



THE IMPORTANCE OF GENETIC MARKERS IN SYSTEMATIC PLANTS (SCIENTIFIC ARTICLE)

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Article history:	Abstract:
Received: 20 th July 2023 Accepted: 20 th August 2023 Published: 24 th September 2023	Biological diversity is a measure of the health of biological systems and the basis on which many studies and research in biology rely. It is a mixture of genetic variations and environmental influences and is relied upon as a value in the management of natural resources. Plant genetic resources are among the components of this science due to the presence of a wide range of variations between species, which A natural formation occurs through which it is possible to obtain new, infinite numbers of genetic combinations. It requires the growth of the plant to a certain stage in order to take a sample, and more than one gene controls the manifestation of phenotypic characteristics. With the progress of genetics and molecular and biological genetics, it has led to the development of many molecular indicators that can be used in studying genetic diversity. There are many molecular indicators available, and each one of them differs from the other in terms of principle, application, amount of DNA, and the amount of variations discovered, as these reflect natural variations. Inherited from the sequence of nucleotides in the DNA of the species and genotypes studied. These DNA indicators have a number of advantages, including their large number, speed of acquisition, and unaffected by the environment, the type of plant tissue, and the age stage of the organism under study. These indicators can detect changes in parts of the coding and non-coding DNA. They are also characterized by going beyond the internal effects of genes, molecular indicators are thus the best alternative in studying genetic diversity and finding the distinctive genetic fingerprint of varieties and genetic structures, which helps in expanding the genetic base and adopting varieties in selection, hybridization, and future breeding programs.

Keywords: Stone moroko, Pseudorasbora parva, meristic features, plastic features, river Chirchik, Uzbekistan

INTRODUCTION

The plant world is characterized by a wide diversity in terms of huge trees, small shrubs, existing and creeping herbaceous plants in terms of their species, types, and varieties, as well as microorganisms, so the different geographical regions on this earth are distinguished from each other in terms of the existence of specific species and types of plants, animals and living organisms. Biological plant diversity in any environment is defined as a wide range of species in terms of genus, type, and class of living organisms that exist naturally within one geographical environment. Mammals and birds and that this diversity (1). An important role and a great function Just as a man did not stand up to the truth about the importance and role of biological diversity in the environment accurately except in recent years, since the 20th century, most people had the impression that biological or vital diversity is limited to the aesthetic aspect in nature. However, the expansion of environmental studies And delving deeper into the specialization related to the relationships between the types of living organisms, it showed the significance of the great role that is played by biological diversity in the environment and human life, as they interact with each other in a complex, accurate and balanced interaction, thus highlighting the importance of the presence of different and disparate types of living organisms. (2) With this diversity of plants within environment and in farms and orchards, many advantages have been achieved, including:

- 1) continuity of benefit and giving
- 2) Diversity of plants is useful in protecting crops from the pests.

- 3) Work to enhance the fertility of the soil.
- 4) Protection from winds, storms, and soil erosion
- 5) Obstruction in spread of fires
- 6) Reducing effort and trouble
- 7) Biodiversity provides shelter and habitat suitable for the diversity of living organisms

Biodiversity is the framework of life on the planet that includes environments, natural places, micro-plant species, and genetic origins. This term (biological diversity) was used in the twentieth century in the field of life and environmental sciences, which represents a modern perspective towards plant and animal revival and is also known as the degree of genetic diversity (3). The species is related to the level of the species and the degree of diversity of ecosystems. And that biological diversity increases in the case of an increase in the diversity of ecosystems from aquatic, terrestrial, and forests. The biota that lives on the globe constitutes an essential and major part of the natural ecosystems, and the total number of species that lived on the surface of the earth throughout the ages and then became extinct by natural extinction is between 50 and 5000 million. A type of plants, microorganisms, and animals. At present, scientists estimate that there are only about 50 million species living on the surface of the globe (4).

Scientists also mention that thousands of plant, animal, and insect species disappear annually. Thus, scientists warn that about 40% of the estimated 11 million species of living organisms may disappear before the end of this century. And that every extinction, whatever its cause, impoverishes biological diversity, that is, the genetic diversity of living organisms, and that the problem is not only in large numbers of these organisms disappearing forever but also that the remaining plants and animals have a genetic makeup and less immunity than those of their species in the past, for example, Farmers and producers were cultivating different varieties of corn and wheat, much more than those they are currently cultivating, as most of the old varieties and species have become extinct (5). Thus, the intensive loss of biological diversity is more than just aesthetic effects, as whenever a plant or other living organism becomes extinct or disappears, We are exposed to danger because plants are a major source of new medicines. If a few types of crops are relied upon, there is a high probability that diseases and pests will destroy them. Thus, the only way for saving a species that is on a verge of extinction is to protect the environment in which it lives, so it depends on us to adopt the Department of Wildlife and modern technology (molecular indicators) or genetic indicators to save such endangered species. Our natural world constitutes a marvel of various scenes, materials, colors and terrains, soil conditions and characteristics, environmental conditions and seas that are havens for the smallest insects and the largest animals, so this is life and this is biological diversity and includes all organisms, species and genetic diversity between them as well as their complex gatherings in ecosystems. Biodiversity is the totality of all plants, animals, fungi, and microorganisms, as well as their genetic diversity and ecosystems (6). Each plant species is a genetic wealth, which opens the way for scientists, researchers, and scholars to devise new strains and varieties of plants and work on breeding and improving them using traditional and modern breeding programs represented by biotechnology informatics, analysis, and sequencing of DNA genetic material (7 and 8).

MOLECULAR MARKERS

Many important phenotypic and hereditary traits are required agriculturally, such as yield, productivity, seriousness, and quality, as well as types and varieties that are resistant to fungal, viral, and insect diseases and resistance to abiotic stresses. Organisms to another and within the same species' class (9). These are quantitative traits, multiple inheritance, multiple factors, or multiple traits. Those regions of the plant genome containing genes that are associated with some certain quantitative trait have been referred to as quantitative trait loci (QTLs). It is very difficult to identify the locations of these quantitative traits based on the traditional phenotypic assessment, so there was an urgent need for a specific technique that helps to display specific genetic markers or markers on the genome before and after the gene to be distinguished in order to facilitate the process of finding and tracking it, i.e., the need for DNA markers emerged (10). Genetic markers had been used in genetic studies to find genetic distance and genetic kinship between species and cultivars within the species of one plant, in addition to building linkage maps and QTL analysis to determine the genetic sites associated with traits through QTL mapping. This is called genome mapping, gene mapping, or Genetic mapping. This type of marker can be utilized as a tool for Marker-Assisted Selection (MAS) plants in the breeding programs and improving the type or plant variety within biological diversity. Many genetic markers have been used by many researchers and farmers in order to achieve the desired goal. The genetic marker is intended as a characteristic used to access and infer the presence of a specific locus on the genome or chromosomes, and knowledge of this site helps to study the inheritance of a specific trait or gene (10). Certain genes very close to the genetic indicator are inherited with it. Several types of genetic indicators are used in studying genetic variation and diversity and in characterizing the types and varieties of plants for horticultural and field crops in addition to forest and woodland plants, including phenotypic, protein or enzymatic and cellular indicators in addition to DNA markers (11 and 12). The genetic fingerprint differs from the genetic index, which means the pattern or shape of the distribution of the bands that are separated by migration on the gel, which results from the analysis of the protein content of the species and individuals being studied (6). When using DNA indicators, the genetic fingerprint means the distribution pattern of divergent bands resulting from cutting the genomic DNA of the studied individuals and species.

The technology of using these markers in plant and animal breeding and the study of genetic diversity has opened up a new field of knowledge: molecular breeding. And understanding the basic principles and methods of

developing DNA markers and selecting with their help will help plant breeders, researchers, and workers in related disciplines work together to achieve the common goal of increasing productivity and quality. Genetic markers represent differences at the genetic level between an organism's species, genera, and taxa, as they don't represent target genes per se but act like flags or signs (12). Those markers located very close to the gene (strongly linked) can be termed as gene tags. And do not impact such markers in the phenotype of studied traits due to the fact that they are located near or closely related to the gene controlling this trait. Such genetic markers occupy places on the chromosomes (legumes) called loci. There are 3 main genetic marker types:-

1) The morphological markers that in themselves are external characteristics, which represent the morphological characteristics that are visually described, i.e., with the eye, such as the color of flowers, the shape, and color of seeds, the colors and shape of petals, and sepals, the nature of growth, the nature, shape, and texture of the leaf, the color and shape of the fruits, etc.

2) Bio-chemical markers, including different alleles of enzymes and are referred to as the isozymes, represent differences in the enzymes which can be detected by electrophoresis and special dyes.

These two markers are limited in number and are impacted by environmental conditions and plant growth phases. Despite their limitations, they are very useful for plant breeders and plant classifiers to show the genetic diversity among individuals within species, genus, and classes of organisms.

3) Molecular markers that show the sites of differences in the DNA. These depend on the apparent variation and differences at the level of small DNA segments (10 and 13). These markers are the most widespread and used among the other markers because of their abundance.

Genetic polymorphic variation can be defined as the simultaneous occurrence of the trait in the plant community in two patterns or non-consecutive patterns, from which it turns out that the molecular markers are nothing but a nucleotide sequence of DNA in the genome that can be located and identified as a result of genetic changes in the structure of the DNA due to mutation in Chromosomes. The basic composition at a specific location of the genome may differ in different plant strains, and these differences in collective form are called polymorphism (14). Markers are important in plant breeding and improvement programs, in addition to their importance in genetic diversity and plant classification through:-

1) Molecular markers give a true representation of the genotype at the DNA level

2) It is stable and not affected by environmental conditions

3) The possibility of detecting molecular markers in the initial stages of growth before the development of the plant to the advanced stages of its life cycle

4) It is possible to increase the number of plant markers as it is required.

DNA MARKERS.

The fundamental progress achieved in the past two decades using molecular biology has resulted in the emergence of a new genetic indicator type that is called DNA markers. It provided opportunities for breeding programs, genetic improvement, and genetic variation and diversity through direct selection, depending on the genes or important regions in the genome. Plant (hereditary bodies) (5). DNA Polymorphism is one of the most common genetic variations in terms of the degree of heritability. It can also be used in plants in the form of three genetic bodies (genomes) related to the nucleus, chloroplasts, and mitochondria. The oldest genetic indicators used in breeding, improvement, and genetic diversity programs are morphological markers (Morphological markers). Phenotypic markers) that can be detected by the naked eye, which is based on their appearance on many genetic factors and their great influence on the environmental conditions surrounding the organism, so relying on it is of a narrow scope (15). The genetic indicator is meant to be a gene or a sequence of DNA whose location on the chromosome is known so that it can be used to identify and identify individuals, species, or plant varieties, and that these are inherited like genetic factors that are, they follow Mendel's laws (segregation and free distribution) in inheritance. It has been shown (16) that the molecular genetic indicator refers to a special part of the genomic DNA that differs from one individual to another and is linked to genetic sites that have relationships with specific characteristics. This part of the variation between individuals and species is called Alleles. After discovering the form of the genetic material (17), Researchers and scholars began to invest in this discovery, which led to an amazing development of theories, applications, and the development of new varieties and species in many quantitative and qualitative traits so that it can be said that the barriers between species have fallen. It has become possible to imagine any genotype that aims to increase productivity or economic value in addition to increasing resistance and immunity from diseases and harmful insects through modern techniques, Biotechnology.

DNA markers are defined as sequences of DNA which may be inferred at a particular location of a genome or chromosome. They are used for studying the genetic relationships and genetic variation between plant species and individuals and to detect the genetic fingerprint due to the fact that they reflect the variations in the genetic information that is stored in the genetic material of these plant species and living organisms. These indicators have been adopted in studies of molecular taxonomy, evolutionary studies, and evaluation studies and the construction of genetic mapping. They have also become important tools for studying genetic diversity, which is an irreplaceable choice in developing appropriate plans for species conservation. These indicators are characterized by the fact that they show variation (18). Which occurs directly at the level of DNA, and as it is known that DNA is the stable genetic material which isn't affected by the environment, these indicators were characterized by stability, unlike genetic

indicators that depend on morphological and phenotypical characteristics which are greatly affected by the environment surrounding the organism. These indicators are also distinguished by the fact that they depend on the DNA present in all organism cells equally so that the analysis of any part of that organism and at any age stage will reflect the genetic condition result of the organism in an accurate manner, which granted this type of inclusive indicators and made them superior to the indicators that Based on protein content analysis. Another advantage of these DNA indicators is their capability for the detection of large numbers of Numerous polymorphic, which makes them capable of finding any discrepancies, despite how slight they are (19).

