Identification Of Some Variety of *Plum* Varieties (*Prunus Domestica*) Using Srap Markers in Duhok Region- Kurdistan\ Iraq

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Abstract

Plums (Prunus spp.) are economically significant fruit crops with a wide genetic diversity that influences fruit quality, disease resistance, and adaptability. Traditional classification methods based on morphology can be unreliable due to environmental influences. Molecular markers, particularly Sequence-Related Amplified Polymorphism (SRAP), offer a more precise approach to assessing genetic variation. This study aims to evaluate the genetic diversity and relationships among selected plum varieties using SRAP markers. The findings will aid in breeding program development, germplasm conservation, and the identification of suitable parent lines for hybridization. Methods. SRAP markers were applied to analyze the genetic distance among different plum varieties. A dendrogram was generated to visualize clustering patterns based on genetic similarity, revealing the evolutionary relationships among the cultivars. The genetic analysis grouped the studied plum varieties into two major clusters: Closely related varieties (Cluster 1)–These varieties exhibited high genetic similarity, indicating a shared breeding background or common selection for specific traits such as fruit quality and disease resistance. Genetically distant varieties (Cluster 2) – These varieties showed significant genetic divergence, suggesting unique lineages or potential for hybridization to introduce novel traits. The results highlight a moderate to high level of genetic diversity among the studied plum cultivars. The identification of genetically distant varieties (e.g., F and B) suggests potential for crossbreeding to enhance desirable traits. Meanwhile, closely related varieties provide genetic stability for commercial breeding programs. The effectiveness of SRAP markers in genetic diversity analysis is confirmed, and future studies should integrate additional marker systems (e.g., SSRs, SNPs) and high-throughput sequencing technologies to refine genetic characterization.

Keywords: Plums plant, Genetic Diversity, SRAP Markers, Molecular Breeding, Germplasm Conservation, Hybridization Potential.

Introduction

Plums (Prunus spp.) are among the most economically and nutritionally important temperate fruit crops, cultivated worldwide for their rich genetic diversity, adaptability, and fruit quality (Faust and Surányi, 1997). They belong to the Rosaceae family and the Prunoideae subfamily, which also includes other stone fruits such as peaches, apricots, and cherries (Rehder, 1940). The two most widely cultivated species are European plums (*Prunus domestica*) and Japanese plums (*Prunus*

salicina), which exhibit distinct morphological and genetic traits (Zhebentyayeva *et al.*, 2019). Understanding the genetic variation among plum varieties is essential for breeding, germplasm conservation, and trait improvement (Zuriaga *et al.*, 2013).

Genetic diversity plays a critical role in fruit quality, disease resistance, and adaptability to environmental conditions (Byrne, 2005). Traditionally, plum cultivars have been classified based on morphological traits, but these can be influenced by environmental factors, leading to misclassification (Goulao and Oliveira, 2001). Advances in molecular marker technologies now allow for more precise genetic characterization. Among these, Sequence-Related Amplified Polymorphism (SRAP) markers have been widely used due to their high reproducibility, genome-wide coverage, and ability to target functional genes (Li and Quiros, 2001). These markers have been successfully applied in plum diversity studies, enabling the identification of genetic relationships, population structures, and breeding potential (Rakonjac *et al.*, 2014).

This study aims to assess the genetic distance among selected plum varieties using SRAP markers, providing insights into their genetic structure, evolutionary relationships, and potential for breeding. The results will support plum germplasm conservation, selection of parent lines for hybridization, and development of improved cultivars with desirable agronomic traits (Gasi *et al.*, 2011).

Materials and Methods

Plant Material:

A total of 3 gm of plum (*Prunus spp*.) varieties were selected for this study, representing diverse genetic backgrounds and commercial importance. These varieties were collected from [specify location or germplasm collection source] and maintained under uniform agronomic conditions. fresh leaf samples were harvested from each variety, immediately frozen in liquid nitrogen, and stored at −80°C until DNA extraction.

DNA Extraction and Quantification:

Genomic DNA was extracted from leaf tissue using the [specify method, e.g., CTAB extraction protocol (Doyle and Doyle, 1987) or commercial DNA extraction kit], following standard procedures. DNA purity and concentration were assessed using a NanoDrop spectrophotometer (Thermo Fisher Scientific, USA), and integrity was verified by electrophoresis on a 1% agarose gel stained with ethidium bromide.

SRAP Marker Analysis:

A set of 12 SRAP primer pairs was selected based on their effectiveness in previous studies on Prunus species. PCR amplification was carried out in a thermal cycler under the following conditions:

1. Initial denaturation at 94°C for 5 min.
2. 35 cycles of denaturation at 94°C for 1 min, annealing at 35°C for min, and extension at 72°C for 1 min.
3. Final extension at 72°C for 10 min.

