

DROUGHT TOLERANCE IN BARLEY (*HORDEUM VULGARE* L.): PHYSIOLOGICAL AND GENETIC BASES AND MODERN BREEDING STRATEGIES

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Abstract. Drought represents a major abiotic stress factor that significantly affects plant growth, as well as physiological and metabolic processes, ultimately leading to reduced cereal productivity worldwide. Under such conditions, plants respond through stomatal closure, decreased photosynthetic activity, osmotic imbalance, and restricted nutrient uptake. In Europe, including Romania, the frequency and intensity of drought and heat stress events have increased, affecting barley (*Hordeum vulgare* L.), a species recognized for its high adaptability and ecological plasticity. Drought tolerance is a complex, polygenic trait involving numerous genes and quantitative trait loci (QTLs) associated with essential adaptive mechanisms. The integration of breeding, physiological, and genetic knowledge is essential for the development of valuable and well-adapted barley genotypes, ensuring yield stability and contributing to food security under the conditions imposed by ongoing climate change.

Keywords: barley, abiotic stress, yield stability, molecular breeding.

DOI [10.56082/annalsarsciagr.2026.1.47](https://doi.org/10.56082/annalsarsciagr.2026.1.47)

1. Introduction

Drought represents one of the primary abiotic stress factors, causing significant modifications at the level of plant growth, physiological processes, and metabolism, with direct effects on global cereal production [28]. From an agricultural perspective, it is defined as a state of soil moisture deficit, insufficient to satisfy the requirements of a crop within a specific time interval [41]. Such

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conditions are associated with reduced water availability, which determines stomatal closure, decreased photosynthetic activity, leaf rolling, osmotic imbalances, and the limitation of nutrient uptake [31].

Tolerance to drought and heat constitutes an essential factor for the stability of agricultural yields, including in Romania, particularly in the steppe zones of the south and east of the country, where these phenomena are frequent. In recent years, drought has manifested increasingly often in the regions of Transylvania as well, having a negative impact on production levels [29].

Starting with the 1980s, the frequency and intensity of drought episodes have experienced a significant increase [35, 28]. Tolerance to drought and heat reflects the capacity of plants to withstand prolonged periods of water stress and to resume their physiological processes without significant reductions in potential yield. In this context, the production level constitutes an essential indicator in the evaluation of these traits. Water stress determines disturbances in the plant's water balance, affecting fundamental physiological functions such as photosynthesis, respiration, the transport of substances, and growth processes [29].

2. Materials and Methods

The method used to draft this paper consisted of documenting, analyzing, and synthesizing specialized scientific literature published in international databases (Scopus, Google Scholar, ScienceDirect). Climate, physiological, and genetic studies relevant to barley cultivation were selected, with an emphasis on identifying the genes involved in the drought response mechanism.

3. Results and Discussions

Climate change simultaneously generates both opportunities and risks for barley production at a global level. Studies highlight that some early-maturing cultivars, although presenting the advantage of avoiding the thermal stress occurring toward the end of the vegetation period, are associated with inferior harvest quality and do not manifest efficient mechanisms for drought avoidance. In this context, under conditions where early forms are correlated with reduced qualitative performance, increasing the number of productive secondary tillers is considered a promising direction for breeding programs [21].

Barley possesses a series of traits that confer a certain degree of drought tolerance, among which high photosynthetic efficiency stands out, associated with more efficient water use and, implicitly, with the formation of a superior harvest index and increased biomass [6]. Nevertheless, these advantages are accompanied by

certain vulnerabilities, the crop being sensitive to variations in soil moisture and thermal regime, particularly during the anthesis and post-anthesis phases, corresponding to the grain-filling period [1].

Traditionally, drought is associated with regions such as Africa and Australia, but recent observations indicate an intensification and expansion of drought phenomena at the European level, these becoming more severe and having a wider geographical distribution across the entire continent [22]. In recent decades, the frequency of periods characterized by water deficit has increased especially in Central and Western Europe. Studies highlight that the drought episodes of 2003, 2006, 2007, 2008, and 2011, particularly in the spring season, had a severe economic impact on the agricultural sector [12]. In this context, climate projections are considered worrying, especially for Central Europe, South-Eastern Europe, and the Mediterranean region, where there is an increased risk of drought intensification in the future.

A study regarding the impact of climate and climate change on European agriculture involved the distribution of qualitative and quantitative questionnaires to experts in agronomy and agroclimatology from 26 European countries. The results indicate that European farmers are in an active process of adapting to climate change, specifically through the use of early-maturing cultivars and the selection of species and varieties with increased drought tolerance. The most severe effects were reported in regions with a continental climate, particularly in the Pannonian zone, which includes Hungary, Serbia, Romania, and Bulgaria. These areas are characterized by a high frequency of heatwaves and drought episodes, and cultivation cannot be planned efficiently for another interval of the year [12].

The analysis of the impact of the stress factor and the phenophase in which drought commonly occurs within a specific area represents an essential premise for the breeding and improvement of drought tolerance [36].

In a study conducted at a local level in Cluj, Romania, it was highlighted that temperatures during the post-anthesis phenophase have recorded a constant upward trend in recent years, exceeding the multi-annual average. This aspect indicates that heat stress phenomena are manifesting even in regions traditionally considered favorable for barley cultivation, see Figure 1 [10].

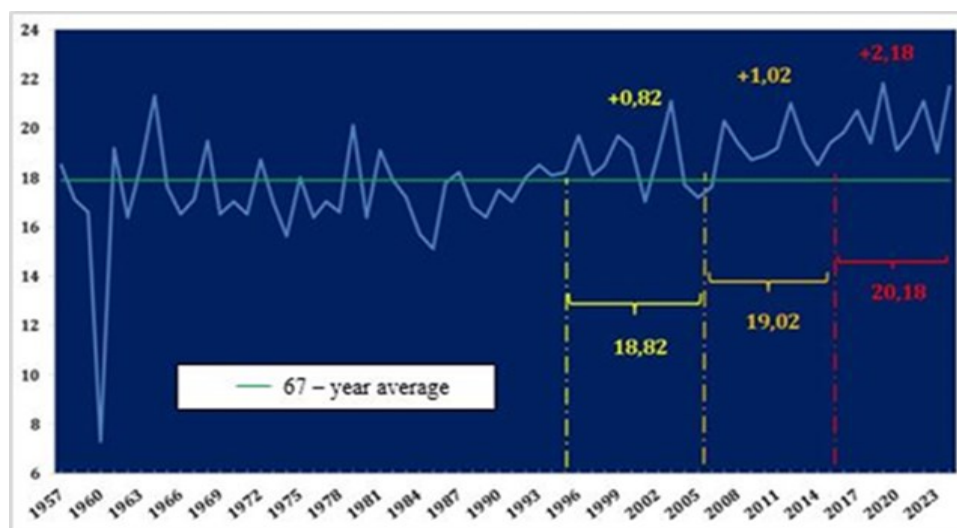


Fig. 1. Changes in the average monthly temperature during the post-anthesis period over the last 67 years (1957–2024) in Turda, Romania [10].

In response to these climatic shifts, the development of new high-value cultivars characterized by enhanced adaptability to current environmental conditions becomes essential. Even in instances where water availability is not the primary limiting factor, cereal crops exposed to elevated temperatures toward the end of the growing season tend to record diminished yields [18, 38]. In the case of spring cereals, this vulnerability is more pronounced due to their susceptibility to heat stress. Within this framework, the work of plant breeders is becoming increasingly complex, requiring the identification of novel sources of genetic material to be utilized as donors for the development of superior genotypes aimed at increasing drought tolerance [40].

Overall, improving drought tolerance in crop species represents an essential requirement for maintaining yield levels and harvest quality [13].

Several studies highlight the existence of certain early-maturing barley cultivars which, despite offering the advantage of early maturity, are associated with reduced harvest quality and do not express efficient drought avoidance mechanisms. Within this framework, the early forms analyzed are correlated with inferior crop performance; consequently, increasing the number of productive secondary tillers is considered a promising direction for breeding programs [21].

At the same time, plant architecture can constitute a relevant indicator for evaluating drought resistance. The development of the root system, oriented toward a more efficient exploration of the soil to access water resources, represents a significant advantage under conditions of water deficit [17]

Furthermore, [37] emphasize that tillering and leaf development represent essential morphological traits involved in drought tolerance mechanisms.

The response of plants to water stress is based on the expression of a large number of genes, which leads to the modification of cellular, physiological, and biochemical processes, each contributing minor effects. Through the use of transgenic techniques, multiple candidate genes (contributing candidate genes - CGs) have been identified and are considered to be collectively involved in the drought adaptation mechanisms of cereals, including barley [34, 20].

Genetic analyses have highlighted the localization of QTLs associated with drought tolerance on chromosomes 2H, 5H, and 7H [9,19], these regions being considered valuable genomic landmarks for the development of barley genotypes with improved tolerance. The relationship between heading date (earliness) and drought tolerance was highlighted by [23]. In this context, QTLs associated with the heading moment were identified, located on chromosomes 2H, 5H, and 7H, which show correlations with QTLs involved in drought tolerance. Furthermore, QTLs related to yield components have been reported, situated in proximity to those associated with earliness [21].

Despite the progress made in this field, a relatively limited number of genes involved in the drought response have been tested, and evidence regarding their direct contribution to increasing tolerance remains insufficient. The products of these genes can be classified into two main categories: functional proteins, involved in processes such as the transport of sugars and prolines, cellular detoxification, the synthesis of late embryogenesis abundant (LEA) proteins, and the regulation of osmotic balance; and regulatory proteins, which include transcription factors, signaling molecules, and enzymes involved in phospholipid metabolism [32].

Embryogenesis Abundant proteins is polygenic in nature; similarly, dehydration processes are polygenically regulated, involving genes such as *Dhn* and *LEA DII* [7, 4].

The literature further highlights other genes involved in drought tolerance mechanisms. Specifically, the *HvARH1* gene is associated with aldehyde reduction processes [8], *SRG6* is involved in protein synthesis under stress conditions [17], and *HVA1* participates in the synthesis of LEA-type proteins [2]. Additionally, the *hVPPRPx* gene is involved in regulating protein synthesis in response to pathogen attack [30].

The *HVA1* gene, involved in the synthesis of LEA-type proteins in barley, was introduced into rice through transgenic methods, leading to increased tolerance of this species to drought and salinity. These results support the hypothesis that LEA proteins play an essential role in plant protection under water stress conditions.

Within this framework, the genes responsible for the synthesis of LEA proteins represent valuable molecular tools in genetic breeding programs oriented toward increasing drought resistance [43].

Abscissic acid (ABA) plays an essential role in mediating the plant response to stress conditions and has been extensively investigated in barley and other cereal species [25]. Within the framework of QTL analyses, traits associated with drought tolerance include parameters such as leaf ABA content, relative water content, and osmotic adjustment capacity [24, 37].

Wild barley germplasm (*Hsp* forms, HOR 11508) represents an important source of QTLs with favorable effects on yield and other agronomic traits involved in increasing resistance to water deficit, particularly in Mediterranean regions [11, 34].

Studies have enabled the identification of several genes involved in drought tolerance, the mechanisms of which can be exploited in modern breeding programs. To this end, 13 genes associated with drought resistance in barley are presented in Table 1, highlighted in a comprehensive research study conducted by [36].

Table 1. Key genes and their functional mechanisms in barley (*Hordeum vulgare* L.) drought tolerance [36]

Gena	Mechanism of action	References
<i>DHNs</i>	Membrane stability (dehydration tolerance)	[15]
<i>Dhn3, Dhn9</i>	Enhanced Chl a, b content, stomatal conductance, biomass, and grain yield	[15]
<i>LEA (HVA1)</i>	Overaccumulation of LEA proteins improves drought tolerance	[16]
<i>DHNs</i>	Membrane stability (dehydration tolerance)	[15]
<i>HvNACs</i>	Leaf senescence and root development	[5]
<i>MYB</i>	Growth and development	[39]
<i>CBF/DREB</i>	Cellular protection against damage and desiccation	[20]
<i>Vm-H1 și Vm-H2</i>	Improved yield stability	[26]

<i>HvTX1</i>	Grain development	[23]
<i>HvDME</i>	Grain development under drought conditions	[14]
<i>HVSRG6</i>	Cellular water absorption and retention capacity	[27]
<i>HvWRKY38</i>	Improved adaptation and biomass accumulation following water stress	[42]
<i>Hsdr4</i>	Osmotic adjustment in barley	[33]
<i>eibi1</i>	Maintenance of leaf water status	[3]

Recent studies in barley have highlighted significant progress in molecular genetics, which has enabled the development and application of modern methods to increase drought tolerance. In this context, several complementary genetic strategies are being utilized. Genome-Wide Association Studies (GWAS) examine the relationship between genetic variation and phenotypic traits, contributing to the identification of candidate genes involved in the response to water stress. Marker-Assisted Selection (MAS) allows for the rapid and efficient identification of tolerant genotypes based on specific molecular markers. In parallel, genetic engineering overcomes the limitations of classical breeding by directly introducing stress tolerance-associated genes into the barley genome. Furthermore, genome editing technologies offer a high level of precision, allowing for targeted modifications of genes involved in plant adaptation to drought conditions [1].

4. Conclusions

The intensifying severity and increasing frequency of drought and heat stress phenomena necessitate a rapid adaptation of agricultural systems through the development of more resilient genotypes. The integration of knowledge regarding the physiological and genetic mechanisms of water stress tolerance, alongside the use of classical methods complemented by modern breeding technologies, represents an essential direction for ensuring yield stability and food security in the context of climate change.

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