Types of DNA markers

Numerous varieties of DNA indications were discovered due to the molecular biology field's rapid development. Depending on the kind of technology utilized for finding and detecting them, these indications have lately been divided into two broad categories:

1) DNA markers Molecular hybridization

The first DNA indicators based on molecular hybridization appeared after the researchers invested in two scientific achievements, namely the discovery of restriction enzymes in 1968 and the southern blotting in 1975, in building the first technology, which is Restriction Fragment Length Polymorphism (RFLP), which is known to inherit differences in the sites of enzymatic cuts that cause In the appearance of different lengths of DNA segments in the agarose gel, and that the RFLP methodology depends on differences in the patterns of segmentation, which occurs due to a single nucleotide mutation at the site of the segment, or by segments added, deleted, or replaced from those sites, which leads to a discrepancy in the lengths of the resulting segments.

2) Polymerase Chain Reaction (PCR) Based markers

The replication reaction of the DNA chain was described for the first time by (20) on the basis that the work of this technology is to multiply a particular DNA piece that is produced from the total genome outside the body of the organism in the presence of primers that are linked to complementary sequence on the DNA template tape, and this discovery The most recent revolution in the world of molecular biology, comparable to the revolution brought about by the discovery of the structure of the double helix of the chromosome (21).

These molecular markers must possess some desirable properties:

- 1) Polymorphic heterogeneity, especially in biogenetic diversity studies
- 2) distributed evenly and sequentially throughout the genome
- 3) Cheap price and fast detection
- 4) It can be repeated

Application of DNA Markers in plant breeding and biodiversity improvement

In general, large numbers of samples, models, and genotypes are involved in breeding and plant improvement programs that must be subjected to several biological statistical analyses. The introduction of modern DNA indicators technology has greatly facilitated the solution to the problem of sample size through the application of PCR technology for that or the conversion of all stages. The work is done automatically by extracting and isolating DNA (22), where the efforts of the plant breeder and classifier focused on examining, classifying, and fixing the desired traits in:

- 1) Check the breeding lines
- 2) Predicting camels
- 3) Linking some indicators with the important characteristics of the plant
- 4) Accelerate the breeding and selection programs
- 5) Construction of chromosomal maps
- 6) Estimating genetic diversity and identifying the fingerprint of genotypes
- 7) Genetic stability test in different plant species and cultivars
- 8) Protection of plant genetic resources
- 9) Determination and examination of the genetic stability of plants resulting from the cultivation of pollen and mycorrhizae
- 10) Knowledge of the evolutionary inheritance of plant communities in the evidence of similarity.

As the genetic indicator may be associated with one gene or with several adjacent genes, there are two types of association

- 1) Tight linkage
- 2) Loose linkage

Bonding within half mega of base has been described as strong bonding (11). He also referred (12) to the uses of genetic indicators in:

- 1) Evaluate genetic variance or genetic diversity
- 2) Detection of the genetic fingerprint
- 3) Estimating the genetic distance between genera, species, cultivars, and plant families
- 4) Detect single sites and quantitatively
- 5) It is considered as an assistant in the various election programs.

Molecular markers can also be divided based on the extent to which they depend on the use of the PCR device in their interactions

1) Non-PCR-based approaches this called markers based on DNA hybridization. Restriction fragment length polymorphism (RFLP) represents the most important one of these markers.

2) Markers based on PCR-based approaches This technology was discovered by (19) This technology is a new molecular indicator that depends on the PCR reaction technique and mobile genetic elements, where pieces are amplified. The DNA located between the two sites of the mobile elements, using a pair of primers with a sequence of nucleotide bases complementary to the nucleotides of the Long Terminal Repeats (LTRs) on both sides of each mobile element and used with high efficiency in genetic mapping, breeding programs, selection and the study of genetic diversity (18) and the most important of these tags

Random amplified polymorphic (RAPD) DNA markers

Simple sequence repeats (SSR)

Amplified fragment length polymorphism (AFLP) and other markers.

Many researchers and scholars have worked to use genetic indicators for the molecular characterization of the biological diversity of many plants and to study cluster analysis of genetic divergence, as cluster analysis has been considered one of the good tools for the plant breeders to assess genetic diversity and specify the sites of quantitative traits (QTL) and preserve the genetic origins, in addition to that it does not require a Making assumptions about data distribution nature (23). (24) studied where they used 34 pairs of primers for mobile elements, 32 pairs of which showed effectiveness in detecting genetic variations between apricot cultivars in Syria, and the study showed that the IRAP technique produced positive, unique markers. It helped distinguish some local cultivars and genotypes of apricot with high efficiency and repeatability. This technology enabled the evaluation of genetic diversity. (25) also studied the genetic divergence of the sunflower plant using cluster analysis, where it was found that the genotypes that fall within a single group are usually the same. Genetic divergence from the rest of the structures under study, this is due to the difference in their genetic origin, which is reflected in the tool of these structures or Positively or negatively, this is due to the different plant origins of these combinations and their possession of some main and preferred genes that are absent in the rest of the genetic combinations.

The primers employed in the study by (26) produced (1002) packages of the genotypes, of which (417 normal bundles and (585) mixed bundles, indicating the feasibility of isolating the genotypes from one another and assessing the genetic diversity degree between them. The number of bundles, which had reached (28) and included (13) unique bundles and (15) absent bundles, was used to distinguish the genetic differences of genotypes under study. The Favad cultivar demonstrated the absence of distinct bundles; either bundle is absent, whereas the ILB-1266 genotype displayed the largest number of unique bundles, reaching four bundles. The genotypes ILD1266, IILB1266, and Luzdeotono stood out for having the most bundles, a total of three. The primers varied and there was no absent bundle for the FBSPN2 genotype. The sizes of the resulting bundles ranged from 1925 to 130 bp, and the highest value for genetic dimension had ranged from 0.110 to 0.269. The lowest genetic dimension has been between the two structures (ILD1266 and FBSPN2), and it was equal to 0.11. The highest genetic dimension was equal to (0.269) between (ILD1266, HISTAL) (ILD1266, Luzdeotono) genotypes. The Dendrogram demonstrates the division of genotypes under study into 2 major groups. Figure 1 divides every one of them to 2 smaller groupings.

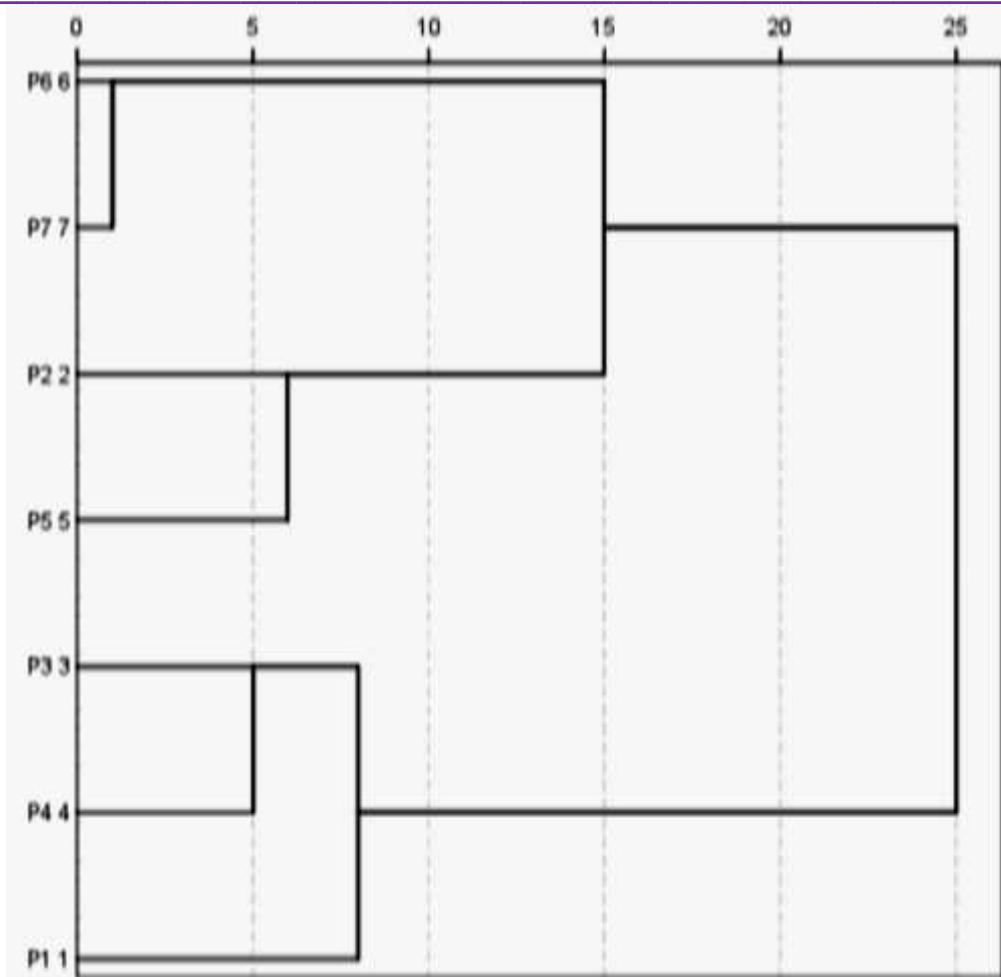


Figure (1). Dendrogram using average linkage (Genetic relationship) of bean genotypes based upon genetic dimension of RAPD technology (24)

RAPD technology was also used to study olive cultivars' genetic fingerprint and biodiversity in Jordan, Egypt, and Morocco (25) Figure 2.

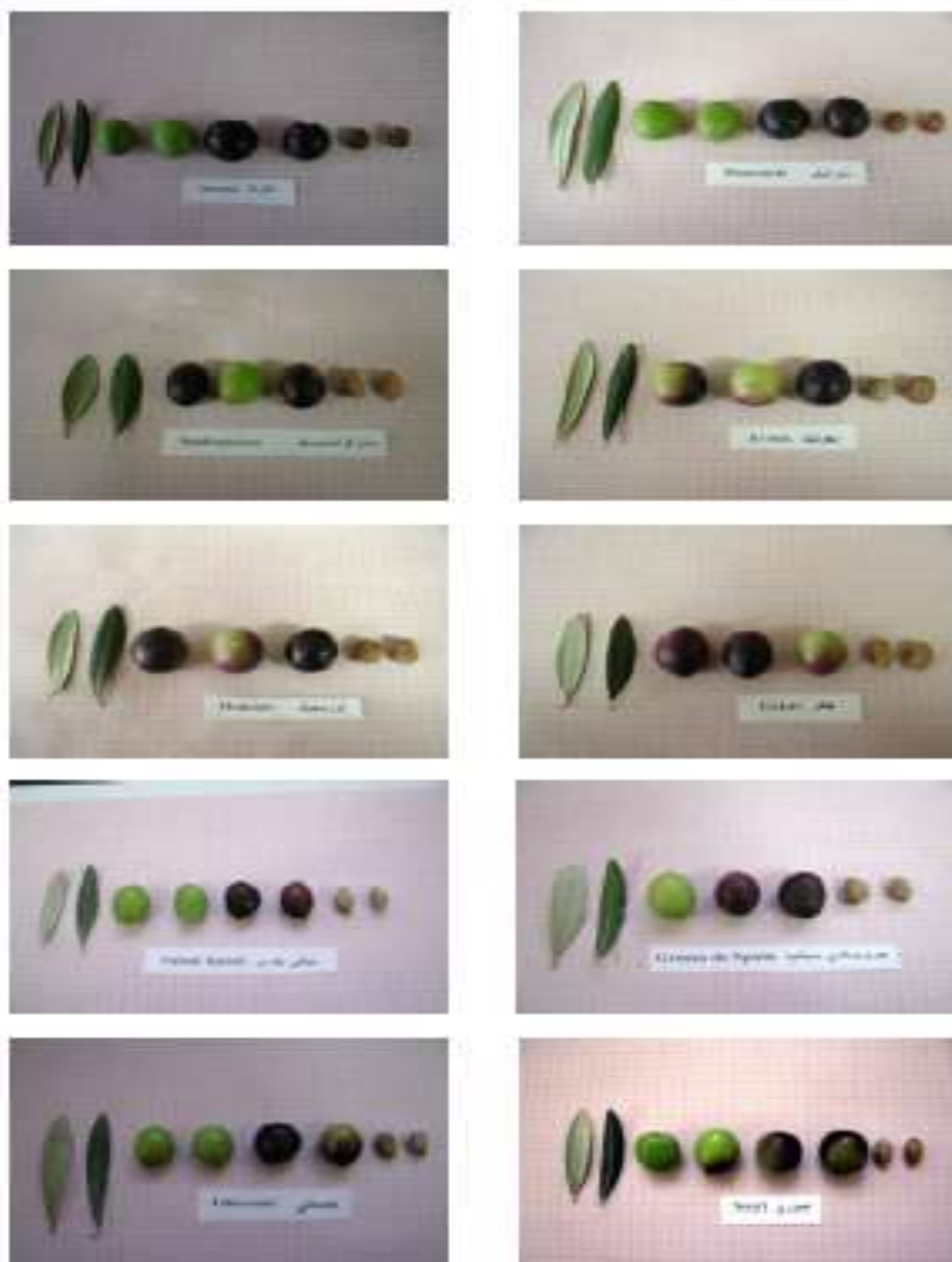
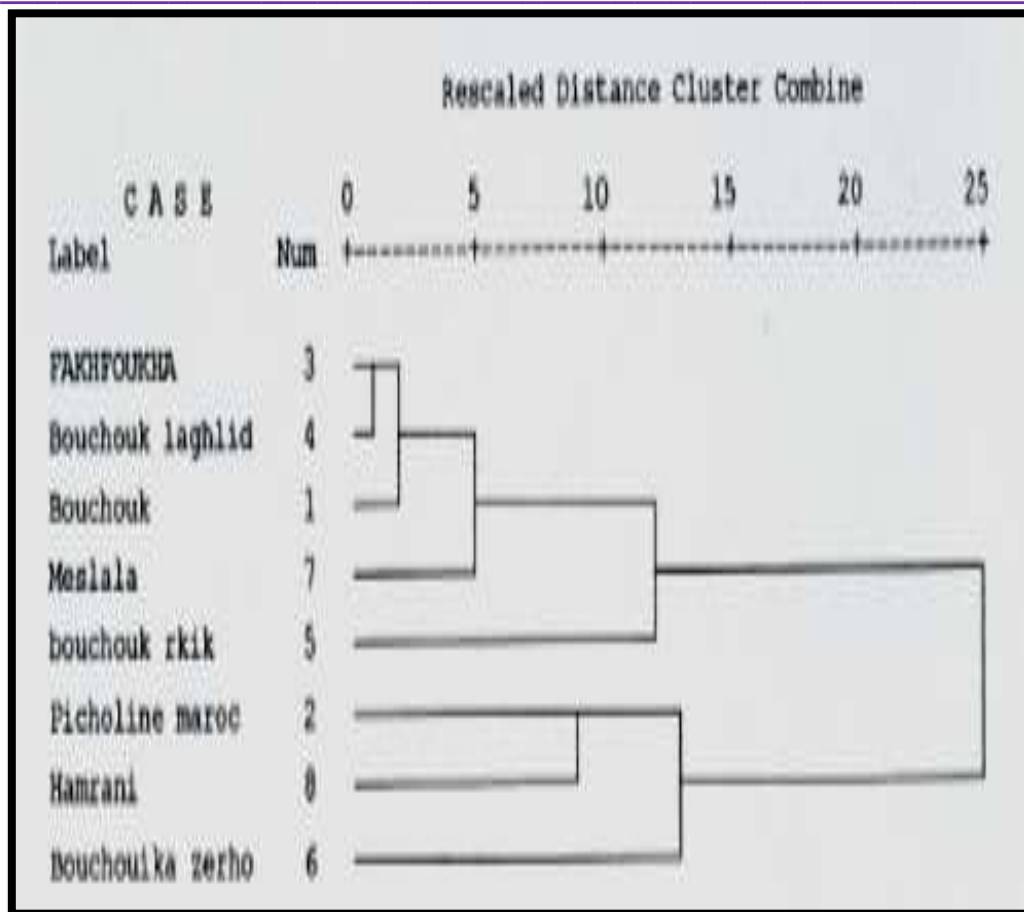


Figure (2). Olive varieties in Jordan show the leaves, fruits, and seed shape (25).



Figure(3) Dendrogram using ward method (RAPD markers)

And the AFLP markers are based on the idea of merging the advantages of two types of molecular markers, namely the RAPD and RFLP markers (25), which allows for obtaining the largest number of morphological variations, which is mainly the result of the process of cutting DNA into pieces of multiple lengths and shapes, by selection enzymes based on the idea of the RFLP tag. This technology is applied in a large number of studies and research. It has been used in genetic diversity and the creation of genetic linkage maps for several plant species and crops (26) and in the analysis of quantitative genetic traits in some crops field, and in identifying sites of resistance to fusarium wilt caused by *Vascularis fusarium* (13), and in elucidating genetic relationships between and within different plant species (27 and 28) and in determining the degree of purity and genetic similarity, and genetic isolations in barley lines and crosses (29) and the study of genotypes and identification of mutation sites and biological diversity in grapes (30, and 31), in genetic mapping of some forest trees (32), in the study of biodiversity in date palms (33), and the study of biodiversity and genetics in citrus (34).

(34) used Rapid Amplified Polymorphic DNA (RAPD) to examine genetic variance in his research work. With the use of 12 random primers, PCR amplification of cultivar DNA produced 1200 random bands, some of which were variant and others of which were different (figure 3). The results of this type of study have been admitted to the computer and private statistical program NTSYS-ps, which indicated that genetic variance reached a value between (0.098 and 1.22), with the high value (1.22) in "Cox" and "conference" cultivars and the low value (0.098) in "Granny Smith" and "Early Gold." The Dendrogram tree (figure 4) demonstrates the division of cultivars into two groups: the first group contains all cultivars of *Pyrus malus* L. species, which are divided to 3 groups based on the genetic similarity, and the second group contains all *Pyrus communis* L. species cultivars, which are also divided to 2 groups, based on the genetic similarity.

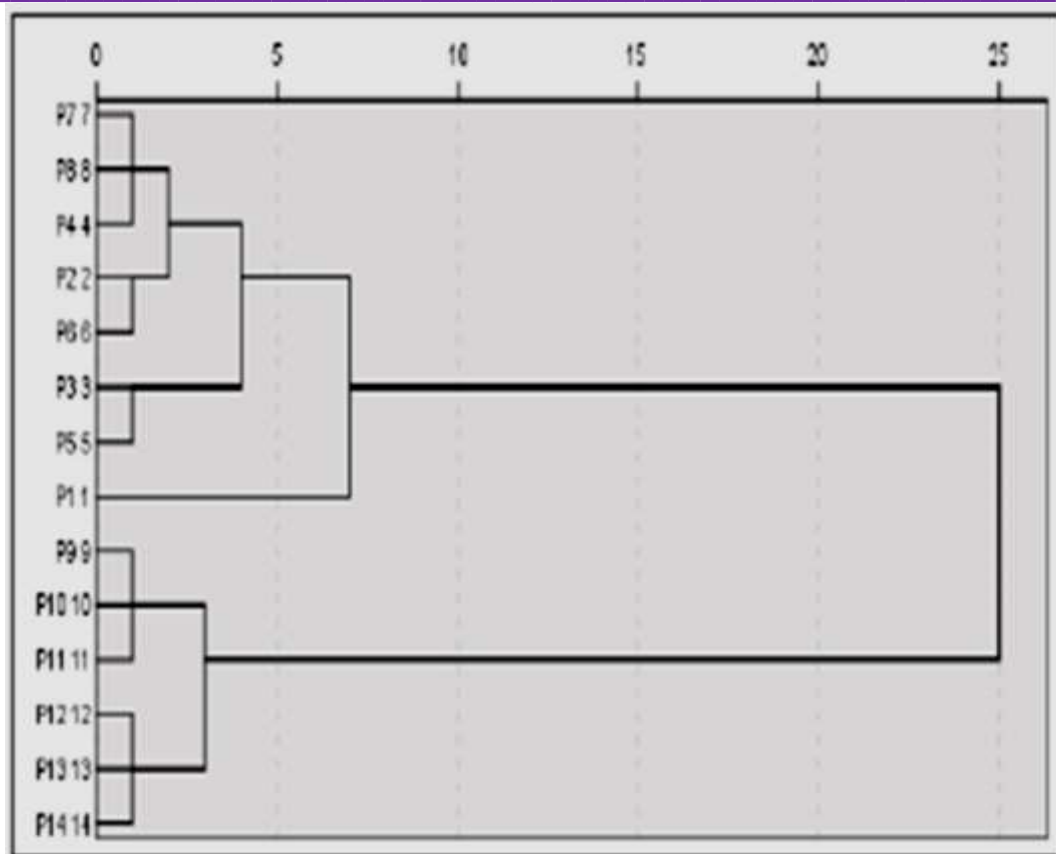


Figure (4) The tree of genetic variance (Dendrogram) of the studied apple and pear cultivars resulted from RAPD data analysis using the UPGMA method.(34)

- 1.Early Gold , 2.Genny Smith, 3.Royal Cala, 4.Red Delicious ,5.Golden Delicious, 6.Honey Crip,7.Mancntosh, 8.Cod, 9.Conefecoca, 10.Decru, 11

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