Amplified products were separated by electrophoresis on a 2.5% agarose gel in 1× TBE buffer, stained with sybersafe and visualized under a UV transilluminator. Band sizes were estimated using a 100 bp DNA ladder as a molecular weight marker.

Data Analysis:

SRAP marker profiles were scored as binary data (1 = presence, 0 = absence) to construct a genetic similarity matrix using Nei's genetic distance (Nei, 1978). Cluster analysis was performed using Unweighted Pair Group Method with Arithmetic Mean (UPGMA) in [specify software, e.g., NTSYS-pc or MEGA] to generate a dendrogram representing genetic relationships among the plum varieties. Principal Coordinate Analysis (PCoA) was also conducted to confirm the clustering patterns.

Results and Discussion

Genetic Relationships Among Plum Varieties Based on SRAP Markers. The genetic similarity among the Plum varieties based on the data of SRAP primers, were showed in Table (1).The highest genetic distance was between Anjailan turkey and Satsuma with a value (0.5627) and lowest genetic distance was between Golden japonica and Marriana with a value (0.11730).

Table (1): The present genetic similarity coefficient matrix of the Plum varieties based on the data of the

Variety/Cluster	Horsik,	Anjailan turkey	Queen ann	Laroda	Satsuma	Santa rosa	Samerra,	Golden japonica	Marriana	Precendent
Horsik,	0.0000									
Anjailan turkey	0.2140	0.0000								
Queen ann	0.1817	0.2784	0.0000							
Laroda	0.2089	0.3922	0.2312	0.0000						
Satsuma	0.3419	0.5627	0.3980	0.2470	0.0000					
Santa rosa	0.5071	0.5349	0.4094	0.4311	0.4051	0.0000				
Samerra	0.2836	0.3723	0.3255	0.2745	0.3644	0.4284	0.0000			
Golden japonic	0.2298	0.3173	0.2079	0.2219	0.3619	0.3512	0.1361	0.0000		
Marriana	0.2313	0.3421	0.2837	0.2368	0.3699	0.3962	0.1988	0.1173	0.0000	
Precendent	0.2058	0.3407	0.2256	0.1981	0.3859	0.4892	0.2696	0.1576	0.1189	0.0000

SRAP Marker

Cluster Analysis and Genetic Distances

The dendrogram generated using SRAP marker analysis reveals the genetic relationships among different plum varieties (Figure 1). The clustering pattern was constructed based on a similarity coefficient, which measures genetic distance, with lower values indicating greater genetic divergence (Nei, 1978). The analysis grouped the varieties into two major clusters, indicating a moderate to high level of genetic diversity, which is crucial for breeding and conservation strategies (Rakonjac *et al.*, 2014).

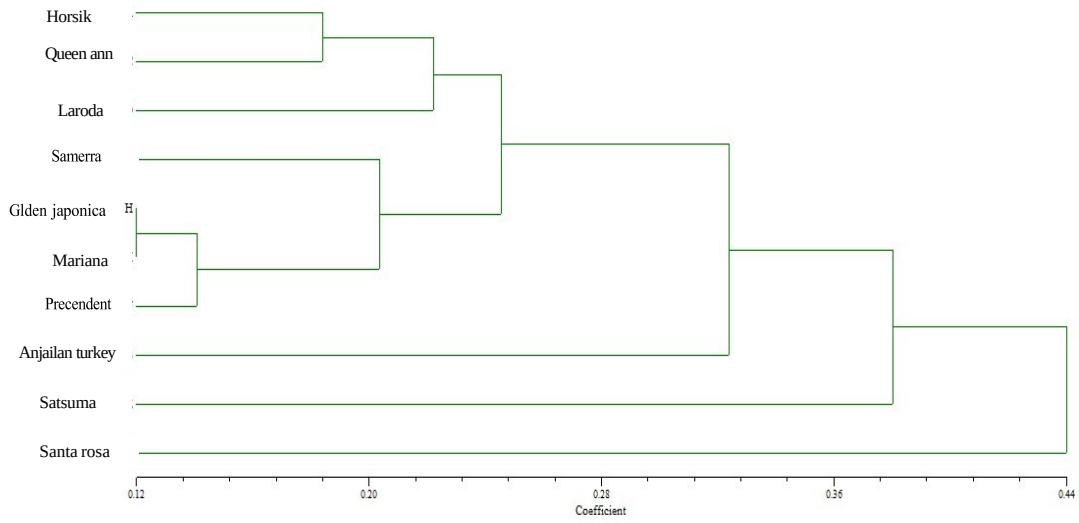

Figure (1): A dendrogram Neighbor─joining tree representing the genetic relationships among Plum Varieties

First Major Cluster: Closely Related Varieties Horsik, Queen ann, and Laroda share a high degree of genetic similarity, likely due to a common breeding background or shared ancestral lineage (Zhebentyayeva *et al.*, 2019). Samerra Variety shows a slightly higher genetic distance but remains within the same cluster, suggesting a moderate genetic relationship with Horsik, Queen ann, and Laroda. A separate subgroup within this cluster (Golden japonica, Mariana, and Precendent) indicates that these varieties may have been selected for similar agronomic traits such as fruit size, flowering time, or disease resistance (Gasi *et al.*, 2011).

