearing, low incidence of pistillate flower abscission, relatively smooth shell, 50% kernel recovery, plump and light-colored kernel, high yielding nuts (6 MT/ha) with large size, and at least moderately resistant to pests and diseases, are all desirable characteristics in a walnut cultivar (Cosmulescu et al., 2010; Botu et al., 2010; McGranahan and Leslie, 2012). The University of California-Davis Walnut Improvement Program (UCD-WIP), which began in the late 1940s with the purpose of generating improved scion and rootstock cultivars for the California walnut industry, is one of the most important walnut breeding initiatives (Tulecke and McGranahan, 1994). In addition, the UCD-WIP, like many walnut breeding programs around the world, aims to increase yields of kernels with desirable visual and taste traits while reducing input demands (such as water and chemicals) and production costs (Leslie and McGranahan, 2014). Furthermore, the first French breeding programs were led by Eric Germain at INRA and allowed the commercialization of 7 cultivars ('Fernette', 'Fernor', 'Ferjean', 'Feradam', 'Ferbel', 'Ferouette' and 'Fertignac') but the programs ended in 2007 with an insufficient choice of cultivars. The new breeding program is led by Ctifl to better respond to current and future needs, especially in the context of global competition, climate change and the reduction of the use of phytosanitary products (Bernard et al., 2018). Regarding China, the Shandong Institute of Pomology has released 17 varieties between 2003 and 2012, including 'Luguo 2' in 2012 by intraspecific hybridization and 'Luwen 1' in 2009 by interspecific hybridization (Zhang et al., 2014). The Xinjiang Autonomous Region program is also investigating the benefits of secondary fruiting found in many early-maturing dwarf walnuts (Wang et al., 2014). Other countries in Asia also have active walnut breeding programs, including Iran, India and Turkey, which has carried out, during the years 1998 and 2015, four main varietal selection programs to find new walnut genotypes with late leafing, lateral bud fertility and high walnut quality (Yilmaz et al., 2017). Concerning the Iranian walnut breeding programs, they have led to the release of six cultivars named 'Jamal', 'Damavand', 'Persia', 'Caspian', 'Chaldoran' and 'Alvand'. Currently, a joint project between CEWIT and the University of California-Davis is underway to understand the mechanisms of drought tolerance and to introduce drought tolerant walnut rootstocks. (Hassani et al., 2020). Similarly, in India, 63 forms of walnut have been selected and the tree that best meets all export standards was selected. High resistance to anthracnose disease was also found

(Sharma et al., 2014). Currently, other genotypes are being evaluated as well as the development of micropropagation is underway (Hassani et al., 2014). Finally, in vitro propagation of walnuts plays a very important role in cultivar multiplication and Iranian teams have been particularly involved in the development of these techniques (Payghamzadeh and Kazemitabar, 2011).

3. Conclusion and perspectives

Using a range of methodologies, from morphological markers to the latest advances in genome analysis, walnut germplasm has undergone several breeding researches since the discovery of heritability of the main agronomic traits in 1972. These practices have led to select superior genotypes, which are allowed to a continuous increase in world walnut production, which has exceeded that of almonds and hazelnuts since 2008. In this regard, the improvement of vegetative propagation methods can be used to ensure rapid multiplication of superior genotypes, avoid the problems associated with variable seed production and act as a safeguard against extinction. Currently the negative impact of climate change on walnut crop must be considered in breeding to provide new materials adapted to local environmental conditions.

