



GENETIC CHARACTERISTICS OF OLIVE (OLEA EUROPAEA) AND THEIR IMPORTANCE IN BREEDING PROCEDURES

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Abstract: Olive (*Olea europaea* L.) is one of the oldest cultivated plants with significant genetic diversity. Studying its genetic characteristics is essential for advancing breeding programs, improving productivity, and developing disease-resistant varieties. Recent progress in genomics and molecular biology has provided a deeper understanding of olive's genetic structure. Techniques such as Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphisms (SNPs) are widely used to investigate genetic variation and optimize breeding strategies. These technologies also play a crucial role in preserving genetic resources and restoring valuable cultivars. This article provides a comprehensive overview of the genetic structure of olives, the use of molecular tools in breeding, and the implications of biotechnological advancements for the future of olive cultivation.

Keywords: Olive (*Olea europaea*), genetic diversity, molecular markers, breeding, SNP and SSR markers, genetic studies

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Introduction:

The olive tree (*Olea europaea* L.) is a highly significant and ancient species, predominantly found in the Mediterranean basin, though its cultivation has spread across temperate regions globally. As one of the oldest cultivated plants, the olive has been a central part of human civilization for thousands of years, offering vital resources for food, medicine, and cosmetics. The fruit, rich in beneficial compounds such as monounsaturated fatty acids, antioxidants, and vitamins, has made olive oil an essential dietary staple, especially in the Mediterranean diet. Moreover, olive oil is widely used in the pharmaceutical and cosmetic industries due to its anti-inflammatory, antimicrobial, and moisturizing properties.

The olive tree is particularly known for its resilience and longevity, with some trees living for centuries, adapting to a wide range of climatic conditions. This adaptability has allowed the olive to flourish in diverse environments, from arid regions to temperate

climates, and it thrives in well-drained soils with Mediterranean-type climates, characterized by hot, dry summers and mild, wet winters. However, despite its resilience, olives face various challenges, including pests, diseases, and changing environmental conditions, making the study of their genetic diversity and improvement through breeding even more critical.

Advancements in the fields of genomics and biotechnology have revolutionized the way we study the genetic structure of plants, including the olive tree. The ability to delve into the molecular level of olives has enhanced our understanding of their genetic makeup and provided a powerful tool for their improvement (Baldoni et al., 2019). The use of molecular markers, especially Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphisms (SNP), has enabled scientists to identify genetic differences between various olive varieties (Muzzalupo et al., 2014; Kaya et al., 2013). These markers are pivotal in optimizing

breeding programs, enhancing genetic diversity, and developing varieties that are more resistant to diseases, pests, and environmental stresses.

Molecular research methods have become indispensable tools in modern breeding programs, providing precise and reliable methods to track desirable traits such as disease resistance, fruit quality, and yield. For example, SSR markers, due to their high degree of polymorphism and reliability, are commonly used to assess genetic variation within olive populations and identify genetic relationships between different cultivars. On the other hand, SNP markers offer a more refined approach, enabling fine-scale genetic mapping and marker-assisted selection for improving traits related to yield and quality.

Moreover, modern biotechnology and genomics not only play a crucial role in enhancing breeding efficiency but are also central to the preservation of the olive's genetic diversity. As climate change and human activities continue to pose threats to biodiversity, genetic resources are at risk of being lost. The application of genomic tools, such as high-throughput sequencing and bioinformatics, allows for the preservation of the olive's genetic pool by identifying and cataloging valuable genetic traits that can be used in future breeding efforts. In this way, biotechnology also serves as a safeguard for the olive tree's future resilience.

Additionally, the study of the genetic diversity of olives provides critical insights into their evolutionary history and origins. Through molecular studies, researchers have uncovered new evidence regarding the domestication of olives, tracing their origins back to ancient civilizations and offering a clearer picture of their spread and evolution across regions. Understanding the genetic makeup of olives helps clarify their domestication process, providing a framework for identifying and conserving ancient cultivars that hold unique genetic traits.

Overall, the high genetic polymorphism in *Olea europaea* is key to its ability to adapt to a wide range of climatic conditions and soil types. This genetic flexibility not only supports the cultivation of olives in various parts of the

world but also allows for the development of new varieties tailored to meet the changing demands of the global market. The vast genetic pool of olives is a resource that continues to fuel innovations in breeding and offers tremendous potential for future improvements.

This paper delves into the genetic diversity of olives, examining the various molecular techniques used to study and enhance their genetic features. It also discusses the significance of these innovations in the context of olive breeding and how modern genomic tools are shaping the future of olive cultivation. Furthermore, it highlights the importance of maintaining genetic diversity in olive trees as an integral part of ensuring their sustainability and resilience in an ever-changing world.

The olive tree (*Olea europaea* L.) is primarily found in the Mediterranean basin and is one of the most ancient cultivated plants. Its fruits and oil are important in food, medicine, and cosmetics. The tree is known for its longevity and adaptability to various ecological conditions. However, studying its genetic diversity and improving it through breeding are vital to enhance yield and resistance to diseases and pests.

Advancements in genomics and biotechnology have enabled deeper investigations into the genetic features of olives. Modern molecular marker techniques, especially SSR and SNP markers, are extensively used to detect genetic differences among olive varieties and to optimize breeding programs. These tools are also significant in preserving the genetic pool and restoring genetic resources. Understanding olive's genetic makeup also helps clarify its origins and evolutionary history. High genetic polymorphism in *Olea europaea* facilitates adaptation to diverse climates and soils.

This paper explores the genetic diversity of olives, molecular research methods, and their importance in breeding. Additionally, it discusses how recent genomic and biotechnological innovations are shaping olive breeding processes.

Genetic Structure and Polymorphism

The olive tree (*Olea europaea* L.) is a



diploid plant with a chromosome number of $2n = 46$, which provides a fundamental framework for its genetic structure. Research has consistently shown that olives possess a high level of genetic diversity, a trait that is essential for their adaptability to various environmental conditions. This genetic variation arises from several key factors, each contributing to the overall polymorphism observed in olive populations.

Geographical Distribution and Environmental Factors: The genetic structure of *Olea europaea* is heavily influenced by the tree's wide geographical distribution. Olive cultivation spans across the Mediterranean basin, as well as parts of Asia, Africa, and the Americas. The variations in climate, including temperature, precipitation, and soil type, play a significant role in shaping the genetic diversity within and among olive populations. For example, olives cultivated in coastal regions may show genetic adaptations to salt tolerance, while those grown in more arid, inland areas exhibit traits that enhance drought resistance (Besnard et al., 2008).

Reproductive Methods: Olives reproduce through both vegetative (asexual) and generative (sexual) methods, and these processes significantly contribute to genetic diversity. Vegetative reproduction, through cuttings, is commonly used in commercial olive orchards, leading to the clonal propagation of specific cultivars. While this method helps maintain desirable traits, it can reduce genetic variability within a given orchard. In contrast, sexual reproduction through seed formation introduces new genetic combinations, fostering a broader range of genetic diversity. This dual mode of reproduction enables the olive tree to maintain both stability in its desirable traits and the ability to adapt to changing environments.

Genetic Impact of Wild Relatives: Another significant source of genetic variation in olives comes from wild relatives, especially *Olea europaea* subsp. *sylvestris* (wild olive). These wild populations are considered an essential genetic resource for the cultivation of domestic olives, as they contribute valuable traits such as pest resistance, drought tolerance, and enhanced resilience to environmental stress (Besnard et

al., 2008). Crossbreeding between cultivated olives and wild olives can introduce new alleles into cultivated populations, improving the genetic base and ensuring greater adaptability to climate change and other ecological pressures.

This rich genetic diversity plays a crucial role in the olive tree's ability to adapt to diverse environmental stresses, including salinity, drought, extreme temperatures, and pest infestations. The unique combination of traits within local cultivars, shaped by centuries of human selection, regional climate conditions, and environmental pressures, has resulted in a wide array of olive varieties with specialized characteristics. These local varieties not only represent the cultural heritage of different Mediterranean regions but also provide valuable genetic resources that are essential for future breeding programs.

The use of molecular marker techniques, particularly Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphisms (SNP), has greatly advanced the study of olive genetic diversity. SSR markers, known for their high level of polymorphism, allow researchers to distinguish between different cultivars and wild populations by detecting variations in specific regions of the genome. (Muzzalupo et al., 2014). These markers are particularly useful for studying genetic relationships, population structure, and the level of genetic differentiation within olive species. They can also identify genetic bottlenecks or inbreeding within specific populations, which is essential for maintaining genetic health in breeding programs.

On the other hand, SNP markers offer even more precise insights into genetic variation (Kaya et al., 2013; Kaya et al., 2021). By examining individual base-pair changes, SNP markers enable the detection of subtle genetic differences that can be crucial for trait selection in breeding. These markers are particularly valuable in fine-scale mapping of traits like disease resistance, fruit quality, and yield improvement. As SNP-based technology advances, it is increasingly used in marker-assisted selection, speeding up the breeding process and allowing for more targeted improvements in olive cultivars.

Molecular marker techniques are not

only fundamental for understanding the genetic structure of olives but also play an essential role in conservation efforts. By assessing the genetic diversity of wild olive populations and local cultivars, scientists can prioritize conservation strategies to preserve rare or endangered varieties. Furthermore, these tools aid in the restoration of genetic resources, ensuring that valuable traits are not lost in the face of environmental challenges or human-induced changes.

In summary, the genetic structure and polymorphism of *Olea europaea* are shaped by a combination of factors, including geographical distribution, reproductive methods, and genetic contributions from wild relatives. The high genetic variability within olive populations is a key factor in the tree's ability to thrive across diverse ecological conditions. Molecular markers, such as SSR and SNP, are indispensable tools for studying this genetic diversity, allowing researchers to uncover hidden genetic resources and optimize breeding programs for enhanced yield, resilience, and sustainability.

Molecular Markers and Genomic Studies:

The application of molecular tools has enhanced the understanding of olive's genetic diversity. SSR and SNP markers help in identifying the origin and genetic relationships of different cultivars (Muzzalupo et al., 2014; Kaya et al., 2013). Studies show that the genetic structure of olive has been shaped by selective breeding and human intervention (Besnard et al., 2008).

Genomic studies have identified genes that influence stress resistance and productivity. For instance, Ole e1 and Ole e10 genes are associated with allergenicity and oil content (Hernández et al., 2020). These findings contribute to developing improved olive varieties. Further, transcriptome analysis has highlighted gene expression profiles related to lipid biosynthesis, fruit development, and flowering time regulation.

Advanced tools like whole genome sequencing (WGS), genotyping-by-sequencing (GBS), and RNA sequencing have expanded our

ability to identify quantitative trait loci (QTLs) linked to economically valuable traits. These discoveries support the development of marker-assisted selection (MAS) strategies (Baldoni et al., 2019; Kaya et al., 2021).

Genetic Diversity and Breeding:

Olive cultivars from regions such as Azerbaijan, Turkey, Spain, and Italy have been subject to different breeding histories and show varying levels of polymorphism. Studies have shown that cultivars from Eastern Mediterranean regions tend to retain more ancestral genetic traits, while Western populations have undergone more intense artificial selection (Duran Sevin Teoman, Aghayeva Saltanat., 2022).

The main goals in breeding include:

- Enhancing resistance to pests and diseases
- Increasing drought and salinity tolerance
- Optimizing fruit size, oil content, and quality
- Improving growth and reproduction characteristics

Modern technologies like genome editing, especially CRISPR/Cas9, allow for more precise and effective breeding. CRISPR/Cas9 has already been demonstrated to target specific genes such as FAD2, which is associated with fatty acid desaturation, opening possibilities for enhanced oil composition (Kaya et al., 2021).

Somatic embryogenesis, tissue culture, and double haploid technologies are also being explored for clonal propagation and rapid development of homozygous lines. These techniques are essential in accelerating the breeding cycle and developing genetically uniform lines.

Conservation of Genetic Resources:

Conservation of olive genetic resources is vital to maintain biodiversity and ensure food security. Ex situ collections, such as field genebanks and cryopreservation of shoot tips and embryos, are crucial for preserving rare and endemic varieties (Baldoni et al., 2019).

In situ conservation through traditional agroecosystems also plays a key role. Many small-scale farmers maintain landraces with unique traits that are often adapted to local



environmental conditions and cultural practices. Preserving this traditional knowledge alongside genetic material is essential for holistic conservation.

International collaborations, such as the Olive Germplasm Bank of Córdoba (Spain),

Biotechnological Innovations in Olive Improvement:

The integration of biotechnology in olive breeding has opened new avenues for sustainable agriculture. Technologies such as genetic transformation using *Agrobacterium tumefaciens*, RNA interference (RNAi), and gene silencing have been investigated to improve traits like oil stability, pathogen resistance, and abiotic stress tolerance (Baldoni et al., 2019; Kaya et al., 2021).

Nanotechnology is an emerging area in plant biotechnology with potential applications in olive cultivation. Nanofertilizers and nanopesticides are being studied to reduce chemical usage and environmental impact while enhancing nutrient uptake and plant protection.

Bioinformatics and machine learning tools are increasingly used to analyze large genomic datasets, predict gene functions, and model phenotypic responses. These computational approaches can guide precision breeding and decision-making in cultivar selection (Zulfiqar Saman et al., 2025).

Conclusion

The genetic characterization of *Olea europaea* plays a crucial role in preserving biodiversity, enhancing breeding programs, and ensuring sustainable cultivation practices. Advances in molecular genetics—especially the use of SSR and SNP markers—have significantly deepened our understanding of the olive's genetic diversity and evolutionary history (Muzzalupo et al., 2014; Kaya et al., 2013). The identification of genes responsible for key agronomic traits, such as oil composition, stress resistance, and adaptability, has opened new avenues for targeted breeding and conservation

contribute to the global efforts of characterization, documentation, and sustainable use of olive genetic diversity (Besnard et al., 2008).

efforts (Hernández et al., 2020; Baldoni et al., 2019).

Moreover, the integration of modern biotechnological approaches, including whole genome sequencing, genotyping-by-sequencing, and CRISPR/Cas9 genome editing, offers unprecedented precision in developing superior olive cultivars (Kaya et al., 2021; Baldoni et al., 2019). These technologies facilitate the selection and enhancement of desirable traits without compromising genetic diversity—an essential requirement for the long-term sustainability of olive cultivation.

The conservation of wild and local olive populations remains a strategic priority. These gene pools are indispensable for maintaining genetic resilience and for adapting to the challenges posed by climate change, pests, and diseases (Besnard et al., 2008; Duran Sevin Teoman., Aghayeva Saltanat, 2022). Thus, integrating classical breeding methods with molecular and genomic tools will accelerate the development of high-yielding, resilient, and high-quality olive varieties.

Future research should focus on:

- Completing high-resolution genome sequencing for a broader range of cultivars (Baldoni et al., 2019),
- Applying genome editing tools (e.g., CRISPR) in practical breeding (Kaya et al., 2021),
- Expanding germplasm collections and encouraging international collaboration for conservation (Besnard et al., 2008).

Ultimately, a multidisciplinary approach—combining genetics, biotechnology, and ecological conservation—will ensure the effective utilization and preservation of olive genetic resources for future generations.

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