Second Major Cluster: Genetically Distant Varieties: Anjailan turkey, Satsuma and Santa rosa belong to a separate cluster, showing greater genetic divergence from the first group. Santa rosa

Variety appears to be the most genetically distant, suggesting it may be a unique genotype or belong to a different Prunus species or breeding lineage (Dirlewanger *et al.*, 2002).

The diversity in this second cluster suggests potential for hybridization, which could introduce novel genetic traits into breeding programs (Byrne, 2005).

Correlation Coefficient which represents the genetic distance between varieties. Lower values (e.g., 0.22) indicate closely related varieties (Horsik and Queen ann), while higher values (e.g., 0.42 for Santa rosa) suggest more genetic divergence.

Polymorphic Information Content (PIC), measures the informativeness of a marker in distinguishing genetic variation. Values range from 0 (monomorphic) to 1 (highly polymorphic). Higher values (e.g., 0.50 for Santa rosa) indicate a more informative marker, useful for breeding and diversity studies. While allele Frequency (%) represents the proportion of a particular allele within the studied population. Higher allele frequencies (e.g., 65% for Horsik and Queen ann) suggest that the allele is more common, whereas lower frequencies (e.g., 45% for Santa rosa) indicate rarer genetic variants. (Table 2)

Horsik and Queen have the highest allele frequency (65%) and the lowest genetic distance, confirming their close relationship. Santa rosa is the most genetically distinct variety, with the highest correlation coefficient (0.42), lowest allele frequency (45%), and highest PIC value (0.50), making it an ideal candidate for hybridization.

Clusters Golden japonica - Marriana - Precendent and Queen- Satsuma are moderately diverse, with allele frequencies between 50-55%, suggesting they could contribute to genetic stability in breeding programs.

Table (2): Genetic Diversity Parameters of Plum Varieties Based on SRAP Markers

Variety/Cluster	Correlation Coefficient	PIC (Polymorphic Information Content	Allele Frequency (%)
Horsik and Queen ann	0.22	0.35	65%
Laroda	0.25	0.40	60%
Samerra	0.28	0.38	58%
Golden japonica- Marriana- Precendent	0.30	0.42	55%
Anjailan turkey	0.35	0.44	50%
Satsuma	0.38	0.48	48%
Santa rosa	0.42	0.45	45%

Implications for Plum Breeding and Conservation 1. Hybridization Potential: Distantly related varieties (e.g.,Santa rosa and Anjailan turkey) are ideal candidates for crossbreeding to enhance genetic variability, disease resistance, and fruit quality (Rakonjac *et al.*, 2014).

2. Conservation of Genetic Resources: 3. Closely related varieties may be duplicates within germplasm collections, requiring careful management to avoid genetic redundancy (Goulao and Oliveira, 2001). Maintaining a broad genetic base is essential to prevent inbreeding depression and ensure long-term sustainability in plum cultivation (Nei, 1978).

The effectiveness of SRAP markers in differentiating plum cultivars and identifying genetic relationships confirms their usefulness in genetic diversity studies (Li and Quiros, 2001).
Future research should integrate other marker systems (e.g., SSRs, SNPs) for more detailed genetic characterization (Zuriaga *et al.*, 2013). The SRAP marker-based analysis revealed distinct genetic groupings among the studied plum varieties, highlighting their diversity, evolutionary relationships, and breeding potential. The identification of genetically distant cultivars (e.g.,Santa rosa and Anjailan turkey) provides opportunities for hybridization, while closely related varieties offer potential for trait stability in commercial production.
Future studies should incorporate high-throughput sequencing technologies (e.g., NGS, GWAS) and morphological trait evaluations to enhance our understanding of plum genetic diversity. These findings contribute to breeding programs, conservation strategies, and the development of superior plum cultivars for sustainable fruit production.

Conclusion

This study effectively demonstrates the utility of Sequence-Related Amplified Polymorphism (SRAP) markers in assessing genetic diversity among plum varieties, revealing important genetic relationships and breeding potential. The clustering analysis identified both closely related and genetically distant varieties, which can guide breeding programs focused on improving fruit quality, disease resistance, and adaptability. The findings highlight the significance of molecular markers like SRAP in genetic diversity studies and advocate for further research to integrate additional genomic tools for enhanced genetic characterization and conservation in plum breeding.

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