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Tables and Figures

Table 1. Main walnut cultivars in the leading producing countries of the World

Country	Cultivars	References
China	Liaoning, Zhonglin, Xiangling, Luguang, Jing, Xifu, Bokexiang, Zha, Wen, Xilin, Bofeng, inlong, Jinxiang, Lubo, Fen Gui, Xinzaofeng, Lipin,	(Serrar, 2007)
Iran	Persia, Caspian, Chaldoran, Alvand, Damavand, Jamal, Chaldoran, Z series (Z12, Z30), Zia8, Kr77, Kr72, Krr111, Kr1-25, Or-64	Hassani et al., 2020
Turkey	Sabin, Yalova 1-2-3-4, Bilecik, Kaplan-86, Kirsehir, Sen-1, Tokat-1, Bursa 95, Maras 18, Sutyemez 1, and Kaman 1	(Ozkan and Koyuncu, 2005), (FAO, 2004)
Italy	Bleggiana, Malizia, Feltrina, Lombardia, Sorrento, Panella, Tonda di S. Martino, Cerreto, Patti, Carvinara	Foroni et al., 2005
India	Gobind, Roopa, Ratna nad, Pratap, Sholding, Hamdan, Sulaiman, CITH-Walnut-1, 2, 3, 4, 5, 6, 7, 8, 9 and 10, Chakrata No-2,4,6,13and 14, Wilson, Kashmir Budded, Placentia, Lake English, Opex Caulchry,	(Rathore, 1986)
Albania	Macrocarpa, tenera, elongata, racemosa, Dura, semidura, and serotina	(Zeneli et al., 2005)
France	Franquette, Mayette, Parisienne, Marbot, Lara, Liba, Solèze, Meylannaise, Ronde de Montignac, Bordelais, Candelou, Carème, Chaberte, Chereba, corne, Fernor, Fernette, Corne, Culpat, Grandjean, Grosjean, Ferjean, Grosvert, R. de Montignac, Solèze, Lozeronne	(Zeneli et a.l, 2005), (FAO, 2004)
USA	Payne, Eureka, Hartley, Franquette, Serr, Ashley, Sunland, Chico, Vina, Tehamo, Amigo, Tulare, Pedro, Howard, Chandler, Cisco, Adams, Gustine, Midland, Pioneer, Sharkey, Vina, Carmello, Chase, Howard, Serr, Payne, Trinta, Howe, Idaho, Manregian, Moyer, Concord, Nugget, Spurgeon, Sunland, Waterloo, Hugnuss, Lampoc, Marchetti,	(Zeneli et al., 2005), (FAO, 2004)
Bulgaria	Drianovski, Djinovski, Cheïnovo, Proslavski, Perouchtenski, Slivinski, Silistrinski, Starozagorski, Mirkovski, Izvor, Kuklenski, Cheinovo, Raikov, Backovski, Drenovo, Dzinovski, Dorka,	(Naples and Mercurio, 2008), (FAO, 2004)
Spain	Mayor, Onteniente, Baldo II, Carcagente, Cerdá, Escrivá, Villena, Del Carril, Gran Jefe, Tivernys, Alcalde, Algaida, Badajoz, Comes, Gales, Ibi, Sendra, Nogon, Cabra, Callao, De Arriba, Enano, Mar Menor, Mollar de Germàn, Nava, Taibilla, Tobilla	Naples and Mercurio, 2008), (FAO, 2004)
Romania	Germisara, Jupâneşti, Sibişel, Miroslava, Velniţa, Anica, Argeșan, Bratia, Geoagiu, Mihaela, Muscelean, Novaci, Orаștie, Peștișani, Roxana, Sarmis, Secular, Șușita, Targu Jiu, Valcor, Valmit, Valrex, Victoria, Ignat Tudor, Iorgulescu, Munteanu, Tehama, Geoagiu 65,	Naples and Mercurio, 2008), (FAO, 2004)
Germany	Geisenheim, Weinsberg, Seifersdorfski, Slifendorfer, Hansen	Naples and Mercurio, 2008), (FAO, 2004)
Portugal	Rego, Arco,	Naples and Mercurio, 2008), (FAO, 2004)
Chile	As-0,1,5 and 7, Pirque	Naples and Mercurio, 2008), (FAO, 2004)
Moldova	Kazak, Kostiuzenski, Ideal, Calaras, Cazacu, Chisinau, Cogalniceanu, Corjeuti, Costiujeni, Schinoasa, Kalaraski, Kisinjevski	(FAO, 2004)
Hungary	Alsoszentivani, Milotai, Tiszacsecsi, Esterhazy II,	(FAO, 2004)
Slovenia	Elit, Maribor, Milanovac, Petovio, Race,	(FAO, 2004)
Yugoslavia	Jasenica, Ibar, Ovcar, Sampion, Vujan, Backa, Novosadski Kasni, Novosadski Rodni, Petovio, Srem, Tisa, Ada, Medveda, Mire, Rasna, Selekcija,	(FAO, 2004)

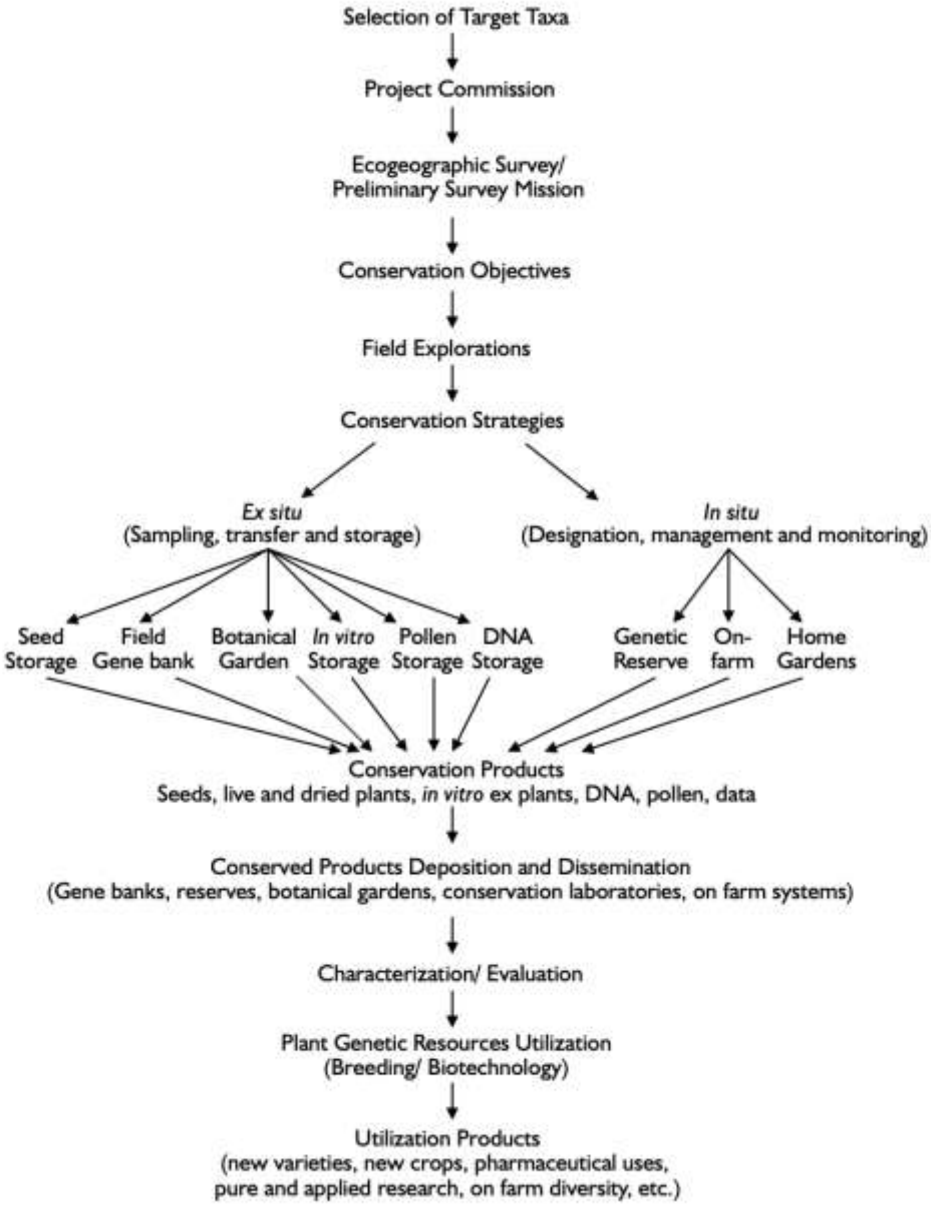

Fig. 1. Proposed model of plant genetic resources conservation (Maxted et al., 1997)