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ABIOTIC FACTORS AND RESISTANCE OF DIFFERENT WINTER WHEAT VARIETIES IN THE CONDITIONS OF SOUTHERN IRAQ

4.1.1. General agriculture and crop production

4.1.2 Plant breeding, seed production and biotechnology

DISSERTATION

for an academic degree of candidate of biological sciences

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На правах рукописи

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АБИОТИЧЕСКИЕ ФАКТОРЫ И УСТОЙЧИВОСТЬ РАЗНЫХ СОРТОВ ОЗИМОЙ ПШЕНИЦЫ В УСЛОВИЯХ ЮЖНОГО ИРАКА

4.1.1. Общее земледелие и растениеводство

4.1.2. Селекция, семеноводство и биотехнология растений

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INTRODUCTION

Relevance of the topic. Global climate changes were a major challenge for many countries, presenting the world with a new reality that includes rising average temperatures, changes in rainfall, and more frequent and severe extreme weather events. Particularly concerning are threats such as droughts, increased soil salinity, and accelerated desertification, which are forcing populations to migrate [1,2]. Soil salinity and drought were the most abiotic threats to crop production worldwide, with drought being the most destructive due to the progressive water scarcity caused by lack of rainfall. Over the past few decades, drought has caused billions of dollars in damage globally, affecting vast agricultural areas across all continents, leading to significant crop losses [3]. Selecting resistant genotypes is one method of mitigating the severity of those abiotic environmental factors [4].

Degree of the development of the research study. Climate change's impact on soil properties, irrigation practices, and global water supplies is a pressing concern, as it threatens the production of strategic crops such as rice, wheat, barley and maize. It’s projected that by 2050, developing countries could face economic impacts from soil and water salinity totalling US$7–8 billion [1], with projected decreases in crop yields between 10 and 25% [5,6]. The broader economic impact could amount to 45% of total production [7]. In Iraq, climate change has caused damage, affecting more than 70% of irrigated land. A significant portion of these (approximately 30%) have become unproductive, primarily due to increased salinity and drought impacts [8].

High temperatures, evaporation, low rainfall, and poor drainage have contributed to the scarcity of irrigation water and increased the concentration of harmful salts in irrigation water and soil, thus leading to a decrease in cultivated area. This impact has exacerbated existing crises, particularly in southern Iraq, threatening food security and population stability [8,9].

Therefore, mitigation efforts have focused on developing and selecting new genotypes capable of resisting drought and salinity [4]. Wheat, due to its large genome,

is used in breeding and genetic engineering programs to create new genotypes adapted to changing climatic conditions [10]. Breeding programs achieved yield increases of 1% to 13% (average 4%), and salinity-tolerant varieties showed benefit-cost ratios of 2% to 3%, confirming their economic feasibility [11].

Subject of the study: Agroecological and productive manifestations of phenotypic plasticity of winter wheat varieties under the influence of a complex of limiting soil and climatic factors (deficit of available moisture, high-temperature stress, secondary salinization of the root layer) in the agroclimatic conditions of Southern Iraq.

The objectives of the study: to identify the level of agroecological adaptation and stress resistance of winter wheat varieties to the complex of abiotic limiting factors (deficit of soil moisture, high vegetation temperatures, and salinity) in the conditions of Southern Iraq for the scientifically based selection of consistently productive genotypes and the development of practical recommendations for optimising the varietal composition in the grain production system of the region.

Research objectives:

1. To evaluate the adaptive potential and stability of the production process of winter wheat varieties under the combined effects of soil drought and salinity through a comprehensive analysis of morphometric traits and yield structure components.

2. To establish correlations between physiological indicators of adaptation (relative water content in leaves, concentration of photosynthetic pigments, and activity of the enzymatic and non-enzymatic antioxidant system) and winter wheat productivity to confirm the agricultural criteria for selecting resistant genotypes under limited conditions.

3. To conduct agroecological differentiation and ranking of varietal material based on an integrated assessment of morphophysiological and molecular indicators for the individualized selection of stress-tolerant genotypes and optimization of regional adaptive assortment.

4. To identify morphophysiological and molecular indicators of winter wheat adaptability to complex salinity and moisture deficiency, substantiating their diagnostic significance for predicting productivity and differentiated selection of genotypes in arid regions.

5. To formulate practical recommendations for differentiated selection of genotypes and adjustment of elements of winter wheat cultivation technology in the soil and climatic conditions of Southern Iraq, ensuring stabilization of productivity and preservation of the technological properties of grain.

Scientific Novelty:

For the first time, a comprehensive agroecological stratification of 23 winter wheat genotypes was performed under conditions of combined salinity and soil drought in southern Iraq, enabling the selection of the Dujela, Faris, and Buhuth 22 varieties as stable components of an adaptive assortment. A unique set of *SSR-PCR* markers, including the stress-specific *Malik 1* and *Malik 2* detectors, was developed, enabling early diagnosis of tolerance and shortening the production variety testing cycle. For the first time, a reliable association between the *DRF1, NAC20L,* and *microsatellite* repeat loci and field-specific stress tolerance parameters has been established. Fourteen sequences deposited in *NCBI GenBank* have been integrated into the predictive variety testing protocol, forming a scientific and methodological basis for optimizing regional variety technologies in limited agroecosystems.

Theoretical significance:

Theoretical principles governing winter wheat productivity development under combined drought-salt stress have been refined. The established correlation between field morphophysiological responses and molecular genetic markers provides a scientific basis for predictable agroecological variety stratification. The identified relationships between integrated yield indicators and rapid diagnostics expand the concept of a controlled production process and form a theoretical basis for designing adaptive variety technologies in limited agroecosystems.

Practical significance:

For the agrotechnological practice of Southern Iraq, the winter wheat varieties Dujela, Faris, and Buhuth 22, which maintain stable productivity under combined moisture deficit and soil salinization, have been selected for production implementation. Rapid diagnostics based on SSR-PCR markers (Malik 1, Malik 2) have been integrated into the scheme for early stratification of seeding material, reducing the field evaluation cycle by 30–40%.

Research Methodology and Methods. The theoretical and methodological framework of the work is based on the principles of adaptive agriculture and the concept of a controlled production process, where winter wheat yield formation is viewed as the result of a controlled interaction between genetic potential and limiting environmental factors. The methodological strategy involves integrating field, physiological, and molecular monitoring into the system of variety and technology support for arid regions. Field trials were conducted in southern Iraq using a randomized block design and zonal agronomic standards. Phenology, yield structure, and productivity were recorded in accordance with VIR and the State Commission of the Russian Federation for Variety Testing. Physiological and biochemical screening (water status, pigment complex, antioxidant activity, and osmoprotectant accumulation) and molecular genetic typing (ISSR/SSR-PCR) were used as diagnostic tools for early assessment of adaptive potential and justification of differentiated cultivation practices. Statistical data processing included analysis of variance, correlation and regression modelling, calculation of ecological plasticity and stability coefficients (Finlay–Wilkinson and Eberhart–Russell methods), and genotype clustering. The reliability of the findings was ensured by multiple replicated experiments, the use of certified laboratory protocols, cross-validation of field and laboratory indicators, and the statistical significance of the relationships.

Provisions submitted for defence:

1. Patterns of winter wheat productivity development under conditions of interrelated salinity and drought stress.

2. Adaptive value of winter wheat varieties Dujela, Faris, and Buhuth 22 under conditions of combined drought and salinity, manifested in the stable development of ear structural elements under critical water-salt conditions.

3. Diagnostic value of a complex of SSR markers, including the stress-oriented primers Malik 1 and Malik 2, providing a rapid assessment of the adaptive potential of winter wheat genotypes to limiting abiotic factors.

4. Coordination of quantitative winter wheat yield indicators with qualitative grain parameters (wet gluten content, grain weight, vitreousness) under conditions of interrelated salinity-arid stress.

Degree of reliability.

The research was conducted using well-established and widely recognised scientific methods. Experimental studies and statistical analyses of the obtained data confirmed the validity of the conclusions and recommendations.

Approval of the work's findings. Abstracts and articles derived from this study were presented at several scientific conferences, including the 2025 University of Kufa Conference on “The Role of Scientific Research in Solving Agricultural Issues” in Iraq; the 2025 Al-Muthanna University Conference on “The 1st Scientific Conference of Directing of Scientific Research for Sustainable Development' in Iraq; and the 2024 People’s Friendship University of Russia Conference on “Food Quality and Safety International Conference” in Russia.

Publications derived from the dissertation research findings: 12 research papers were published based on the dissertation findings, including 3 articles in scientific journals indexed in Scopus/WoS, 2 articles in peer-reviewed journals included in the BAK database, 4 additional articles published in another scientific journal and 3 participations in scientific conferences.

Personal contribution of the author. The author formulated the study's goals and objectives, collected and analysed the data, processed and interpreted the results, and prepared research publications.

The structure and content of the dissertation.

The dissertation consists of 215 pages, divided into an introduction, three main chapters, and a conclusion. It includes 44 tables, 46 figures, and 19 appendices. The list of references comprises 212 sources.

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LITERATURE REVIEW

Wheat

1.1.1 The economic importance

Wheat is one of the major agricultural staples and nutritional resources in the globe [12]. Average world production (2017-2021) was roughly 776 million tonnes, according to data from FAO Figure 1.

In terms of strategy, this cereal comes second after sugarcane and maize. In human and animal nutrition it is important because it provides essential proteins and carbohydrates for large populations in many developing nations.

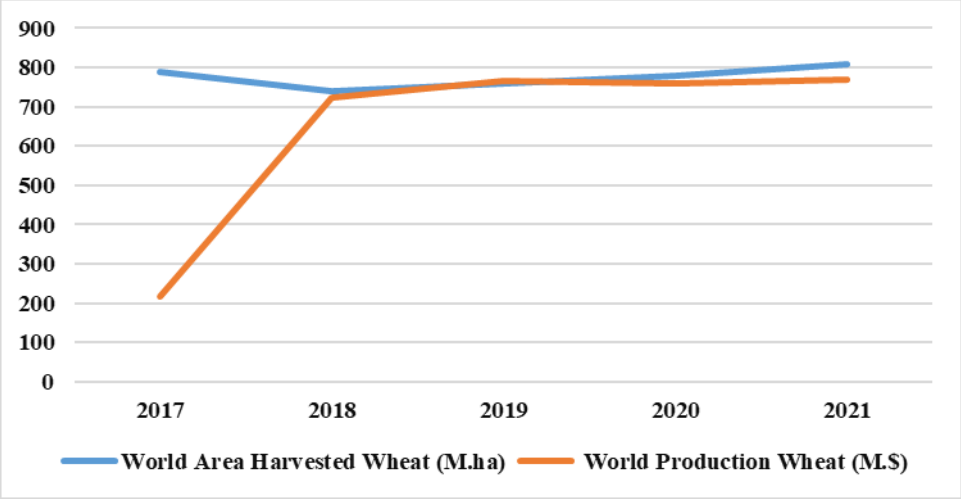


Figure 1.Wheat production for the years (2017-2021).

Other types of wheat, which represent a small part of production, include ancestral forms and durum [13]. Common wheat is prevalent worldwide Figure 2 [14].

Asia's share of global wheat production was substantial between 2017 and 2021. Technological advances such as precision farming and the development of drought-tolerant cultivars have increased productivity. Favourable climatic conditions allow large-scale cultivation. This production is supported by the needs of livestock and by domestic consumption. This means Asia is a key part of the world's wheat supply chains.

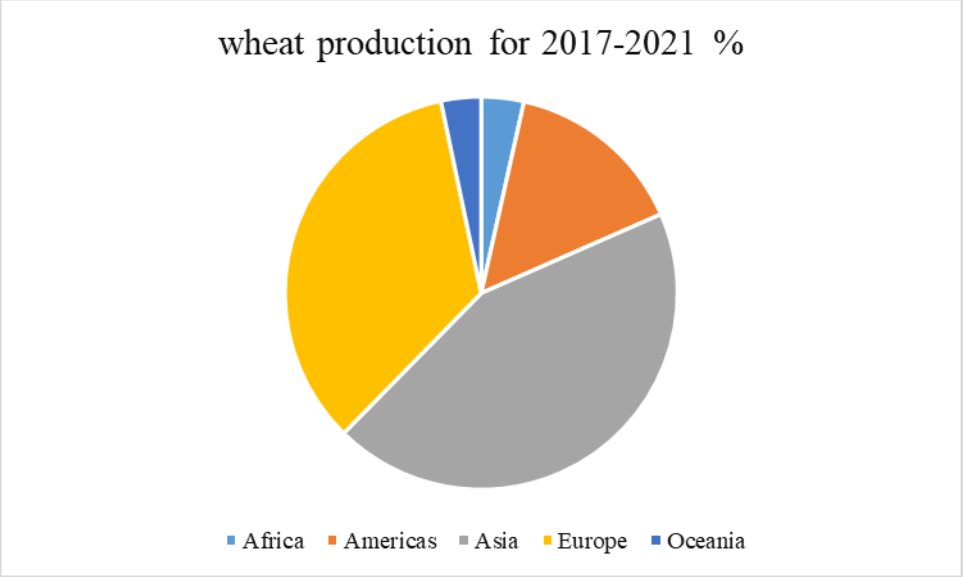


Figure 2. Percentage of wheat production in continents

The population growth exacerbates this phenomenon, because the current production cannot meet the growing demand for nutrients. The demand for wheat is growing steadily, and food supply has become critical [15].

In developing countries consumption growth is expected to continue [16]. Recently Iraq has concentrated on cultivar improvement to meet nutritional requirements, as domestic production is subject to economic and environmental uncertainties [17]. There have been several assessments [18] that wheat will be key to feeding the world in 2050. Genetic improvement has made a greater contribution than improved agricultural practices in increasing crop productivity [19], Breeders and geneticists have been concurrently working on the development of superior cultivars [20] to meet the challenges of food security.

1.1.2 Wheat taxonomy

Wheat and its wild relatives belong to:

Genus: *Triticum L.* ,

Family: *Gramineae* ,

Tribe: *Triticeae.* ,

Family: *Poaceae*,

which includes crops such as: wheat, oats, barley, rye, corn, and rice. Tribe *Triticeae* includes: 300 species that are characterised by: chromosome number (x=7), (2n=14), (2n=28) and (2n=42) [21]. The genus (Triticum) includes six species: *T monococcum L.*(AA); T urartu (AA); *T turgidum L.* (AABB); *T timopheevii*(AAGG); *T aestivum L.*(AABBDD); and *T zhukovskyi*(AAAAGG).

The tetraploid forms of wheats from a hybridisation between *T. urartu* and *Aegilops speltoides* species, resulting in wild emmer wheat *T. turgidum spp. Dicoccum* in Figure 3 [22]. Winter wheat *T. aestivum*(*AABBDD*), originated from a spontaneous hybridization between *T. turgidum ssp.*(*AABB*) and *Aegilops tauschii*(*DD*).

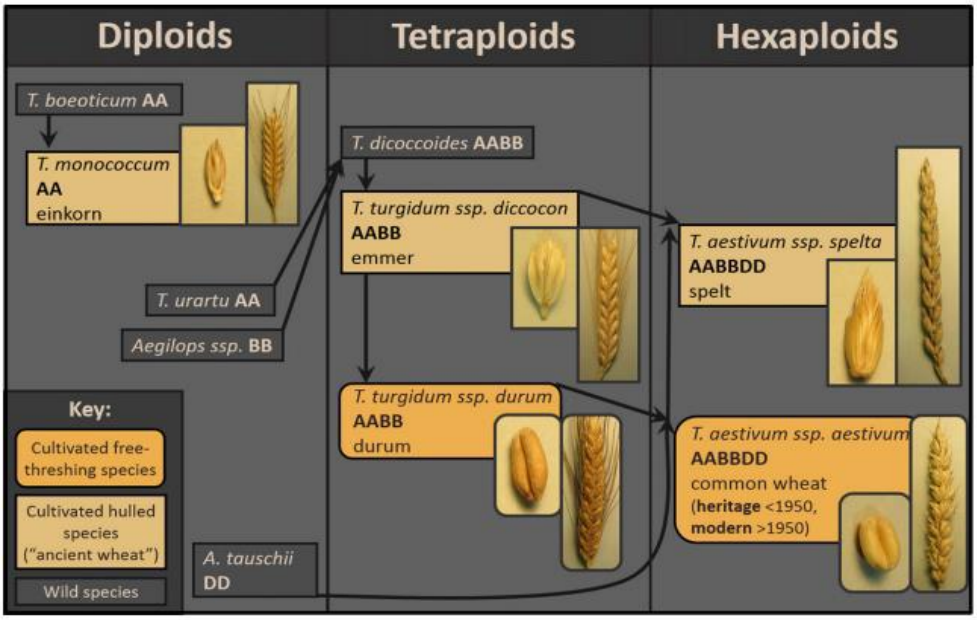


Figure 3. Genealogies of wheat [22].

1.1.3 Wheat genome

Wheat genome has a length (15–17) billion bp and 42 chromosomes. It is a hexaploidy (2n =6x) in (A,B,D genomes), with about 80-90% of repetitive sequences [23]. Wild relatives of wheat have significant genetic diversity [24]. Commercial wheat includes primarily of soft wheat and pasta wheat [21]. About seventy million years ago, wheat, maize, and rice all came from the same origin [25], these crops differ in genome size, wheat has the largest genome of crops, a size about 17gb, with each subgenome about 5.5 gb, about 8 times larger than the maize and about 40 times larger than the rice [26].

1.1.4 Domestication of wheat

The extensive genetic diversity in wheat has enabled breeders to develop cultivars resistant to both biotic and abiotic constraints. Despite this genetic richness, diversity in modern cultivated varieties has been diminished through sustained artificial selection [27]. Consequently, genetic diversity underpins improvement via breeding programmes targeting trait enhancement and elevating yield gains from the

current annual rate of approximately 1% towards the required 2.4% per year (Figure 4).

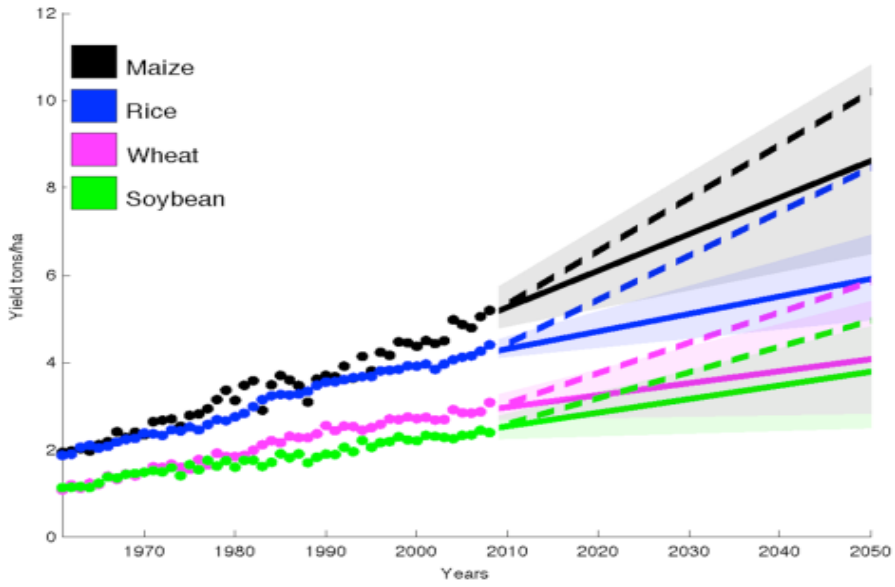


Figure 4. Yield for crop, as described in [27].

Plant Stresses

Ecological disturbances imposed by non-living physical agents and biotic factors curtail physiological functions and developmental trajectories in vegetation, ultimately determining reproductive success and harvestable outputs [28]. Anthropogenic climatic shifts have amplified the probability of agricultural species confronting novel stress combinations, often surpassing previously documented extreme episodes [29]. Although considerable scholarly attention has examined plant reactions to individual stressors—particularly hydration scarcity, ion excess, and thermal variability—the translational applicability of such research for predicting concurrent stress conditions remains inherently constrained [30]. Recent investigations have substantially advanced our comprehension of molecular, biochemical, and organismal responses to simultaneous environmental challenges across evolutionarily diverse angiosperms [30].

Mounting evidence indicates that each stress category elicits a distinctive spectrum of adaptive demands, subsequently triggering specialised metabolic circuits and intercellular signalling cascades in a coordinated fashion. These integrated defensive and restorative strategies encompass adjustments in photosynthetic light acquisition, reinforcement of radical-scavenging machinery, reorganisation of hormonal regulatory frameworks, and re-establishment of moisture equilibrium through osmoprotectant accumulation—all operating synergistically to sustain organellar integrity and biosynthetic continuity under unfavourable edaphic and climatic circumstances [31]. In fact, inanimate ecological stress is a major limiting factor to global farming productivity and has been shown to reduce yields by >50% in susceptible hereditary stocks [28].

Abiotic Factors

Environmental factors are the basic regulators of the physiological functioning of crop species and have a profound effect on growth patterns and developmental sequences. Three major categories of environmental limitations that negatively impact agricultural productivity are temperature extremes (high and low thermal conditions), water availability constraints (including moisture shortages) and soil-related problems (such as irrigation issues and salt accumulation) [28]. Each stressor has characteristic physiological and structural effects on cereal specimens, leading to sophisticated adaptive responses that ultimately determine the success of the harvest. In the following sections of this review, we shall consider each stress factor in detail, describing their functional effects on wheat cropping systems and considering possible amelioration strategies reported in the scientific literature.

1.1.5 Heat stress on plants

High thermal stress is a significant reason for the decrease in cereal productivity in various geographical areas [32]. Above-ambient temperatures of 34°C increased foliar deterioration, directly affecting kernel development and final yield that can be harvested. High temperatures usually cause a 45–60% reduction of the reproductive phase, mainly because the translocation of photosynthates to the developing kernels is reduced, and this affects both quantitative and qualitative yield characteristics [33].

Modelled projections consistently indicate that a 1°C elevation in baseline global temperatures corresponds to estimated yield reductions of 4–10% across major production areas [34,35].

The actual magnitude of thermal injury remains contingent upon multiple interacting variables, including stress period, peak intensities, and synchrony with sensitive developmental windows. Flowering and early kernel development are especially sensitive to supra-optimal temperatures.

1.1.6 The photosynthetic

Robust photosynthetic activity during the flowering phase builds up substantial sink capacity, which in turn supports high grain production [36]. The period when the number of grains is determined is very critical and occurs around 10–15 days before anthesis. To improve productivity, a good understanding of the molecular determinants controlling grain establishment during this period, especially those related to carbohydrate availability and signalling cascades therewith [37] is needed. The main controlling factor for grain and spikelet number is photosynthetically derived carbohydrates. Modern studies [38,39] apply the latest monitoring technologies to study the gas exchange dynamics of metabolically active leaves, as well as to assess photosynthetic performance as a potential way to increase the yield.

1.1.7 The Salts and minerals

Sodium chloride (NaCl) is a water-soluble compound that accumulates in cereal foliage as Na^+ . The accumulation of Na^+ in excess impairs the absorption of essential trace elements, especially K^+ and Ca^{2+}, that are important for normal metabolic functioning [40]. Salt-induced damage. One of the critical determinants is to keep a favourable (K^+/Na^+) balance. A decrease in productivity can be observed when the salinity of soil or irrigation water reaches about (EC=6–8) [41]. In the early stages of soil salinisation, plant growth is restricted by osmotic stress, and ion toxicity causes damage to the plants [42,43]. Approximately a 25% of the world's arable land is under salt stress, and this is expected to increase progressively [44].

Geological salt accumulation accounts for the bulk of the projected one billion hectares of saline-affected terrain, equivalent to roughly 7% of the global landmass. Salt impact extends to approximately one-third of irrigated farmland, corresponding to about 70 million hectares. Future estimates indicate that saline regions will expand by around 1-2 million hectares each year [45].

1.1.8 Drought and soil moisture

Diminished water resources induce drought stress. Drought frequency has escalated globally due to erratic precipitation patterns. By 2040, it is projected that forty per cent of agricultural land will face significant water shortage [46]. Water scarcity during the wheat life cycle significantly hinders optimal crop production. Drought is regarded as one of the most important constraints to global agricultural production. Impact on agricultural productivity is highly variable depending on the stage of crop growth, intensity of the stress and its duration [47,48]. Drought stress can also be combined with high temperatures, soil salinity, high irradiance, wind and biotic stressors, resulting in significant reductions in production [49]. The field capacity suitable for the growth of plants and the microbial respiration in soil is between -0.01 and -0.03 MPa, according to studies [50]. The water content of soil at field capacity is

strongly influenced by soil texture and normally ranges from 10–20% by volume in sandy soils, 25–30% in loamy soils, and 35–45% in clay-dominant soils [51]. Selection of wheat germplasm having high early vigour is beneficial for yield improvement under climate change constraints and for enhancing the input-use efficiency.

1.1.9 Variation in wheat tolerance to salt and drought stress

Research has shown that drought and salt stress negatively affect wheat growth and yield, but their effects are different. Drought stress has generally a more pronounced effect on wheat than salt stress at similar potentials [52]. Water stress causes a huge reduction in plant biomass and grain production [53]. Salinity also reduces these parameters, but generally to a lesser extent [53]. Wheat is more tolerant to salinity than to drought due to the accumulation of higher levels of compatible osmolarities and higher water uptake efficiency [52]. Both stresses reduce chlorophyll and relative water content and increase proline and soluble sugar concentrations [54]. Salt-tolerant wheat cultivars experience less decline in production under stress than salt-sensitive wheat cultivars [54].

Effects of a changing climate on Iraq

Iraq was one of the country's worst hit by atmospheric unpredictability, which continually jeopardises the viability of the farming sector and the welfare of agrarian communities. Sustainable cultivation methodologies have narrow margins given the dwindling potable water resources and increasing aridity episodes. Uncontrolled exploitation of natural resources, large arid areas that characterise the topography of the country and increasing salinisation in the mid-southern areas have intensified the depletion and mismanagement of hydrological resources. Therefore, a cross-institutional strategy is imperative to overcome the interconnected obstacles of terrestrial degradation and edaphic salt infestation with the involvement of multiple interested parties [4].

Iraq has endured an acute water deficit attributable to deficient precipitation regimes, resulting in the involuntary migration of over eight hundred thousand residents [55]. These evolving ecological conditions have exercised detrimental repercussions upon both agronomic and pastoral activities [56]. The estimated deleterious consequences may escalate to seven per cent, potentially compromising the sustainability of life within these territories [57]. Heightened ionic accumulation and diminished substrate water content represent outcomes attributable to planetary thermal alterations; accordingly, ameliorative interventions have become imperative to counteract these detrimental outcomes [58]. Climatological perturbations within Iraqi territory have precipitated the exhaustion of aquatic stores within the southern palustrine ecosystems, culminating in total depopulation of both indigenous fauna and resident human congregations, as illustrated in Figure 5 [59].

Figure 5. Marshes in southern Iraq [59].

Mercurial peaks during summer achieve 50°C, which, in conjunction with heightened evaporative fluxes and inadequate pluvial patterns (depicted in Figure 7, Figure 6) , promote gradual edaphic alkalisation and declining ground humidity levels [60].

Figure 6. Surveying on the surface of the soil.

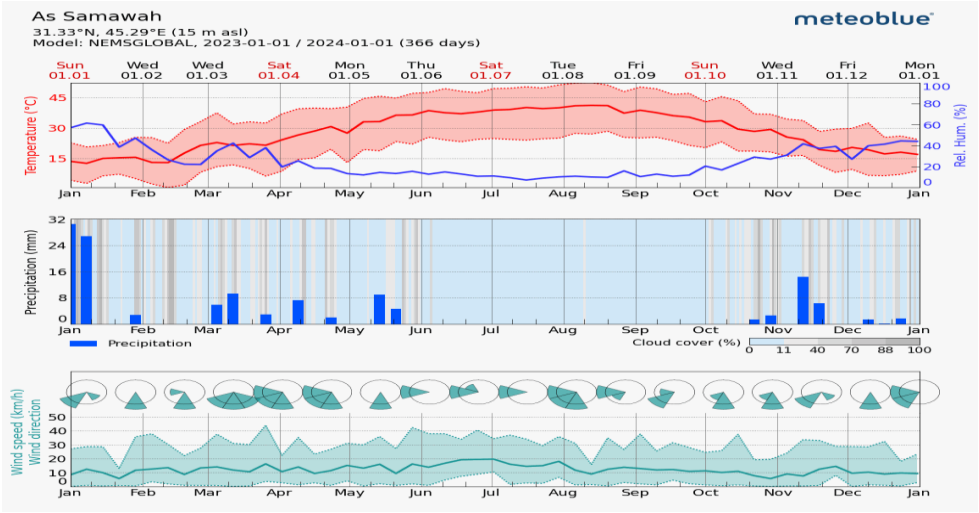


Figure 7. Temperature and rainfall amount in southern Iraq [60].

Reduced upstream hydrological contributions have had serious consequences for farm commodity production and biodiversity along both major waterways. This declining trend is quantitatively substantiated through hydrographic evidence pertaining to fluvial discharge quantities, as presented in Table 1, [61,62].

Table 1. Water yields in Iraq [63,64].

	Pre-1990s	**2011**	**Decrease**	**Yearly decline**	**Forward estimates**
Euphrates	$1006m^3.sec^{-1}$ ($29km^3.y^{-1}$)	$627m^3.sec^{-1}$ ($4.4km^3.y^{-1}$)	90	$0.245km^3.y^{-1}$	$290m^3.sec^{-1}$
Tigris	$677m^3.sec^{-1}$ ($20.9km^3.y^{-1}$)	$526m^3.sec^{-1}$ ($9.7\ km^3.y^{-1}$)	57	$0.1335km^3.y^{-1}$	$301m^3.sec^{-1}$
Total	$1683m^3.sec^{-1}$ ($49.9km^3.y^{-1}$	$1153m^3.sec^{-1}$ ($14.1km^3.y^{-1}$)	147	$0.378km^3.y^{-1}$	$591m^3.sec^{-1}$

Grain outputs continue to be lower because of the inconsistent hydrological provision and the lower standards for cultivation [2,8]. Crop productivity is greatly constrained by the high salinity of agricultural lands. The construction of impoundment structures in the upstream reaches of both primary waterways has reduced hydrological inflow to the downstream, resulting in the recession of marshy environments and aquatic systems and the development of conditions favourable to windborne particulate events. This is especially true across the central southern governorates, where the water table has risen due to outdated water transmission systems and diminishing wastewater disposal mechanisms. Consequently, cultivable terrain productivity persistently degrades due to incremental accretions of salt residues [65].

Causes of salinization and drought in southern Iraq

The main causes

Precipitation amounts and the depletion of the atmospheric moisture budget are natural determinants of significant influence on the processes of terrestrial salinisation and aridification. Southern Iraq has the following unique climatological characteristics that make it especially susceptible to the accumulation of edaphic salt: very high vapour losses and low rainfall [4].

Evaporation and heat-Higher evaporative demands and the region's topography have led to higher saline concentrations in both the agricultural soils and irrigation water supplies, particularly in the central and southern governorates [8,9]. Climatological forecasts foresee increasing thermal averages, with reduced pluvial precipitation, conditions that will probably worsen freshwater scarcity and accelerate desertification phenomena [66].

Scarce precipitation. The inadequate rainfall regimes have led to the inadequate percolation of soluble salts through the pedological profile and their progressive concentration towards the surface horizon during periods of water deficit [67]. Annual precipitation totals are characteristically low with strong spatial heterogeneity between the relatively humid north-eastern highlands and the considerably more xeric southern lands. The main rainy season is from Dec to Feb, during which most of the annual rainfall is received, but there is considerable interannual variability. Maximum evaporative losses occur in the summer months, when increased solar irradiance incident on the Earth's surface accelerates desiccation of the substrates and enhances salinisation.

Underground water level. The groundwater table is generally found to be in the range of approximately 1.5–2 m below land surface (Figure 1) in the central parts of the country area with corresponding saline levels of 8–12 EC=(dS/m). The southern provinces, by contrast, have shallower groundwater depths (1–2 m) but considerably higher ionic content (>30 EC). At least partially, the salt accumulation within overlying pedological strata is attributable to the pronounced mineralisation of the underlying aquifer systems [68]. These hydrogeological phenomena are mainly characteristic of the alluvial lowlands, but beyond this sedimentary plain, groundwater resources are found at greater depths or with reduced salinity, with a substantially different hydrogeological configuration [4].

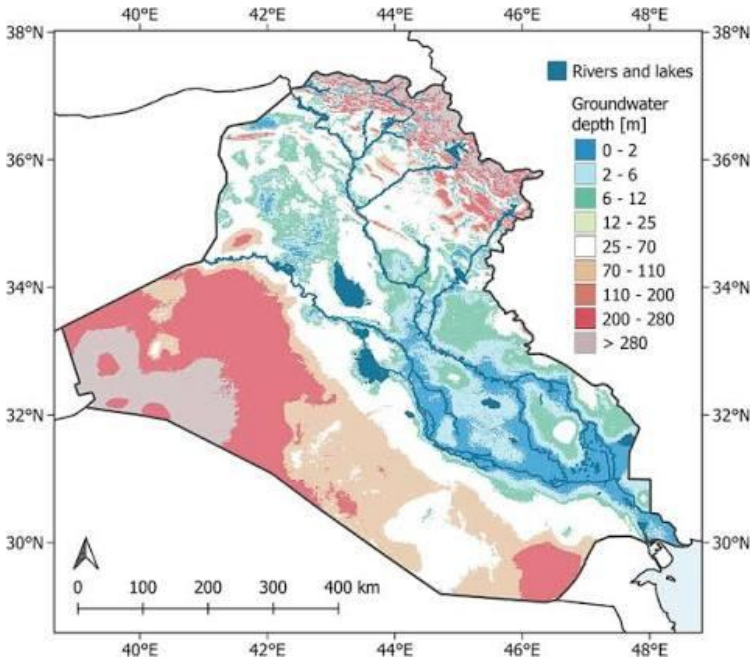


Figure 8. Subsurface water depth in Iraq [69]

Accordingly, the utilisation potential of groundwater resources may be ascertained through their saline content, as delineated in Table 2 [69].

Table 2. Utilisation of subsurface water.

Category	**Application**	**Salt concentration . g.L^{-1}**
1st	Potable water	< 1
2nd	Crop irrigation	From 1 to 3
3rd	Irrigation - limited	From 3 to 5
4th	Irrigation – more limited	From 5 to 10
5th	Subsurface water (unsuitable for utilisation)	From 10 to 20
6th	Salty	> 50

In the northern sector, the groundwater salinity is about 8-10 g/L in the upper sedimentary plain, then it increases gradually towards the southern latitudes and reaches about 20-25 g/L in the vicinity south of the central metropolis and north of the mid-southern urban centres, where some underground conduits are already unsuitable

for use. After that, salinity concentrations keep trending upwards through the southern areas, reaching above 50 g/L in some localities [70].

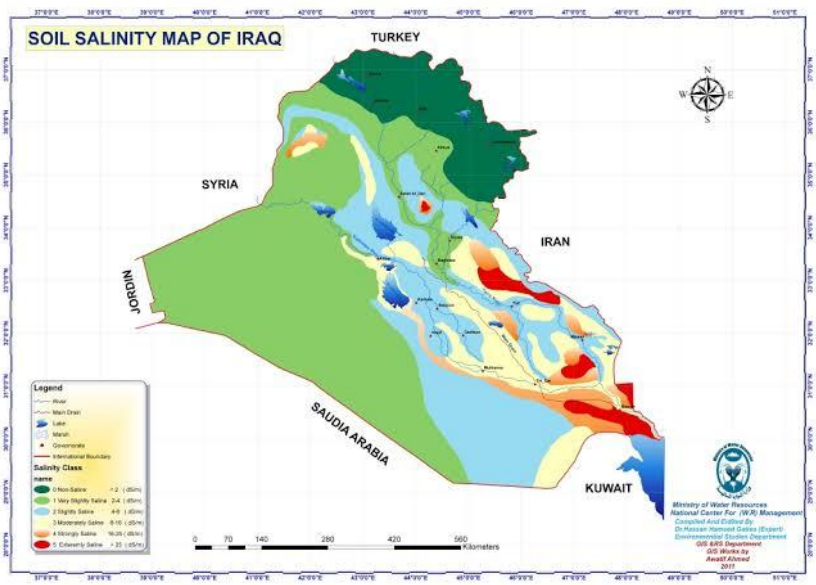


Figure 9. Subsurface salinity in Iraq [69]

The saline content of ground water within the western desert expanses varies between 1-3g/L which is permissible for irrigation purposes. The fresh ground water channels with salt content less than 1g/L are present within the western depression zones. The southern desert is more saline than the western desert: 3–5g/L in the western desert and more in the sedimentary plain depression . Groundwater in the northern highlands is potable freshwater, usually less than 1g/L. Saline concentrations within limits for irrigation water, usually less than 3g/L, are found in some areas in the uplands and large parts of the lower hill country, especially the eastern slopes (Figure 9) [70].

Features of agricultural water

In 2017, an assessment was conducted to determine the hydrological footprint of cereal cultivation in a number of administrative governorates in Iraq using crop water requirements algorithms integrated into specialised computer modelling platforms [71]. The aggregate water consumption attributable to grain production

amounted to 1,9 cubic metres per metric tonne. Provincial analysis revealed that the northern governorate exhibited the most substantial water footprint, followed in decreasing magnitude by Samawa Province, the western territories, and the south-eastern provinces. Fluvial water quality within the study area is governed by an interplay of both external and internal determinants, which may be categorized as either controllable or uncontrollable according to their etiological characteristics and source mechanisms [72].

Uncontrollable factors are represented by changes in climatological patterns and their associated impacts, e.g., reduced precipitation regimes and increased thermal conditions. These climate anomalies have exacerbated water scarcity in the region, threatening the sustainability of agriculture and domestic water security [73]. Quantitative projections indicate that total water demands will rise to about 72.1km^3 per annum by 2020 and available supplies are projected to fall to about 63.1 km^3 per annum , leaving a volumetric deficit of 8.6 km^3 [62].

Increasingly large gaps between demand and supply indicate increasingly severe limitations on irrigated agriculture. This has special relevance for cereal-producing regions which are heavily dependent on surface water allocations. Furthermore, the deteriorating quality of available water resources compounds the quantitative deficits, as elevated salinity levels and contamination from various sources progressively reduce the suitability of remaining supplies for cultivation purposes. Falling flow quantity and declining quality constitute a dual threat for agricultural productivity. Integrated water resource management approaches are needed that address both quantity and quality issues simultaneously.

Impact on Agricultural Productivity in Iraq

Iraq is currently experiencing a severe rise in temperature beyond previously recorded extremes and a rainfall deficit not seen in the last 40 years [74]. These combined climatic anomalies have seriously affected the production of the main cereal

crops, with the yield reductions of the main grains, especially wheat and barley, being between 50 and 70% [56].

Simultaneously, frequent droughts over the past few decades have accelerated landscape degradation, intensified desertification processes and compromising soil stability throughout large arable zones. Furthermore, hydraulic infrastructure projects developed by upstream riparian nations have significantly reduced transboundary river flows to downstream agricultural regions, severely limiting the availability of irrigation and threatening the sustainability of large-scale agricultural enterprises [56,74].

Mitigation measures

1.1.10 Breeding for Stress-Tolerant Varieties

Genetic engineering for salt tolerance improvement is a viable solution for the anticipated rise in rhizosphere salinity [75]. This approach is substantiated by proven examples of successful application of tolerant genotypes as the base of salinity management programmes [76]. Genetic selection and breeding programmes still constitute important strategies for improving agronomic performance [4]. The detection of genotypes with high resistance to biotic and abiotic stresses is necessary to maintain agriculture under harsh environmental conditions.

1.1.11 Improved Watering Techniques

On-farm water distribution systems must be improved due to the detrimental effects of climate volatility on soil alkalisation and desiccation. The key interventions are subsurface drainage networks for improved irrigation infrastructure and to enable the removal of excess moisture from the soil profile. These techniques allow leaching the salt below the root zone, thus improving productivity and ionic regulation, while balancing crop hydration needs, applied water quantities and existing groundwater

levels [77]. Moreover, it is recommended to adopt sophisticated water supply systems, drainage channels for wastewater, and techniques for capturing precipitation to prevent the accumulation of salt in arable soils [4].

The Effect of Genotype and Irrigation Regimes on Wheat Yield

Field studies in the area showed that irrigation timing, which is based on soil moisture extraction thresholds, water retention properties or phenological stage, strongly influences crop water productivity in cereal production [78].

When the depletion was 40% (435-466 mm) water was added and the productivity of cereal was 1.85 kg/m3. However, at 70% depletion (365-385 mm) productivity was significantly reduced to 1.01 kg/m3. Full irrigation at 100% field capacity produced harvestable outputs of 3.78–3.87 t ha^{-1}, with water use efficiency ranging from 5.40 to 5.77 kg m^{-3}. Supplementary irrigation during key growth stages achieved notably higher efficiency, approaching 15 kg/m^3. Genotypic variation in moisture utilisation was evident, with the accession Mawaddah performing better under 40% depletion, whilst Babel113 exhibited reduced efficiency at 70% depletion [78]. Further assessment under four depletion levels (25%, 50%, 75% and non-stressed control) revealed that accession Buhuth was superior to other genotypes such as N29, N12, Aba99, N14 and N28 [79]. Taken together, these results suggest that both the inherent genetic variation among the accessions and the local edaphic and climatic components significantly affect the irrigation responsiveness and overall water productivity.

Morphological indicators of wheat under abiotic stress

1.1.12 Salinity and drought stress on plant height trait

Structural and productivity parameters are negatively influenced by saline and hydric pressures [80,81]. Several studies have shown that severe moisture deficit conditions and sodium concentrations (60–75 mM NaCl) significantly inhibited ear elongation (17–20%) and vertical growth (16–35%), mainly due to osmotic stress, ionic imbalance and disturbed cell proliferation [81]. Significant genetic variation with resistant genetic lines displaying superior functionality through varied manifestation of pressure-responsive genetic elements (TaDREB1A, TaLEA3) is well documented in academic literature. Recent studies have found quantitative trait loci associated with pressure resilience on chromosomes 1A, 1B, and 2A that could be useful targets for marker-assisted selection [82]. As a result, an integrated approach that combines physiological evaluation and genomic technologies is currently used to produce climate-resistant cereal cultivars for sustainable production under less-than-ideal circumstances.

1.1.13 Salinity and drought stress on flag leaf area trait

The uppermost layer of the canopy is important for carbon assimilation in cereal crops, as it is the main source of photosynthates for kernel development. The upper leaf surface is reduced by the saline and hydric pressures, and the assimilatory potential is limited. The stress due to deficiency of moisture in the growing season also decreases leaf expansion, eventually influencing the total crop productivity [83].

In bread wheat, traits such as foliage pigmentation, epicuticular coating and foliar inclination are beneficial as they reduce vapour loss and lower the thermal conditions on the upper surface, thus improving plant resilience under adverse environmental conditions. In one study, the effect of epicuticular wax on the physiological parameters of some accessions of bread wheat was investigated, and the

presence of significant genotypic variation in wax deposition patterns was recorded [84].

1.1.14 Salinity and drought stress on the plant of tillers trait

Salinity and water stress have a significant effect on the tillering and the overall productivity of cereal crops. Both stressors decrease the population of initial and subsequent shoots and the number of fruitful culms [85]. Number of lateral branches is an important determinant of grain crop yield. Resistant wheat accessions show lower reductions in shoot number and seed yield compared to susceptible varieties under stressful environments [85]. In genetic lines that are sensitive to the effects of salt, removal of axillary buds can increase salt resistance. This could be due to decreased competition for photosynthates [86].

1.1.15 Salinity and drought stress on spike length trait

Saline and hydric pressures exert negative effects on cereal development and production by decreasing P.H , ear length, and kernel number per ear [87]. Research shows that these stresses could lead to ears that are shorter and narrower, with fewer kernels, thus reducing yield. Cereal varieties respond differentially in ear architecture to moisture deficit, and in certain environments late-maturing accessions perform better than early-maturing types in dry conditions, challenging the traditional “aridity avoidance” approach [88]. The ability of a specimen to compensate for agricultural losses caused by strain is mainly controlled by two factors: the timing and duration of the exposure to moisture deficits [88]. These observations together illustrate the complex interactions between environmental pressures and crop developmental characteristics.

1.1.16 Salinity and drought stress on the grains in spike trait

Both saline and hydric conditions have diminished kernel numbers within cereal ears. Such stresses have been shown by research to upset reproductive development in

bread wheat, causing a decrease in ear fertility and hence seed set. Agriculture losses are from lack of moisture during flowering and kernel maturation. Stress interferes with meiosis in floral reproductive structures, resulting in nonviable male gametes or non-productive flowers, and thus fewer kernels and an increased overall harvest loss [89].

1.1.17 Salinity and drought stress on grain weight trait

Kernel mass reduction in bread wheat under salinity and water stresses. These strains appear to reduce kernel weight mainly because of impaired mineral acquisition and reduced carbon assimilation, directly affecting the quality and quantity of the harvested produce. Moisture deficit generally has a more detrimental impact on relative water content than salt stress, and bread wheat is more tolerant to salinity than to aridity through increased compatible solute accumulation and less lipid peroxidation [52].

1.1.18 Salinity and drought stress on the 1000-grain weight trait

According to previous literature, these strains can limit moisture and mineral availability needed for kernel development, leading to reduced and less dense grains [85,90]. Under adverse environments, the reduction of yield parameters in resistant wheat accessions is lesser than that of susceptible varieties [54]. Autumn-planted wheat varieties are often more salt tolerant than spring-planted varieties, and durum wheat is often more resilient than the standard bread wheat [90]. Reduced thousand-kernel mass has been reported under saline irrigation regimes [91,92].

1.1.19 Salinity and drought stress on the yield trait

Study Studies on bread wheat have shown that saline and hydric stresses have a significant impact on its development, functioning and productivity. Salt and moisture stress reduce the pigment content, potassium concentration and yield parameters; however, resistant varieties are less affected than susceptible ones [85]. Moisture

deficit causes a reduction in phenological duration, such as days to flowering, anthesis, maturity and productivity attributes such as harvestable yield and organic matter per unit area [93]. High-throughput phenotyping platforms have been shown to reliably predict biomass differences between cultivars in different stress conditions, providing useful tools for breeding programmes aimed at improving stress tolerance [82].

1.1.20 Salinity and drought stress on biomass trait

Wheat genotypes differ in their resistance to non-living stressors, and there is a large variation in organic matter accumulation and seed yield under stress [94]. The relationship between productivity and soil salt concentration is almost inversely proportional and usually [95]. A detailed analysis showed that cereals suffer an average productivity loss of 27.5% due to moisture deficit, with the impacts varying between development stages, but cereals generally suffer similar proportional yield losses across the growth cycle [81]. The amount of organic matter during the beginning of vegetative stages is a promising trait to enhance the aridity resilience of cultivars [96]. The extent of productivity reduction depends upon both genetic constitution and the developmental stage subjected to strain [97]. Both salt and moisture stress decrease organic matter build-up and plant stature in broadly comparable fashion [98]. The combined influence of salinity and aridity can produce additional decreases in organic matter and kernel productivity in bread wheat [82].

Salinity and drought stress on grain content and quality

1.1.21 Salinity and drought stress on grain moisture content

Salinity stress impacts on wheat grain moisture content and bread-making quality parameters. In wheat genotypes, grain moisture is generally decreased and protein content is increased under saline conditions [91,99]. Both salt and water stress affected the moisture content of the grains, but the effect differed with stage and variety

[91]. Other results showed that water stress improved several quality parameters, with a decrease in quantity of grains and their moisture content.

1.1.22 Salinity and drought stress on protein content in grains

Several studies indicated that salinity increased wheat grains' protein content [91,92]. The effect of salinity on gluten content and SDS is consistent, and these are important parameters in the assessment of bread quality. On the other hand, salinity stress often decreases other quality parameters like glutenin, fat and fibre content. The accumulation of salt was found to increase the protein content in different varieties of wheat. The stabilisation of nitrogen metabolism resulted in an increase in protein concentration. [100]. Water stress strongly affects bread-making quality and protein content of wheat, but the relationship is complex. Drought stress led to increased grain protein content but reduces loaf size and grain yield [101].

1.1.23 Starch content in grains affected by salinity and drought stress

Salt treatment reduces photosynthetic ability, which in turn reduces starch synthesis and accumulation in wheat grains, according to a number of studies [90,100]. Increased groundwater salinity levels lower bread wheat starch content to 61.9% to 67.8%, according to [99]. Among wheat types, winter wheat exhibits greater salt tolerance than spring wheat, and durum wheat outperforms common bread wheat [100]. Water stress significantly influences starch quantity and bread quality in wheat grains, including the intricate interplay between physiological responses and grain composition. Severe water deficit (25-50% water holding capacity) reduces grain yield, flag leaf area, and chlorophyll content and accelerates senescence [102]. Mild water deficit during grain filling, however, can modify starch composition and improve bread-making characteristics, though typically at reduced total yield.

1.1.24 Gluten content in grains affected by salinity and drought stress

Multiple field studies show that gluten content typically increases under stress conditions. [92] observed notable increases in both wet and dry gluten content in durum wheat subjected to combined salt and drought stress. However, gluten quality revealed variable reactions. [91] observed reduced glutenin levels under salt stress. [101] observed that when the amount of gluten increased, the gliadin/glutenin ratio similarly rose. This increase might possibly contribute to a decline in baking quality. The rise in protein is associated with higher gluten content, gluten index, and sedimentation values, while concurrently showing decreased grain moisture content and thousand kernel weight [101].

Physiological indicators of wheat under salinity and drought stress

1.1.25 Salinity and drought stress on the activity of enzymes antioxidants in wheat

Reactive superoxide radicals are converted to hydrogen peroxide (H_2O_2) or other less harmful products by free-radical scavenging systems, which are necessary for this purpose. The peroxidative damage caused by reactive oxygen species (ROS) such as H_2O_2, O_2 and OH disturbs the intracellular oxidation-reduction equilibrium, resulting in tissue damage and organism death [103]. To protect from peroxidative injury, plant tissues have an elaborate protective quenching apparatus that reduces reactive oxygen species by different catalytic proteins such as guaiacol peroxidase (POD), superoxide dismutase (SOD) and catalase (CAT). These catalytic proteins are endogenous protective mechanisms against stressors and ecological and organic agents, and the responses and metrics of these mechanisms can be used to quantify the magnitude of injury. A wide variability in the quenching capacity has been reported among the cereal genetic lines, and therefore, the selection of accessions with an improved protective potential is essential to alleviate the peroxidative pressure [104].

1.1.26 Salinity and drought stress on the activity of non-enzymatic antioxidants in wheat

1.1.26.1 Salinity and drought stress on proline content in wheat

Plant tissues harbour diverse non-proteinaceous quenching agents that contribute to preventing injury induced by reactive oxygen species; these substances transform aggressive radicals, including singlet oxygen, hydroxyl radicals, hydrogen peroxide and other activated molecules, into less detrimental derivatives. Proline represents one such non-proteinaceous protective compound that shields vegetation from hydration deficit by functioning as an osmotic modulator and facilitating the preservation of biomembrane and catalytic protein integrity under strain [105]. Salt and hydration deficits represent primary non-living agents that elevate reactive oxygen species activity, inducing peroxidative injury in cereal specimens [106]. Both stressors lead to increased synthesis of protective substances, such as proline and soluble carbohydrates, for osmotic adjustment [107]. Plants recover from injury by osmotic regulation and accumulation of compatible solutes such as proline to maintain osmotic balance within cells [108]. Some of the different protective strategies employed by cereal species against abiotic stress are leaf rolling, increased epicuticular deposition, and synthesis of protective polypeptides and proline [109].

1.1.26.2 Salinity and drought stress on chlorophyll content

Pigment content is a measure of the health of the plant. In general, the flag leaf of cereal crops shows lower pigment concentrations in conditions of salt or water increase. Typically, chlorophyll a decreases, whereas chlorophyll b and carotenoids may increase in an adaptive response [52]. This reduction in efficiency of photosynthesis, which is vital to growth and yield, high salt concentrations have been found to dramatically reduce the content of chloroplast pigments, resulting in lower rates of photosynthesis and significant yield losses [110]. Portable chlorophyll meters provide readings correlating well with true chlorophyll and carotenoid content even

under stress conditions and are therefore useful for non-destructive monitoring [111]. Stress-tolerant genotypes usually have better stomatal conductance, chlorophyll fluorescence and pigment indices compared to stress-susceptible lines [112].

1.1.26.3 Salinity and drought stress on Relative Water Content

Saline and hydration deficits decrease the relative water content and integrity of biomembranes and increase the accumulation of lipid peroxides in cereal foliage [52]. Salt stress generally decreases the relative water content of leaves, and salt-tolerant cultivars tend to have a higher relative water content than salt-susceptible cultivars. Salt alone causes a reduction in relative water content in leaves of cereals with considerable variation in cultivar resilience to salt [113]. The relative water content of cereal leaves under hydration deficit was considerably reduced but to different degrees in cultivars. The relative water content decreases with the degree of the hydration deficit, with an acute deficit causing greater losses. Drought tolerant cultivars have higher relative leaf water content than susceptible types. Reduction in relative water content is generally accompanied by reduction in pigment content and changes in mineral composition, particularly lower potassium and calcium levels [114].

Biochemical indicators of wheat under salinity and drought stress

1.1.27 Salinity and drought stress on sodium and potassium ion exchange

Development and function of cereal crops under saline and hydration deficits the present investigation was carried out to study the effect of water and salt stress on wheat plants through physiological and biochemical parameters. High levels of sodium and chloride ions in plant tissues may inhibit the uptake of vital nutrients from the soil and interfere with plant metabolism. In salt-affected cereal varieties, the uptake of sodium and chloride increased while the absorption of potassium, calcium and zinc decreased [110]. Salt-tolerant cereal varieties have better ion regulation by limiting the accumulation of sodium and maintaining higher potassium concentrations than salt-

sensitive varieties. One of the key cellular mechanisms for plants to adapt to saline environments is to restrict sodium intake and maintain a favourable sodium/potassium ratio [115].

1.1.28 Salinity and drought stress on Nitrogen (N) ion exchange

The deficit of hydration causes a decrease in the accumulation and activity of organic matter and nitrate reductase and a decrease in the contents of N and K in plants [103]. Hydration deficit, which causes lower substrate moisture and reduced root systems, limits nutrient acquisition by decreasing the uptake and transport of micronutrients (nitrogen, phosphorus, and potassium) in plants. Water limitations with low nitrogen availability adversely affect the relative water content, pigment percentage, and the activity of carbon assimilation, thereby limiting cereal productivity [116]. Lack of irrigation causes changes in the ionic balance of plants, reducing the presence, uptake and transport of nutrients within the plant. Therefore, a suitable macro- and micronutrient status may be a promising criterion for the selection of cultivars that are resilient and adapted to deficit-irrigation conditions [103,115].

Molecular parameters and markers contributing to tolerance to abiotic stress in wheat

Hexaploidy wheat is one of the main cereal commodities worldwide, and its productivity is severely affected by water shortage and soil salinization [117,118]. Such extreme climatic conditions cause a variety of complex changes in vegetation at structural, functional, biochemical and hereditary levels [119]. The genetic basis of drought tolerance in hexaploidy wheat is very complex because it is controlled by many quantitative trait loci, which makes traditional breeding methods for specific improvement very difficult [118]. For non-living stress signalling, vegetation needs a set of genes with specialised functions that include genes that encode transcriptional modulators of DREB class, glutamine synthetase proteins and vacuolar Na + /H + antiporters [120]. Improved acclimation to highly saline and moisture-restricted

environments has been associated with increased transcriptional activation of several candidate genes such as TaGS1, TaGS2 and TaDREB2B [120]. Furthermore, studies of heredity have revealed single nucleotide polymorphisms in loci associated with salt sensitivity, such as allelic forms of NRAMP-2 and OPAQUE1, with differential patterns of expression in stress-resilient and stress-susceptible genetic lines [121]. Collectively, these observations provide promising hereditary targets for developing salt-resilient wheat genotypes. Modern genomic methodologies, such as quantitative trait locus mapping and transcriptional profiling, can help in the systematic identification of genetic resources with desirable stress responses, and a thorough understanding of these mechanistic frameworks are necessary prerequisites for successful cultivar development [117,119].

1.1.29 Molecular genetic markers

Hereditary molecular markers represent one of the most accurate instruments employed in plant molecular genetics, delivering highly informative data concerning genetic variation [122]. Most marker platforms depend upon in vitro amplification of nuclear DNA via polymerase chain reaction, facilitating the detection of sequence variations within particular genomic regions as differentially sized amplicons, contingent upon the marker category employed. These markers can reveal distinct hereditary differences among specimens that display similar external characteristics yet differ genetically. The association between molecular markers and other hereditary characteristics renders them potent instruments for characterising diverse biological materials and for diagnosing and managing plant genetic resources. Generally, molecular markers are linked to particular genomic locations that can be identified by specific hybridisation probes or oligonucleotide primers. They can be used for detecting chromosomal locations that are linked to specific characteristics. Nucleic acid sequences are normally shown with 3' and 5' ends, but the markers may not be at the end of the chromosome [123].

1.1.29.1 DNA markers

DNA markers are short nucleotide sequences located at specific chromosomal sites and are required for the assessment of genetic and molecular diversity in plant species. They detect genomic variations due to structural rearrangements such as deletions, duplications, inversions or insertions. DNA markers, in contrast to morphological markers, do not directly influence phenotypic traits but are usually found close to genes that control those traits. These molecular tools exhibit a dominant or co-dominant inheritance and offer many advantages over traditional markers. Major categories of DNA markers are SNPs, SCARs and SSRs that have been applied extensively in pedigree analysis, quantification of genetic diversity and construction of high resolution linkage maps [124].

Technological progress in DNA marker systems has significantly advanced genetic mapping and genomic research. The introduction of PCR-based markers has revolutionised the field, allowing for significant improvements in time and cost efficiency over previous hybridisation techniques. These markers allow fast and accurate genotyping using primers designed to the regions of interest [125]. RFLPs, RAPDs, STSs, AFLPs, SSRs (microsatellites) and SNPs are common types of DNA markers. The advantages and disadvantages of these are summarized in Table 3.

Table 3. Features of molecular markers [126]

Features	RFLP	RAPD	AFLP	SSR	SNP
Genomic frequency	H			M to H	VH
Genomic representation	low-copy sequences	Entire genome			
Genetic behaviour	Co-dominant	Dominant	(Dominant&co-dominant)	Co-dominant	
Locus density	S(<1000s)		M(1000s)	H(10000s)	VH(>100000)
Cloning	Y	N		Y	
PCR dependency	N	Y			
Repeatability	H	L	H		
DNA quantity (µg)	H(5-50)	S(0.01-0.1)	M(0.5-1)	S(0.05-0.12)	
Screening efficiency	L		H		
Economic feasibility	M to H	L	M	M to H	H
Discriminatory power	L	M			M
Completion time	H	L	M	L	
Allelic richness	1-3	1.5-5	20	1-3	1
Main usage field	Genetic	Diversity	(Diversity&genetic)		

Note: Small(S), Moderate(M), High(H), Very High(VH), Low(L), Yes(Y), No(N)

1.1.30 Molecular PCR Techniques

The polymerase chain reaction (PCR), as outlined in [127], enables the in vitro multiplication of targeted DNA segments through molecular markers, yielding distinct amplicons suitable for subsequent examination.

1.1.30.1 Simple Sequence Repeat Marker (SSR)

Microsatellite markers, or SSRs, or STRs, are extensively applied in botanical genetics [128]. SSRs consist of repeats of 1–6 nucleotide units in nuclear genomes, with polymorphism due to copy number variation at specific chromosomal locations [129]. These markers occur in transcribed and non-transcribed regions as well as in organellar genomes. SSR analysis demands minimal template DNA and employs site-specific oligonucleotide pairs for target amplification. Amplicon sizes differ between samples due to repeat number, leading to multi-allelic signatures at particular sites. SSR applications are widely used in many cultivated species for characterisation, mapping, genomics, systematics, and evolution [130,131]. SSRs are co-dominant, highly variable, and informative. However, primer synthesis is expensive and needs flanking information [132]. SSR repeat regions are highly mutable, but flanking sequences are generally conserved, facilitating robust amplification in individuals and across populations. SSR are classified as perfect, imperfect, and compound repeats [132]. These markers have been useful to identify loci involved in adaptation. Diversity is observed in the cereal varieties which enables selection and correlation [133],[134],[135],[136].

1.1.30.2 Inter Simple Sequence Repeat (ISSR) Marker

ISSR markers are based on microsatellite techniques using oligonucleotides attached to the ends that amplify the interspersed regions or flanking regions. This leads to genome-wide coverage, a large number of amplicons and high variability. These markers prove valuable for investigating plant genotyping [137,138]. ISSRs are dominant, economical, thermostable under elevated temperatures, require micro-sampling, are facile, and provide genome-wide representation [139]. They do not require pre-knowledge and can be visualised on electrophoretic media. ISSRs effectively enable discrimination and trace phylogenetics among cereal genotypes [140]. The ISSR-clustering was effective in subdividing genotypes based on

relatedness and stratification [141,142]. ISSRs are reproducible bands that help in allele-mining and parentage for varietal development under diverse adaptability [143,144].

1.1.31 Preparing the Primers

For genetic diversity studies across plant populations, (ISSR) primers offer greater versatility than (SSR) primers because ISSR can be applied across a wider range of plant phylogenetic diversity. They are also relatively easy to develop, cost-effective, and highly informative for assessing genetic polymorphism within and between species [145–149].

1.1.32 Importance of Molecular Markers

Molecular markers are an important part of plant genomics and are indispensable tools in the measurement of genetic variation, population structure and phylogenetic relationships among plant taxa. These markers can be used to detect new genotypes, monitor genomic changes, and improve plant conservation and management strategies [150]. The advent of next-generation sequencing methods has been followed by a wider use of genetic markers for the assessment of genomic diversity, linkage map construction and crop improvement. These advanced resources help to identify ancestral relatives of domesticated species that contain beneficial alleles for resistance to pathogens and tolerance to environmental stresses, thus accelerating selection programmes towards the development of climate-adaptive varieties while increasing the overall efficiency of plant improvement.

1.1.33 Genetic fingerprinting of wheat genotypes

Genetic fingerprinting of wheat genotypes using molecular markers has been widely employed to assess relationships among varieties and landraces, as well as genetic variation and diversity analysis in wheat. Various marker systems have been utilised, including SSR, AFLP [151], and ISSR [152]. These markers were efficient in

discriminating wheat genotypes and estimating genetic diversity. Studies with polymorphism rates from 70% to 84.8% [152,153] have shown that there are large degrees of polymorphism between wheat varieties. The genetic similarity between varieties ranged from 47 to 94% [152].

1.1.34 Quantitative Traits Loci (QTLs), genetic and environmental factors

The quantitative traits of wheat, such as grain yield and quality, result from interactions between genetic and environmental factors. Many QTLs for yield traits are located on wheat chromosomes, some of them in specific regions. Both additive and epistatic effects contribute to trait variation, with additive effects generally being more important [154]. Environmental factors like temperature, precipitation and soil properties have major effects on wheat quality traits and often compete with genetic effects in magnitude. The relative importance and the extent of influence of genetic and environmental factors vary according to the trait and the extent of the study [155]. Breeding efforts have focused on the incorporation of yield-enhancing morpho-physiological traits to improve grain yield potential and stress resilience [156]. Genetic factors controlling quantitative traits in wheat have been identified by cytogenetic methods such as monosomic analysis and chromosome substitution [157].

MATERIALS AND METHODS

Study Scope and boundaries

These themes, places and time periods acted as boundary conditions for the scientific research in an effort to get accurate results and results that applied to the environmental and genetic situation that was wanted:

Geographical and Temporal Delimitations - The experiment was carried out in a farm field in the southern part of Iraq (31.351830983330583° N, 45.22119602351606° E) for three growing seasons, 2021-2022, 2022-2023, and 2023-2024. The climatic conditions of the Sammawa district are typical of arid desert environments. According to the Köppen-Geiger classification system, the atmospheric conditions prevailing in this territory are designated as "BWh". Maximum thermal readings occur during August, when mean temperatures reach approximately 39.4°C (102.9°F), while the lowest average temperatures are recorded in January, at about 11.9°C (53.5°F). Annual precipitation totals approximately 93 mm (3.7 inches) [158]. Weather data for both growing seasons (2021-2022, 2022-2023 and 2023-2024) were obtained from the Meteorological Department in Sammawa City and Meteoblue site [60], as shown in Table 4.

Table 4. Temperature and amount of precipitation in the experiment region for 2022 to 2024 years.

The first year (Oct 2021 – Apri 2022)				
Month	Max Temp (°C)	Min Temp (°C)	Precipitation (mm)	Rel. Humidity (%)
Oct	33.5	20.2	0	28
Nov	24.8	13.5	4	45
Dec	18.2	8.4	15	58
Jan	16.5	6.2	10	62
Feb	20.1	9.5	5	50
Mar	27.2	14.8	8	38
Apr	33.4	19.1	3.5	30
The second year (Oct 2022 – Apri 2023)				
Oct	34	21	5	32
Nov	25.5	14.2	12	48
Dec	19.1	9	8	60
Jan	17.2	7.1	18	65
Feb	21.5	10.4	6.5	52
Mar	26.8	15.2	15	42
Apr	32.9	20	12	35
The third year (Oct 2023 – Apri 2024)				
Oct	34	23	1.2	30
Nov	27	16	24.5	45
Dec	19	10	3.2	55
Jan	17	7	0.5	50
Feb	20	10	15	45
Mar	27.5	15	5	27
Apr	32.5	20	24.5	25

Genetic Material – This study utilised twenty-three genotypes of soft wheat (*Triticum aestivum L.*) in Table 5. Genotypes were brought from several sources: the Iraqi GeneBank, the Iraqi Ministry of Agriculture, Al-Muthanna University and RUDN University.

Table 5. Genetic sources used in the research.

	Genotype	***Sample***	***Pedigree***	***Genetic origin***	***Source***
1	Baraka	AB	IARI × STD	Iraq/ Hybridization	Ministry of Science and Technology \ Seed Technology Centre
2	Wafia	BW	Attila / 3* Pastor, (CIMMYT, ICARDA)	France/ Hybridization	Shuruq Al Nahar Agricultural Supplies Trading Company
3	Latifiya	CL	Australian breed × Aras	Iraq/ Hybridization	Ministry of Science and Technology \ Agricultural Research Department - Latifiya Research Station
4	Binakal	DB	BISU/3/YAV79/ALOI/ALTARS4 / CD93683.7Y.040M-03 OY-LPAP.B	Spanish/ Hybridization	Alreef Alkhadraa company for General Trading and Agricultural Supplies. The Spanish company Fito Semillas.
5	Uruk	EU	Inia 66 (Rad) Radiation of seeds of Enya 66	Iraq / Radiation	Institute of Genetic Engineering and Biotechnology\ University of Baghdad
6	Fateh	GF	MixPac × Aras	Iraq / Hybridization	Ministry of Agriculture /Agricultural Research Department
7	Buhuth 10	HB	Abaa 95 × Abaa 99		
8	Abaa 95	QA	Veery eer (CIMMYT)		
9	Abaa 99	RA	Ures/Bow's'//Pollmer's (CIMMYT and ICARDA)		
10	Buhuth 22	TB	CMSS96Y03236M-050M-040M-020M-050Sy-020sy-IM-0Y	Iraq / Radiation	
11	Buhuth 158	IB	119-S2/57-S2. Cr7.S2		
12	Sham	FS	W-3018-A/JUPATECO-73		
13	Babul 113	JB	MEXIPAK/R23	Iraq / Radiation	Iraqi Atomic Energy Organization
14	Al Iraq	KA	Radiation of Mexipac seeds with full cobalt 60 doses and 10 kilos rad, Max. (Rad)		
15	Bwru	LB	H31/Trapf21 / Enesco	Italy/ hybridization	Debbana Modern Agriculture Company
16	Baghdad	MB	MX105-6MVLT40 / BNSN	Iraq / Hybridization	Ministry of Science and Technology Department of Agricultural Research and Food Technology
17	Abo ghurayb	SA	Ajeeba × Lian 12 × Mexico24		
18	Buhuth	PB	118//S2/57-S2-CR7-S2		
19	Faris	NF	STAR/TR77/773/SLMS	Iraq / Radiation	

20	Tammuz	OT	Exposing the resulting hybrid (Maxipac x Saber Beek) to radiation	Iraq / Hybridization and Radiation	Iraqi Atomic Energy Organization
21	Dujela	UD	8409644HS2-6H	Iraq / Radiation	College of Agriculture - Al-Muthanna University
22	Nemchinovka	VN	(Donshchina × Pamyati Fedina) × Moskovskaya 39	Russia/ Hybridization	Agricultural Technological Institute -RUDN
23	Abo Raghif	WA	Inia 66 / 2 * Mexipak	Turkey/ Hybridization	College of Agriculture - Al-Muthanna University

Experimental and Statistical Scope – Field experiments were carried out using a Split-Plot Design with three replicates, each replicate being designed as a randomised complete block design (RCBD), for both salinity and water stress experiments. The experiment' land was divided into three main blocks (replicates). Each block contained three randomly assigned main plots corresponding to salinity treatments.

Salinity Stress – The treatments in the salinity stress experiment were: T1: 5 ds/m, T2: 10 ds/m, and T3: 15ds/m. Treatment (T1) represented (control) because the salinity level of natural irrigation water from the river ranged between 4.64 and 5 ds/m; as for the other treatments, sodium chloride ($NaCl_2$) was added to the irrigation water to reach the required level for each treatment (Figure 10).

Salinity experiment 2022-2023

R1

1m	JB1	IB1	KA1	UD1
1m	CL1	GF1	QA1	EU1
T2	AB1	TB1	WA1	PB1
	BW1	SA1	NF1	RA1
	LB1		DB1	VN1
	OT1	HB1	MB1	FS1

R2

1.5m	FS2	HB2	IB2	NF2
	LB2	JB2	TB2	DB2
T1	UD2	PB2	QA2	MB2
	KA2	GF2	SA2	OT2
	BW2	AB2	RA2	WA2
	EU2	CL2	VN2	

R3

JB3	IB3	SA3	BW3
OT3	TB3	CL3	UD3
EU3	GF3	WA3	LB3
NF3	AB3	DB3	FS3
QA3	HB3	PB3	RA3
	KA3	VN3	MB3

1.5m

	UD1	JB1	NF1	OT1
	MB1	PB1	SA1	HB1
T1	BW1	DB1	KA1	GF1
	LB1	EU1	RA1	AB1
	FS1	CL1	TB1	WA1
	VN1	QA1	IB1	

	WA2	QA2	MB2	OT2
	GF2	VN2	PB2	IB2
T3	UD2	DB2	SA2	HB2
	JB2	EU2	KA2	LB2
	FS2	CL2	RA2	
	BW2	NF2	TB2	AB2

BW3	IB3	OT3	UD3
QA3	DB3	TB3	MB3
SA3	HB3	CL3	PB3
FS3	WA3	VN3	LB3
GF3	EU3	RA3	AB3
	NF3	JB3	KA3

	QA1	GF1	IB1	DB1
	TB1	NF1	LB1	KA1
T3	CL1	BW1	JB1	FS1
	EU1	AB1	RA1	OT1
	UD1	PB1	WA1	MB1
	SA1	VN1	HB1	

	LB2	GF2	FS2	OT2
	JB2	KA2	MB2	PB2
T2	HB2	EU2	VN2	RA2
	NF2	DB2	WA2	IB2
	QA2	BW2	UD2	
	SA2	CL2	AB2	TB2

PB3	CL3	JB3	OT3
GF3	VN3	TB3	DB3
IB3	HB3	WA3	SA3
AB3	FS3	RA3	UD3
EU3		QA3	NF3
LB3	MB3	KA3	BW3

Figure 10. Design and preparation of a salinity experiment.

The unit of measurement used to measure water salinity in the experiment was decisiemens per metre (ds/m), where 1 ds/m = 1 millisiemen per centimetre (mS/cm). The salinity percentage was measured before the irrigation process using a portable device (*HANNA, HI98304 DiST 4*) Figure 11.

Figure 11. HANNA, HI98304 DiST4.

Drought Stress – The drought stress treatments consisted of a mild control (T1=90% FC), moderate stress (T2=60%), and severe stress (T3=30%). Each main plot contained subplots for the 23 genotypes with randomised experimental unit placement. The space between one main plot and another was 1.5 m, and the space between one subplot and another was 35 cm. The subplot (genotypes) was divided into 69 experimental units for each treatment. The area of the experimental unit was 1 m^2, with dimensions of 1x1 m.

A drip irrigation system was employed to ensure precise water delivery. The water stress treatment levels were applied gradually after germination until the target levels and harvest were reached. A drip irrigation system with 85% efficiency was used [159].

The pressure plate method was used to test soil retention properties for water, soil moisture content at field capacity (θ_{FC}), soil moisture content at the permanent wilting point (θ_{PWP}) and the total available water (TAW), according to [160]. Prior to planting, undisturbed soil samples (100 cm^3) were collected at a depth of 60cm using

metal cylinders, then sealed tightly and took it to the laboratory at Al-Muthanna University.

Following Richards' method, the samples were saturated and placed on ceramic plates inside a pressure chamber. A pressure of -33 kPa (0.33 bar) was applied to determine θ_{FC} and θ_{PWP} of -1500 kPa (15 bar) until equilibrium was reached. The samples were dried in an oven at (105°$_C$ for 24 hours) to calculate water content. The results showed that the soil was silty clay loam. The irrigation requirements for the experiment were estimated in Table 6, where the efficiency of the drip irrigation method (E_{irr}) used in the experiment was 85% [159], and the wheat root depth (D) was 60 cm (600 mm) [161]. According to [162]:

$TAW = (\theta_{FC} - \theta_{PWP}) \times D$ (mm) ……(1)

Irrigation Threshold (θ_{irr}) = FC Level × θ_{FC} ……... (2)

Net Irrigation Requirement (Net) = ($\theta_{FC} - \theta_{irr}$) × D ……(3)

Gross Irrigation for each Event (Gross) = Net / E_{irr} …..……..……(4)

Irrigation was applied when the soil moisture content reached 90%, 60% and 30% of field capacity thresholds. At each threshold, water was added to bring the soil moisture to 100% of field capacity.

Table 6. Irrigation treatments and water requirements under different field capacity thresholds during three years.

Treatment	FC Level	Depletion from FC (%)	Irrigation Threshold (% of FC)	Net Irrigation per Event (mm)	Gross Irrigation per Event (L/m²)	Number of irrigations (2022-2024)	
Light	90% FC	10%	90% of FC	21.6	≈ 25.4	12 -14	frequent irrigation
Moderate	60% FC	40%	60% of FC	86.4	≈ 101.6	8 - 10	Moderate irrigation
Heavy	30% FC	70%	30% of FC	151.2	≈ 157.9	4 - 7	infrequent irrigation
Soil: Silty Clay Loam, θ_{FC}: 36%, θ_{PWP}: 18%, TAW: 108mm, (by pressure plate method)							

Drought experiment 2022-2023

	R1					R2					R3			
	1 m													
1 m	JB1	IB1	KA1	UD1	1.5 m	FS2	HB2	IB2	NF2		JB3	IB3	SA3	BW3
	CL1	GF1	QA1	EU1		LB2	JB2	TB2	DB2		OT3	TB3	CL3	UD3
T1	AB1	TB1	WA1	PB1	T3	UD2	PB2	QA2	MB2	T2	EU3	GF3	WA3	LB3
	BW1	SA1	NF1	RA1		KA2	GF2	SA2	OT2		NF3	AB3	DB3	FS3
	LB1		DB1	VN1		BW2	AB2	RA2	WA2		QA3	HB3	PB3	RA3
	OT1	HB1	MB1	FS1		EU2	CL2	VN2				KA3	VN3	MB3
	1.5 m													
	UD1	JB1	NF1	OT1		WA2	QA2	MB2	OT2		BW3	IB3	OT3	UD3
	MB1	PB1	SA1	HB1		GF2	VN2	PB2	IB2		QA3	DB3	TB3	MB3
T3	BW1	DB1	KA1	GF1	T2	UD2	DB2	SA2	HB2	T1	SA3	HB3	CL3	PB3
	LB1	EU1	RA1	AB1		JB2	EU2	KA2	LB2		FS3	WA3	VN3	LB3
	FS1	CL1	TB1	WA1		FS2	CL2	RA2			GF3	EU3	RA3	AB3
	VN1	QA1	IB1			BW2	NF2	TB2	AB2			NF3	JB3	KA3
	QA1	GF1	IB1	DB1		LB2	GF2	FS2	OT2		PB3	CL3	JB3	OT3
	TB1	NF1	LB1	KA1		JB2	KA2	MB2	PB2		GF3	VN3	TB3	DB3
T2	CL1	BW1	JB1	FS1	T1	HB2	EU2	VN2	RA2	T2	IB3	HB3	WA3	SA3
	EU1	AB1	RA1	OT1		NF2	DB2	WA2	IB2		AB3	FS3	RA3	UD3
	UD1	PB1	WA1	MB1		QA2	BW2	UD2			EU3		QA3	NF3
	SA1	VN1	HB1			SA2	CL2	AB2	TB2		LB3	MB3	KA3	BW3

Figure 12. Design and preparation of a drought stress experiment.

The seeds were planted in November in three lines in the experimental unit, parallel to the drip irrigation pipes, and the space between one line and another was 20–30 cm [163]. The drip irrigation method was used in the field for controlling the distribution of the irrigation water in an even manner, as well as to prevent the treated water from leaking into other treatments or experimental units. Three tanks were assigned for irrigation water, each with a capacity of 2000 litres. One tank was allocated for each treatment in the experiment. In both experiments, treatment levels for salinity and drought stress were applied directly after germination until the required treatment level was achieved and continued to harvest.

Properties of experimental soil – involved testing random samples from multiple locations in the experiment's area, taken at a deepness of (30cm); the results indicated that the soil (pH=8.0), (EC=3.5dS/m), and the percentage of organic matter was (550 mg/kg). The soil texture was a silty clay loam.

Other agricultural operations – Fertiliser application and weed suppression measures were performed according to the established cultivation instructions. In soil preparation before sowing, diammonium phosphate (DAP) fertiliser was incorporated at an average rate of 0.25 t/ha. Nitrogen supplementation was performed using urea (46%), administered in two separate applications. The mean quantity of seeds planted per experimental plot was approximately (10g/m²) [164]. Remove weeds mechanically (hand hoeing) weekly.

Collection of morphological indicator data

In the experiment, after 80% of the plants were in the flowering stage, ten plants were randomly selected from the subplot. The equation calculated the flag leaf area (Fl.A) [165]:

$$Fl.A\ (cm^2) = \text{max length} \times \text{max width} \times 0.95 \quad \text{.....(5)}$$

Harvesting was carried out after the plants reached full maturity in each experimental unit to determine grain yield and biological yield. Plants were harvested

on April, and May (Figure 13). The following parameters were considered for data collection: Organic mass for plant(Bio.Pl) g, organic mass for square meter (Bio.Sq) g, grain yield (t/ha), grains weight in spike (W.G.S) g, 1000 grains weight (W.1000) g, and weight of seed (S.W)mg were measured by using an electronic scale.

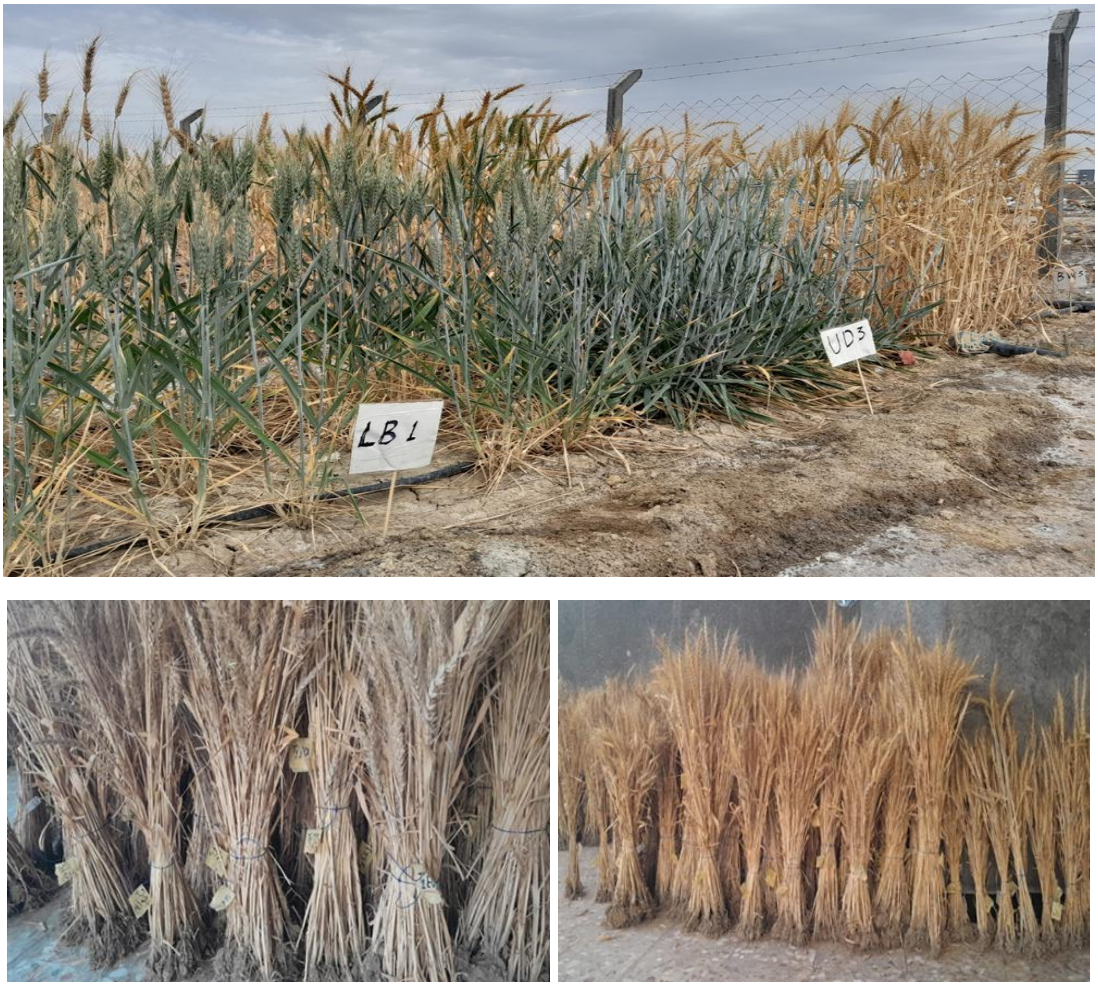


Figure 13. Harvesting wheat biomass.

The length of the spike (L.S) cm and plant height (P.H) cm were measured using a tape measure. P.H was measured from the tip to the base of the main stem (Figure 14).

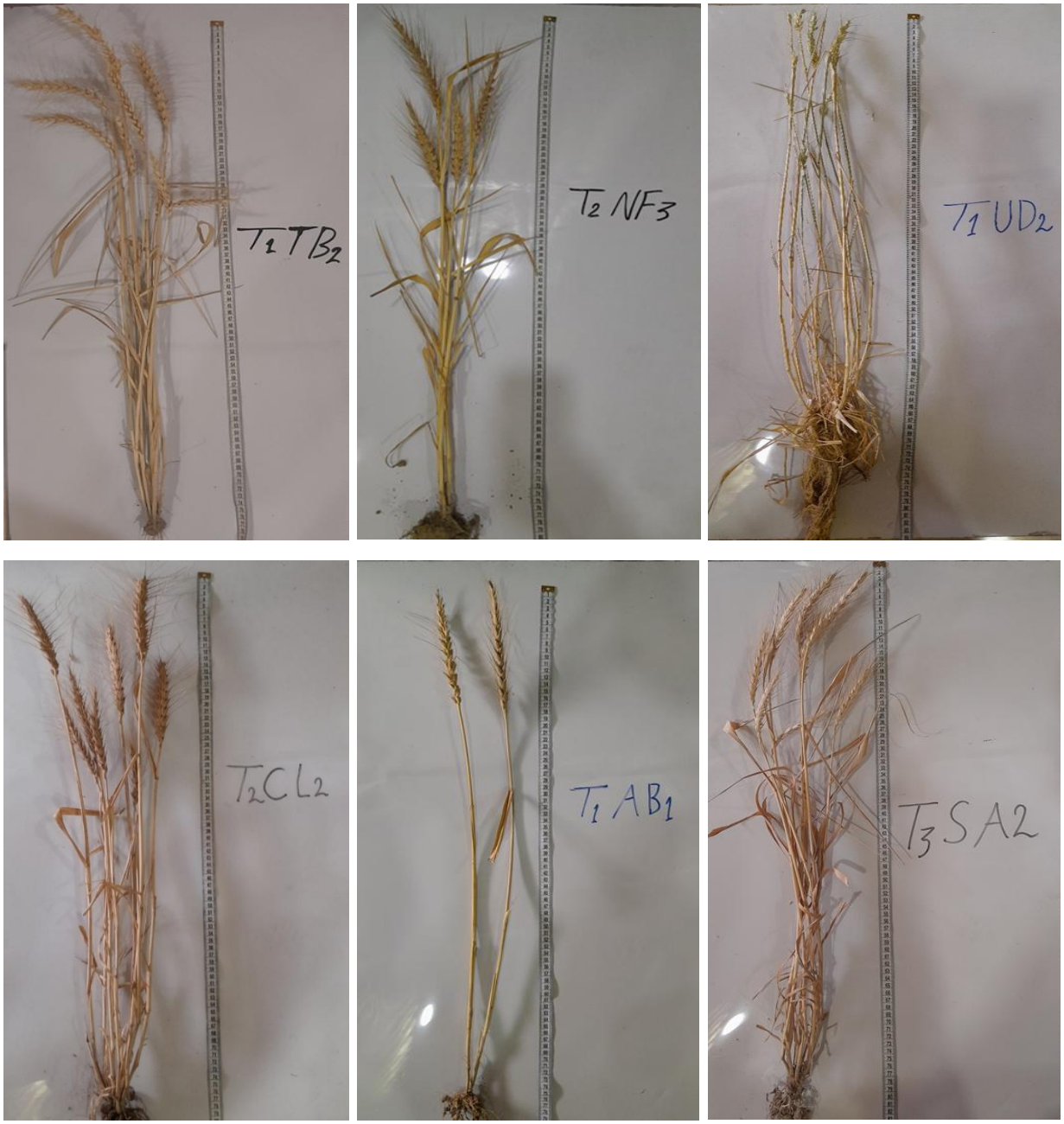


Figure 14. Measuring (P.H) cm, Spike Length (L.S) cm, and N.T.P.

The No. of tillers for plant (N.T.P), the Number of Spikes in plant (N.Sp.P), The Number of Spikes in Square meter (N.Sp.Sq), Number of Grains in spike (N.G.Sp) were measured by observation (Figure 15).

Figure 15. Measuring the components of the yield.

1.1.35 Estimating the sensitivity of genotypes to stress on yield.

The yield of the grains (t/ha) was determined by harvesting all plants from a 1 sq. m area in every plot and weighing the grains on a digital scale.

- Stress intensity(SI) values are between zero and one, according to [166]:

  (SI)=1-$\bar{Y}$s/$\bar{Y}$p .....(6).

- Yield Index (Yl) according to [167]:

  Yi=Ys/$\bar{Y}$s .....(7).

- Yield Stability Index(YSI) equation of [167]:

  YSI=Ys/Yp.....(8).

- Stress Tolerance Index(STI) equation [166]:

  STI=(Ys×Yp)/$\bar{Y}p^2$.....(9).

- Stress Susceptibility Index (SSI) by using the equation [168]:

  SSI=(1-Ys/Yp)/SI .....(10)

Where: *SSI*=Variety sensitivity index to salinity and water stress, *Ys*=Grain yield weight (t/ha) of the variety under stress conditions, *Yp*=Grain yield weight (t/ha) of the variety under normal conditions, $\bar{Y}s$=Average grain yield per variety (t/ha) under stress, and $\bar{Y}p$=Average grain yield per variety (t/ha) under normal conditions.

Collection of physiological indicator data

1.1.36 Estimation of non-enzymatic physiological parameters

1.1.36.1 Estimation of Chlorophyll content in flag leaf

80-100% of the plants were in the flowering stage; 10-13 plants from each plot were examined to measure chlorophyll content (SPAD units), an indicator of the crop's growth status, as shown in Figure 16, and was measured using a SPAD device after the emergence of the flag leaf [169].

Figure 16. Measurement of chlorophyll content using SPAD.

1.1.36.2 Proline content in flag leaf

Proline was extracted and quantified according to the protocol described by Bates [170] In brief, 0.5g (W) of oven-dried leaf tissue (drying at 65–70°C) was homogenised with 10 ml (Vt) of 0.03% sulphosalicylic acid ($C_7H_6O_6S$) using a mortar and pestle. The homogenate was filtered through Whatman No.1 filter paper. Then 3ml aliquot (Va) of the filtrate was put in a test tube and mixed with 3ml of ninhydrin reagent and 3 ml of glacial acetic acid. The tubes were then incubated in a boiling water bath at 100°C for 1 hr and cooled to room temperature. Then 5 ml of toluene was added to each tube and the mixture was shaken vigorously for 20 s. The upper

toluene layer, which developed a red colour, was recovered, and its absorbance was measured spectrophotometrically at 520 nm using a blank of 5 ml toluene alone. A standard calibration curve was made from serial dilutions of pure proline to establish the correlation of absorbance with concentration of proline (C). Fresh ninhydrin reagent was prepared by dissolving 1.25g of ninhydrin in a mixture of 21 ml of glacial acetic acid and 31ml of 4M phosphoric acid, heating and stirring continuously on a vibrating hot plate until the solution was complete. The reagent was prepared and used within 32 hours and stored at 2°C. The proline content was determined as µg/g dry weight (dw) according to the formula described by Bates [170]:

Proline (µg/g dw)=C×(Vt/Va)/W .....(11)

Where:

C=The proline concentration (µg) as determined from the standard calibration curve, corresponding to the spectrophotometric absorbance reading of the toluene phase at 520 nm. Vt=The total volume (ml) of the initial crude filtrate obtained after homogenisation and filtration. Va =The volume (ml) of the filtrate aliquot taken for the reaction with the acid ninhydrin reagent. W=The dry weight (g) of the plant tissue sample used for extraction.

1.1.36.3 Determination of Relative Water Content (RWC)

Fresh leaf specimens were collected at the stage of full flowering (100% anthesis) and immediately weighed to record their fresh mass (FM). The excised leaves were subsequently immersed in deionised water and incubated under illumination at ambient temperature for a period of 4 hours to allow full hydration. After incubation, the leaf samples were gently blotted dry with tissue paper to remove surface moisture and their turgid mass (TM) was recorded. The samples were then oven-dried at 70°C for 48 h in a forced-air oven and the dry mass (DM) determined. The RWC was computed according to the equation proposed by Barrs and Weatherley (1962) [171].

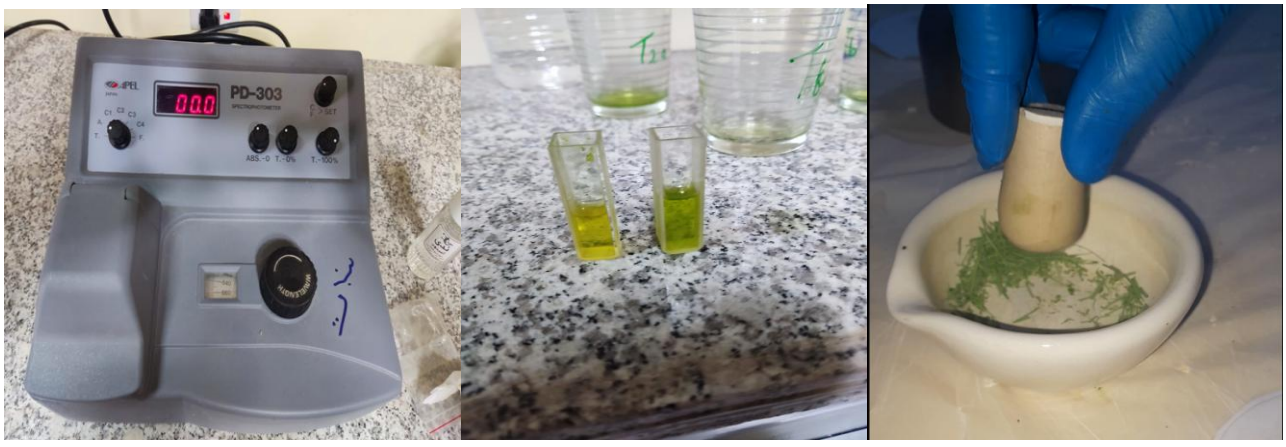
RWC(%)=(FM–DM)/(TM−DM)×100 .....(12)

Where:

FM=Fresh mass (g) of the leaf tissue at the time of collection. TM =Turgid mass (g) after full rehydration in distilled water for 4 hours under light. DM =Dry mass (g) after oven-drying at 70°C for 48 hours. RWC (%) =Relative water content, expressed as a percentage, reflecting the tissue water status.

1.1.37 Assessment of enzymatic physiological indicators

Fresh leaf specimens were collected during the early morning hours and promptly placed in plastic vials within an ice-cooled portable container to preserve tissue integrity. The samples were then immediately transported to the research laboratory at the College of Pure Sciences, Al-Muthanna University, for further processing. The activities of oxidative stress markers, including hydrogen peroxide (H_2O_2), as well as the enzymatic antioxidant defense system—comprising catalase (CAT), peroxidase (POD), and superoxide dismutase (SOD)—were quantitatively evaluated following standardized and well-established analytical protocols.



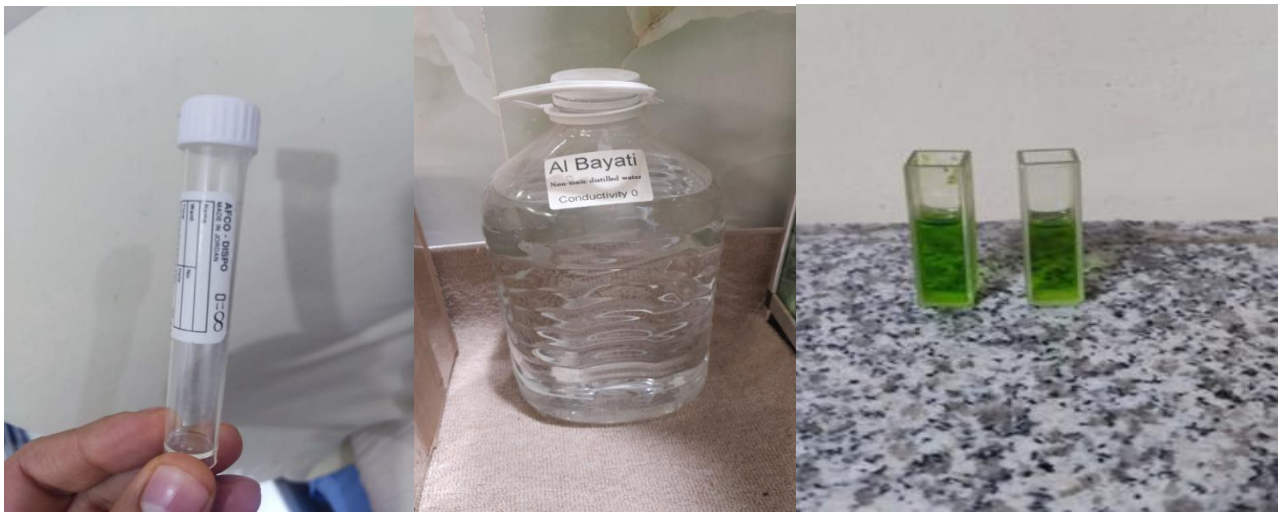


Figure 17. Preparing materials for testing physiological parameters

1.1.37.1 Determination of hydrogen peroxide activity (H_2O_2)

The concentration of H_2O_2 was determined spectrophotometrically by measuring the absorbance of the titanium-hydroperoxide complex at 415nm as described by[172]. The titanium reagent was prepared by heating a mixture of 150cm^3 of concentrated sulphuric acid, 1g titanium dioxide and 10g potassium sulphate on a hot plate for 4h. The digested mixture was then diluted to about 500ml with distilled water and heated to 70–80°C under continuous magnetic stirring until a clear transparent solution was formed. The solution was then cooled to ambient temperature and adjusted to a final volume of 500 ml with distilled water.

In a temperature-controlled chamber maintained at 10°C, a fresh leaf sample (0.5g) was homogenised with 10ml of chilled acetone. Then the homogenate was filtered through (Whatman No.1) filter paper; 4ml of the titanium reagent and 5ml of ammonium solution were added to the filtrate to promote the formation of the titanium–hydroperoxide complex. The reaction mixture was centrifuged at 10,000 rpm for 10 minutes in a Beckman J2-21 centrifuge. The obtained precipitate was dissolved in 2ml of 2M H_2SO_4 and the solution was centrifuged again. Absorbance of the supernatant was measured against reagent blank at 415nm in a UV-visible

spectrophotometer. The H_2O_2 content of the samples was determined by a standard calibration curve in the concentration range of 100-1000 nmol.

The H_2O_2 concentration was calculated according to the equation described by Mukherjee and Choudhuri (1983):

H_2O_2 (µmol / g FW) = C × Vt × Vf / W × Va …… (13)

Where: C = H_2O_2 concentration from the standard curve (µmol), Vt = total volume of acetone extract (10ml), Vf = final volume of H_2SO_4 used to dissolve the precipitate (2ml), W=fresh weight (g) of the specimen (0.5g), and Va = volume of the acetone extract aliquot used (4ml).

1.1.37.2 Assessment of Peroxidase Activity (POD)

The activity of POD was determined spectrophotometrically according to the method of Chance and Maehly (1955)[173]. The reaction mixture was composed of a 20mM guaiacol solution, a 12.3mM hydrogen peroxide (H_2O_2) solution and a 0.1M phosphate buffer (pH 7.0). Fresh flag leaf tissue (1.0 g,W) was ground to powder in a pre-cooled ceramic mortar at refrigerated temperature with 10ml of ice-cold 0.1M phosphate buffer. The resulting homogenate was transferred to centrifuge tubes, centrifuged at 10,000–12,000 rpm for 20min at 4°C, and the supernatant was stored at 2°C until analysis.

The enzymatic activity was monitored by measuring the increase in absorbance at 436 nm, corresponding to the oxidation of guaiacol, using a spectrophotometer. The change of absorbance was recorded after 30 sec intervals for 5 min.

The POD (EC:1.11.1.7) activity was calculated using the following equation:

POD Activity (U.mg^{-1} FW) = $\Delta A_{436} \times Vt / \varepsilon \times Vs \times W$ .....(14)

Where: ΔA_{436} =The change in absorbance per minute (slope, min^{-1}) at 436nm, which is indicative of the enzyme oxidation rate. Vt =total reaction volume (ml) in cuvette =3.18ml (3.00ml phosphate buffer + 0.05ml guaiacol solution + 0.10ml enzyme extract + 0.03ml H_2O_2 solution). ε=The molar extinction coefficient of the

oxidized guaiacol product at 436 nm, 6.4 mM^{-1} cm^{-1}. Vs=The volume (ml) of enzyme extract used in the reaction, 0.10ml. W=Fresh weight (g) of the flag leaf sample (1.0 g).

1.1.37.3 Estimation of Catalase Activity (CAT)

The activity of CAT was assayed by the spectrophotometric method of Aebi (1984) [174]. Fresh flag leaf tissue (1.0g) was ground in an ice-cold ceramic mortar with 10ml phosphate buffer solution (pH7.0,20mM) containing 0.3g polyvinylpolypyrrolidone (PVPP) to remove phenolic compounds. The homogenate was filtered through cheesecloth/gauze and centrifuged at 10000rpm for 10min at 4°C. The supernatant obtained was used as an enzyme source.

The enzymatic reaction was initiated by adding 40µL (Vs) of the enzyme extract to 2.0mL of a reaction mixture containing 10mM H_2O_2 prepared in the same phosphate buffer (20mM, pH7.0). A blank was prepared by substituting the enzyme extract with 40µL of phosphate buffer (20mM, pH7.0) in 2.0mL of 10mM H_2O_2 solution. The spectrophotometer was zeroed against a blank before sample measurement. The absorbance at 240nm, as an index of H_2O_2 consumption, was recorded every 15s for 1min immediately after the addition of the enzyme extract. Change in absorbance/min (ΔA_{240}/min) was then determined.

The calculation for CAT activity was done by the equation:

$$CAT\ (Unite/mg\ FW) = (\Delta A_{240} \times Vt \times Vext) / (\varepsilon \times Vs \times W \times \Delta t) \quad .....(15)$$

Where:

ΔA_{240}=The rate of decrease in absorbance per minute (min^{-1}) at 240nm, which reflects the enzymatic decomposition of H_2O_2. Vt=The total reaction volume (ml) in the cuvette was 2.04ml (2.0ml H_2O_2 solution + 0.04ml enzyme extract). Vext=Total volume (ml) of extract (10ml). ε=Molar extinction coefficient of H_2O_2 at 240nm (0.0436 mM^{-1} cm^{-1}). Vs=Volume (ml) of enzyme extract employed in the reaction (0.04ml). W=Fresh weight (mg) of sample (1.0g=1000mg). Δt=Reaction time(1min).

1.1.37.4 Assessment of Superoxide Dismutase Activity (SOD)

SOD activity was assessed pursuant to the methodology of Markland [175]. The reaction consisted of 50 microlitres of the extraction solution, 2ml of Tris buffer, and 0.5ml of a 3mM pyrogallol solution. The solution absorbs light at a wavelength of 420nm. 1g of fresh flag leaves was pulverised and admixed with 10 ml of 50 Mm phosphate buffer (pH = 7.4). The extract was filtered using a gauze cloth, and the precipitate was subjected to centrifugation at 10,000 rpm at 4°C. 50µL from the supernatant were then taken, and 2ml of Tris buffer (pH=8.2) and 0.5ml of pyrogallol reagent were incorporated. The change in absorbance of the test specimen was then compared to the change in absorbance of the reference specimen (50µL distilled water instead of the enzyme, 0.5ml of pyrogallol and 2ml of Tris solution). The blank consisted of distilled water. The unit of measurement was the amount of enzyme that could inhibit pyrogallol oxidation by 50%.

SOD (EC 1.15.1.1) activity estimation equation:

SOD Activity (Unite/mg FW) = I%×Vt×Vext / 50%×Vs×W.....(16)

Where: I% = inhibition percentage calculated as:

I%= ΔAcontrol−ΔA sample / ΔA control×100 .....(17)

Where: ΔAcontrol =absorbance variation per minute of the reference (devoid of enzyme). ΔAsample= absorbance variation per minute of the specimen (with enzyme)., Vt = total reaction volume (2.55ml), Vext =total extract volume (10ml), Vs = volume of enzyme extract used in the reaction (0.05ml), W=fresh weight of sample, which was 1.0g (equivalent to 1000mg). 50%=the inhibition percentage defining one unit of SOD activity.

Biochemical parameters

1.1.38 Estimation of Nitrogen (N) in the vegetative part of plant

The nitrogen The nitrogen content was determined by the Kjeldahl methodology as described in [116,176] (Figure 18).

The Kjeldahl method consisted of three basic steps:

1. Digestion-The organic matter in the specimens was digested with concentrated sulfuric acid (H_2SO_4) to yield a solution of ammonium sulfate as the final product.
2. Distillation-The acidic digestate was diluted and made alkaline by the addition of NaOH to convert NH_{4+} to NH_3, and then boiled, and the NH_3 vapor was condensed into a receiving solution. In this procedure, a Kjeldahl flask, water-cooled condenser and heating source were used to separate the ammonia gas (NH_3) from the digestion mixture. The end of the condenser was placed in a flask of acid solution to catch the distilled ammonia.
3. Titration: The ammonia content of the receiving solution was then determined. The nitrogen content was measured as the concentration of ammonium ions in the receiver solution. During the first 5 to 10min. of the boiling, most of the ammonia (NH_3) was distilled off and held in the receiving acid solution. The usual standard protocol uses a distillation rate of around 7.5 ml per minute.

Plant foliage was washed, dried at 60-70°C and ground through a mesh screen of 2 mm. A subsample of 0.5 g of dehydrated powdered leaves was taken from each specimen, weighed, and put into a Kjeldahl flask. Added potassium sulfate (1 g) and copper sulfate (0.5 g) as catalytic agents. The specimen was then digested with 10 ml of concentrated sulfuric acid. The mixture was slowly heated to boiling until the solution was clear and pale in colour and then diluted to 100 ml with distilled water, as described by [176]. NaOH (a strong base, typically 40%) was gradually added until the medium became strongly alkaline (pH > 9–10) to convert the NH_4^+ to gaseous NH_3. The most important step in this process is the distillation of the NH_3-bearing steam into

a receiving flask containing boric acid solution (with indicator) to capture the ammonia. The captured solution was titrated with H_2SO_4 to determine the amount of NH_3 collected. The volume of the blank (V. blank) and the volume of the titrant (V. sample) and the difference between them were calculated according to the equation:

$$\%N = \{[(Vs - Vb) \times N.\ acid \times 14.007]/\ W.\ sample\} \times 100 \quad \text{.....(18)}$$

Where:

Vs=volume of titrant consumed by the sample (mL). Vb=volume of titrant consumed by the blank (mL). N. acid=normality of the acid titrant. W. sample = weight of the specimen (mg). 14.007=atomic mass of nitrogen.

Figure 18. Kjeldahl Method for Determining Nitrogen Content

1.1.39 Estimation of sodium and potassium ions in the plant

The procedure for quantification of Na^+ and K^+ contents was performed as described previously by Yoshida [177]. Dried foliar samples of wheat were ground to a fine particulate consistency. A 100mg subsample was transferred to a clean vessel and washed thoroughly with 25ml of 1N HCl from a dispensing burette so that the

powder was well wetted. The specimen was allowed to stand for 24hours with brief intermittent agitation, after which the mixture was filtered through Whatman No.1 filter paper. A reagent blank comprising 1N HCl was prepared identically. An aliquot of 1 ml of the filtrate was withdrawn and transferred into a 40 ml graduated cylinder, then diluted to 40ml with 1N HCl. The Na^+ and K^+ emissions were subsequently recorded using a flame photometer (model FF-200, Figure 19) at their respective characteristic wavelengths. The concentrations of Na^+ and K^+ were computed as percentages by interpolation from 2 separate calibration curves. Then, the Na+/K+ ratio of genotypes under control and saline conditions was calculated using the formula [115]:

$$Normality\ of \boldsymbol{HCl} = ((\mathbf{0.1\ x\ 10}))/(\boldsymbol{Volume\ of\ HCl\ titrated}) \quad \text{.....(19)}$$

Where: 0.1 = Normality of the standard NaOH solution used for standardization. 10 = Volume (mL) of the standard NaOH solution taken for titration. Volume of HCl titrated (mL) = The volume of HCl consumed during the titration against the standard NaOH.

$$\boldsymbol{Na^+ / K^+} = (\%\ \boldsymbol{Na\ in\ leaf}) / (\%\ \boldsymbol{K\ in\ leaf}) \quad \text{.....(20)}$$

Where: %Na in leaf tissue =The sodium content expressed as a percentage of dry weight, derived from the calibration curve. %K in foliar tissue =The potassium content expressed as a percentage of dry weight, derived from the calibration curve.

Figure 19. Flame Photometer (Model FF-200)

Estimation of Grain Content and Quality

1.1.40 Estimation of Protein, Starch, Gluten, and Moisture Content in Grains

The grain content of 23 genotypes Figure 21 resulting from salinity and drought stress was measured to assess grain quality. The samples were sent to the laboratory, Al Muthanna University, in the academic year 2023-2024. The protein, starch, gluten, and moisture content of the seeds were assessed based on the dry weight of the whole grains with a near-infrared (NIR) reflectance spectrometer, specifically the Perten Instruments AM 5200-M (Figure 20).

Figure 20 . Perten Instruments AM 5200-M

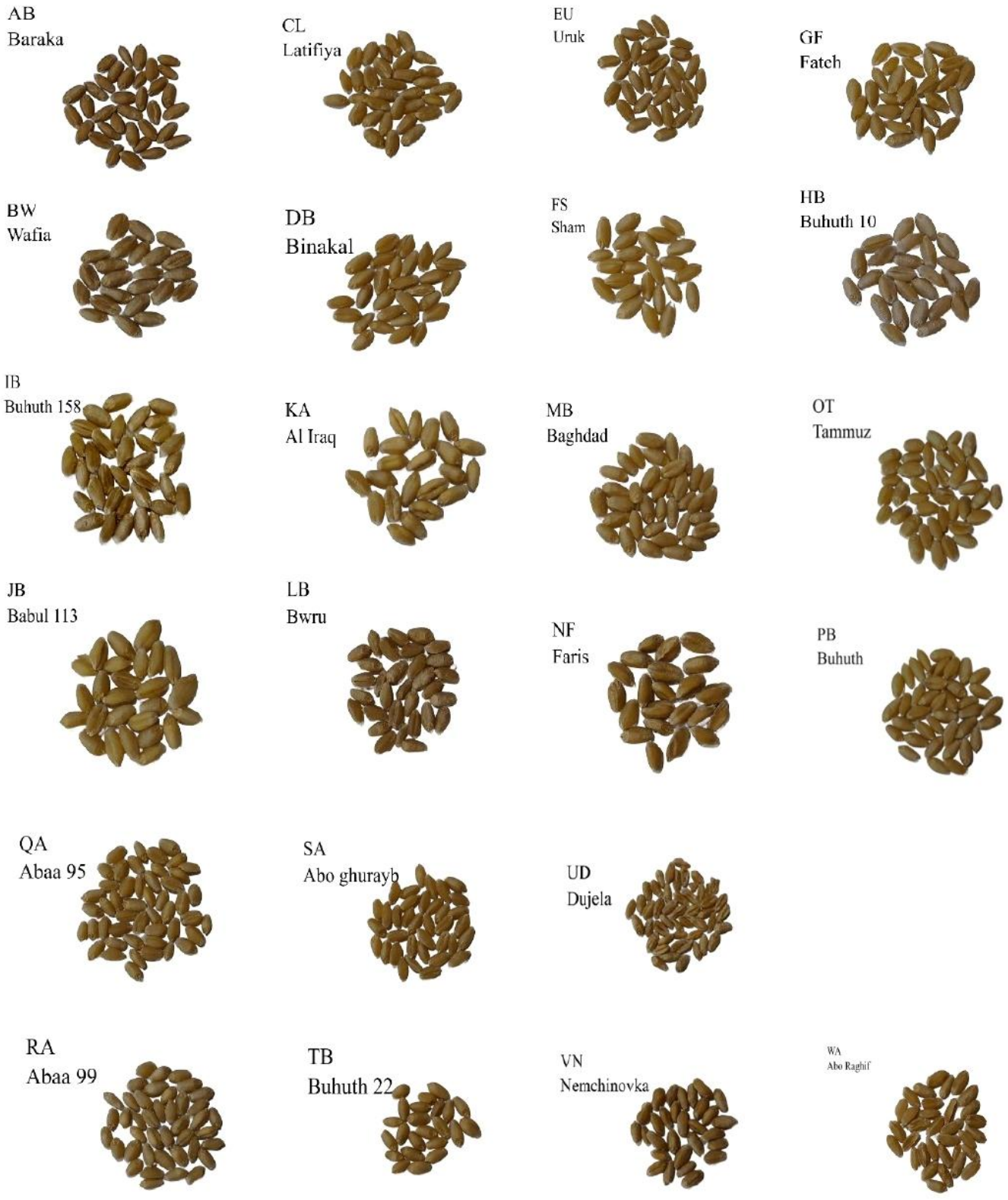


Figure 21. Samples of Wheat Genotype Grains

Molecular Markers

1.1.41 DNA Extraction

In Appendix 0-16 Table of equipment used in a laboratory. DNA Extraction Protocol Using Silica Spin-Column Method (FavorPrep Plant Genomic DNA Extraction Maxi Kit) (According to Appendix 0-8 and Appendix 0-7):

1. Specimen Pulverisation — The first step is to reduce the vegetative material to a fine powder in order to break down the integrity of the cellular structure and allow for the subsequent liberation of genetic material in Figure 22.

Figure 22. Crush the walls using liquid nitrogen.

2. Membrane Disruption — This step is designed to disrupt the cellular and nuclear membranes to release the chromosomal DNA and to degrade contaminating proteins and RNA species.
3. Nucleic Acid Immobilisation This step is aimed at fixing the freed DNA on a chromatographic support, hence separating it from soluble cellular components.
4. Contaminant Wash – This wash step removes any residual salts, proteins and other contaminants, while the DNA remains bound to the solid matrix.

5. Recovery of DNA The purified genetic material is eluted from the column using a small volume of buffer, resulting in a concentrated preparation of nucleic acids.
6. Quality Verification – The concentration and purity of the isolated DNA are spectrophotometrically checked, and the samples are standardised to a consistent concentration [178] (Appendix 0-7).

1.1.42 Optimizing annealing temperature for DNA amplification

Several variables such as the annealing temperature influence the quality of the amplification products. To determine the most appropriate annealing temperature for each primer combination, a thermal gradient was examined, since each primer pair has a characteristic optimal annealing temperature. For the assessment of the annealing temperature gradient, the number of samples was 920 for ISSR-PCR and 368 for SSR-PCR.

PCR reaction mixture was formulated following the supplier's specifications (Transgenbiotech Inc., China). The master mix components were assembled according to the manufacturer's protocol, as detailed in Table 7 [179] .

Table 7. Master Mix

Materials	**Volume (×1)**
DNAPolymerase	500U
10×Buffer($Mgcl_2$)	1.2ml
2.5mM(dNTP)	800µl
(6×DNALoading)	1ml

1.1.43 The PCR-ISSR and SSR Tests

In the present investigation, the PCR approach was employed to evaluate genetic diversity and generate molecular profiles of the examined genetic lines using ISSR marker analysis, as well as to conduct molecular characterisation of salinity- and drought-tolerant genotypes via SSR marker screening. The principal constituents of the PCR amplification mixture are presented in Table 8.

Table 8. Main compositions of the PCR-SSR and ISSR tests.

Contents	SSR(µl)	ISSR(µl)
F(10µM)	0.5	1
R(10µM)	0.5	
2xMaster Mix	12.5	12.5
T DNA	2	2
N-free-water	9.5	9.5
volume	25	25

1.1.44 Thermocycling Conditions of PCR

The settings for the thermal cycling in the PCR were done with the standard amplification system shown in Figure 23. The basic PCR protocol involves three critical phases, denaturation, annealing and extension, which enable exponential copying of a defined target sequence within the DNA template as summarised in Table 9.

Table 9. Thermal cycling in the PCR

Stage	Temp	Timer	N0. of cycles
Initial denaturation	94˚C	3mins	1
Denaturation		30sec	32
Annealing	Primer temperature		
Extension	72˚C	1min	
Final extension		5min	1
Hold tempe	4˚C	-	-

Figure 23. Conventional PCR Device – Bio-Rad

1.1.45 Preparation of Buffersand Solutions

Standard buffer systems containing Tris-borate-EDTA (TBE) and Tris-acetate-EDTA (TAE) solutions were used for electrophoretic separation of nucleic acids . The buffers help maintain the ideal pH conditions to keep DNA soluble and negatively charged to migrate towards the positive electrode. To protect the nucleic acids from enzymatic degradation by sequestering divalent cations, a chelating agent (EDTA) was added. The running buffer was prepared from Tris-HCl, boric acid and EDTA, adjusted to the correct pH and kept at low temperature before use. Dilution of concentrated stocks was used to prepare working solutions and a tracking dye (sucrose and bromophenol blue) was used to follow the progress of the electrophoresis Figure 24.

Figure 24. Tris-Borate-EDTA(TBE) Buffer and Agarose

1.1.46 Gel electrophoresis

1. DNA Quantification — DNA specimens were resolved on 1% agarose gels prepared in TBE buffer. Electrophoresis was conducted at 125V for 25 minutes. Bands were visualised under UV light. A total of 23 specimens were processed [180].
2. ISSR-PCR Analysis — Amplification products were separated on 1.5% agarose gels prepared according to Sambrook and Russell (2001). Electrophoresis was performed for 25 min at 125 V and then for 1 h at 75 V. Gels were visualised under UV illumination Figure 25. Screening was performed on 460 samples.
3. SSR-PCR Analysis — PCR amplicons were resolved on 3% agarose gels. Electrophoresis was carried out at 125V for 25 minutes and then at 75V for 1 hour. