

Review Article

Genetic Analysis Of Drought Tolerance and Identification of Candidate Genes in Grapevine (*Vitis Vinifera*) Genotypes

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Abstract

Drought stress is one of the major environmental factors limiting grapevine growth, productivity, and fruit quality, particularly in regions affected by increasing water scarcity and climate variability. Grapevine (*Vitis vinifera*) genotypes exhibit substantial genetic variation in their responses to water deficit, making the identification of genetic factors associated with drought tolerance important for the development of resilient grapevine cultivars. In this review, we discuss the genetic and molecular mechanisms underlying drought tolerance in grapevine, with particular emphasis on genes involved in water regulation, stress signaling, antioxidant defense, osmotic adjustment, and transcriptional regulation. We also examine the potential of molecular markers, gene expression analysis, transcriptomic approaches, and other genomic tools for identifying candidate genes associated with drought-responsive traits. Understanding the genetic basis of drought tolerance may facilitate the identification and characterization of superior grapevine genotypes and support marker-assisted selection and molecular breeding programs. Further investigation of candidate drought-responsive genes could contribute to the development of grapevine cultivars with improved adaptation to water-limited environments and help maintain grape production under changing climatic conditions.

Keywords: grapevine, drought tolerance, drought stress, genetic diversity, candidate genes, plant genetics, molecular markers.

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1. Introduction

Grapevine (*Vitis vinifera* L.) is one of the most economically important perennial fruit crops worldwide and is cultivated extensively for wine, table grapes, juice, and dried fruit production. Because grapevine cultivation is strongly influenced by environmental conditions, the availability of water is a major factor determining plant growth, productivity, and fruit quality. Many grape-producing regions are characterized by warm and dry growing seasons, and increasing temperatures together with irregular precipitation patterns are expected to increase the frequency and severity of drought events. Consequently, water scarcity has become an important challenge for sustainable viticulture, particularly in regions where irrigation resources are limited [1], [2].

Drought stress affects grapevines at multiple physiological and biochemical levels. A reduction in soil water availability can alter stomatal conductance, photosynthesis, water transport, osmotic regulation, and antioxidant activity, ultimately affecting vegetative growth and berry development. Grapevine cultivars also differ considerably in their responses to water deficit, indicating that drought adaptation is influenced by genotype as well as environmental conditions. Differences among genotypes have been associated with traits such as stomatal regulation, hydraulic conductivity, root characteristics, aquaporin activity, abscisic acid (ABA) dynamics, and osmotic adjustment [1].

The molecular response of grapevine to drought involves complex regulatory networks rather than a single physiological mechanism. ABA-mediated signaling has an important role in the response to water deficit by regulating processes associated with stomatal closure and plant water balance. In addition, drought stress can induce changes in the expression of genes involved in hormone signaling, reactive oxygen species (ROS) metabolism, osmotic adjustment, carbohydrate metabolism, and cellular protection [2].

Transcriptomic investigations have further demonstrated that grapevine genotypes can activate distinct sets of genes under water-limited conditions, suggesting that genotype-dependent molecular responses contribute substantially to differences in drought adaptation [3].

The identification of genes associated with drought-responsive traits is therefore an important component of understanding the genetic basis of drought tolerance in grapevine. Advances in molecular genetics and genomics have provided several approaches for investigating this genetic basis, including molecular markers, gene expression analysis, transcriptomics, genome-wide association studies (GWAS), and comparative genomic analyses. For example, a GWAS study involving different *Vitis* species identified significant marker-trait associations related to stomatal conductance during progressive water deficit and identified candidate genes potentially involved in drought response. The study demonstrated that genetic variation can be associated with physiological traits that contribute to water-use regulation in grapevine [4].

2. Physiological and Biochemical Responses of Grapevine to Drought Stress

2.1. Water Relations, Stomatal Regulation and Photosynthesis

Water availability strongly influences the physiological performance of grapevine and determines how effectively the plant can maintain growth and carbon assimilation during periods of drought. When soil moisture declines, the movement of water from the soil into the plant becomes increasingly restricted, creating changes in leaf water status and hydraulic functioning. Grapevines respond to these changes through coordinated adjustments in water uptake, xylem transport, transpiration, and stomatal behavior. The interaction between these processes determines the capacity of a plant to maintain water balance under prolonged water limitation [5], [6]. Under water deficit, grapevines reduce stomatal conductance and transpiration to limit water loss [7]. The intensity of this response varies among genotypes and is influenced by hydraulic properties and ABA signaling [8]. Grapevine genotypes may adopt contrasting isohydric or anisohydric strategies under drought, involving differences in stomatal regulation, ABA response, xylem pH, and hydraulic adjustment. Stomatal closure also restricts CO₂ entry into leaves, resulting in reduced photosynthetic activity [9], [10]. Under moderate drought, photosynthesis can be maintained despite partial stomatal closure, whereas severe drought causes additional limitations in carbon fixation and photosynthetic processes [11]. Therefore, differences in stomatal regulation and photosynthetic maintenance among genotypes can be useful for identifying drought-tolerant grapevine varieties [5], [7].

2.2. Oxidative Stress and Antioxidant Defense

Drought stress disrupts cellular redox balance and promotes the accumulation of reactive oxygen species (ROS), including superoxide radicals and hydrogen peroxide [5]. Excessive ROS can damage lipids, proteins, and nucleic acids, whereas controlled ROS production can also function as a signaling mechanism during stress adaptation. The strength of this antioxidant response differs among grapevine genotypes and can contribute to their contrasting levels of drought tolerance [12]. Recent evidence also indicates that drought-responsive transcription factors such as VvNAC33 can enhance grapevine drought tolerance by promoting antioxidant activity and ROS detoxification [13].

Grapevine possesses a complex antioxidant network that helps maintain cellular redox balance during drought stress [13]. This network includes enzymatic components such as superoxide dismutase, catalase, and peroxidases, together with non-enzymatic antioxidants including ascorbate and glutathione [14]. The activity of these protective systems may vary between grapevine genotypes, which can partly explain differences in their ability to tolerate water deficit [15]. In addition, changes in the expression of antioxidant-related genes can contribute to the regulation of ROS levels during drought [16]. The coordinated activation of these defense mechanisms helps

reduce oxidative damage and supports the maintenance of cellular functions under prolonged water limitation [13], [16].

3. Molecular Mechanisms of Drought Tolerance

3.1. ABA Signaling and Drought-Responsive Pathways

Abscisic acid (ABA) is a major hormonal regulator of grapevine responses to drought stress. Water deficit promotes ABA accumulation, which contributes to stomatal regulation and activation of stress-responsive genes. As water availability decreases, increased ABA signaling helps the plant coordinate water conservation with broader cellular responses to drought. This regulation is particularly important because stomatal closure reduces excessive water loss while simultaneously influencing CO₂ uptake and photosynthetic activity [2]. At the molecular level, ABA is perceived by PYR/PYL/RCAR receptors, which inhibit PP2C and allow SnRK2 kinases to become active. The activation of this signaling cascade provides a molecular connection between the perception of water deficit and the regulation of downstream stress responses [17]. Activated SnRK2 proteins subsequently regulate downstream transcription factors, including ABF/AREB proteins, leading to the expression of drought-responsive genes [2], [17]. Through this pathway, ABA signaling can influence several physiological processes associated with drought adaptation, including stomatal behaviour, cellular protection and regulation of stress-related gene expression. Studies in *Vitis vinifera* have identified multiple components of this signaling pathway, including PYR/PYL receptors, PP2Cs, SnRK2s and ABFs [17]. Differences in the expression of ABA-related genes among grapevine genotypes may contribute to variation in drought tolerance [18]. Such differences may affect the intensity and timing of ABA-mediated responses and consequently influence how individual genotypes respond to prolonged water limitation,

3.2. Osmotic Adjustment, Aquaporins and Stress-Responsive Genes

Drought causes a decline in cellular water availability, and grapevine can partially compensate for this change through osmotic adjustment. Grapevines can maintain cellular water balance during drought by accumulating compatible solutes and mineral ions, which support the preservation of cell turgor under low water availability [1]. Among these compounds, proline, soluble sugars, potassium, and calcium have been associated with osmotic regulation, although their contribution may vary depending on the genotype. The accumulation of these compounds can help cells retain water and maintain metabolic activity when external water availability becomes limited. Osmotic adjustment is therefore an important mechanism that allows grapevine tissues to tolerate changes in cellular water potential. Among these compounds, proline, soluble sugars, potassium, and calcium have been associated with osmotic regulation, although their contribution may vary depending on the genotype.

In addition, drought activates numerous stress-responsive genes involved in ABA signaling, osmotic regulation, antioxidant defense, and carbohydrate metabolism, demonstrating that grapevine drought tolerance is controlled by a complex molecular network [3]. These genes participate in different stages of the stress response and allow grapevine cells to coordinate water conservation with cellular protection. Changes in carbohydrate metabolism can also influence the availability of soluble sugars that contribute to osmotic adjustment. At the same time, activation of antioxidant-related genes helps protect cells from oxidative damage associated with drought stress. The expression of these stress-responsive genes may differ between grapevine genotypes, suggesting that genetic variation contributes to differences in drought adaptation. Overall, osmotic adjustment, aquaporin regulation, and stress-responsive gene expression function as interconnected mechanisms that help grapevine maintain cellular stability under water-limited conditions [1], [3].

4. Identification of Candidate Genes Associated with Drought Tolerance

4.1. Transcriptomic and Gene Expression Approaches

Transcriptomic methods, particularly RNA-sequencing, are widely used to investigate grapevine responses to drought stress. These approaches allow researchers to identify differentially expressed genes involved in ABA

signaling, carbohydrate metabolism, antioxidant defense, and stress regulation [3], [19]. Gene expression patterns can vary among grapevine cultivars, providing insights into their different drought-adaptation strategies [15]. Therefore, transcriptomic analysis is useful for identifying candidate genes and molecular pathways associated with drought tolerance [19].

RNA-sequencing also makes it possible to examine large numbers of genes simultaneously, providing a broader view of the molecular response to water deficit. Changes in transcript abundance can reveal which biological processes are activated or suppressed when grapevines experience drought conditions. This information can be particularly useful for distinguishing early responses from changes that occur after prolonged stress. Transcriptomic comparisons between stressed and well-watered plants can therefore provide information about the molecular reprogramming that accompanies drought exposure [3], [19]. The analysis of differentially expressed genes can identify functional groups associated with stress perception, signal transduction, and cellular protection. Genes related to transcriptional regulation may also play an important role because transcription factors can coordinate the expression of multiple drought-responsive genes. In addition, alterations in genes involved in carbohydrate metabolism may reflect changes in carbon allocation and osmotic regulation during water limitation. Similarly, changes in antioxidant-related transcripts can indicate the activation of mechanisms responsible for controlling oxidative stress [3], [15].

An important advantage of transcriptomic analysis is that it can reveal differences between grapevine cultivars exposed to the same environmental conditions. Some cultivars may activate particular stress-related pathways more strongly or at an earlier stage than others, contributing to their contrasting drought responses [15]. Such genotype-dependent expression patterns can help explain why grapevine varieties differ in their ability to maintain physiological activity during water deficit. Transcriptomic data can also be combined with physiological measurements to establish relationships between gene expression and traits such as stomatal conductance, photosynthesis, and water-use efficiency.

Furthermore, transcriptomic studies can provide a starting point for identifying candidate genes that require further functional investigation. Genes showing consistent associations with drought-related responses may subsequently be examined using molecular and genetic approaches. The integration of transcriptomic analysis provides an important molecular framework for studying grapevine drought responses and identifying biological ways that may contribute to the development of more drought-tolerant genotypes.

4.2. Molecular Markers, GWAS and Candidate Gene Identification

Molecular markers are valuable tools for identifying genomic regions associated with drought tolerance in grapevine. Techniques such as SSR and SNP markers, together with genome-wide association studies (GWAS), enable the detection of marker-trait associations linked to physiological responses under water deficit. GWAS analyses have identified several candidate genes involved in stomatal regulation, water transport, and stress signaling, providing important targets for marker-assisted breeding of drought-tolerant grapevine genotypes [4]. GWAS can also narrow the search for genes located within genomic regions associated with drought-related characteristics.

5. Application of Genetic Knowledge in Grapevine Breeding

5.1. Identification and Selection of Drought-Tolerant Genotypes

The identification of drought-tolerant grapevine genotypes requires the evaluation of several physiological and agronomic characteristics rather than relying on a single trait. Parameters such as stomatal conductance, water-use efficiency, photosynthetic performance, yield, and root characteristics can help distinguish genotypes with better adaptation to water deficit [20]. Because drought responses are strongly influenced by environmental conditions, combining multiple traits provides a more reliable basis for selecting promising genotypes. Such screening can support the selection of suitable cultivars and rootstocks for breeding programs aimed at improving grapevine drought tolerance.

5.2. Molecular Breeding and Future Biotechnological Approaches

Molecular breeding can accelerate the improvement of drought tolerance by combining genetic markers, genomic information, and physiological traits during selection [20]. Genome-editing technologies, particularly CRISPR/Cas systems, provide an additional approach for investigating and modifying genes involved in drought-response pathways [20]. These technologies may help develop grapevine genotypes with improved water-use efficiency and stress adaptation while reducing the time required for conventional breeding. The integration of genomic selection, transcriptomic information, and gene editing is therefore a promising direction for future grapevine improvement.

6. Conclusion

Drought stress represents one of the major environmental challenges affecting grapevine growth, productivity, and long-term adaptation, particularly under changing climatic conditions. The response of grapevine to water limitation involves a complex interaction between physiological, biochemical, and molecular mechanisms. Regulation of stomatal conductance and photosynthesis allows plants to balance carbon assimilation with water conservation, while antioxidant systems help protect cells from oxidative damage caused by excessive reactive oxygen species. At the molecular level, ABA signaling, osmotic adjustment, and drought-responsive genes contribute to the coordination of these responses.

Genetic and transcriptomic approaches provide further opportunities to understand the mechanisms underlying differences in drought tolerance among grapevine genotypes. RNA-sequencing, molecular markers, and GWAS can facilitate the identification of candidate genes and genomic regions associated with important drought-related traits. Combining these molecular approaches with physiological screening may improve the selection of genotypes capable of maintaining water status, photosynthetic activity, and cellular stability under water deficit. Such integration is particularly valuable for grapevine improvement because drought tolerance is controlled by multiple interacting traits rather than by a single gene or mechanism.

Overall, integrating traditional genetic approaches with modern biotechnology can contribute to more efficient grapevine breeding and support sustainable grape production under increasingly limited water availability. A more comprehensive approach to grapevine improvement can be achieved when DNA-based marker data are interpreted alongside ampelographic observations. Such integration allows for more accurate cultivar identification and supports the selection of genotypes that combine stress tolerance with desirable agronomic and enological traits. Moreover, combining molecular fingerprinting with morphological descriptors enhances the conservation and sustainable utilization of genetic resources, providing a robust framework for germplasm management in breeding programs [21].

Future research should therefore focus on combining physiological measurements, genomic information, and functional gene analysis to obtain a more comprehensive understanding of grapevine drought adaptation. Molecular breeding, genomic selection, and genome-editing technologies may provide additional opportunities to accelerate the development of drought-resilient grapevine varieties. Overall, integrating traditional genetic approaches with modern biotechnology can contribute to more efficient grapevine breeding and support sustainable grape production under increasingly limited water availability.

Author Contributions

The author conceived and designed the study, conducted the research, analyzed the data, and wrote the manuscript.

Conflict of Interest

The author(s) declare no conflicts of interest.

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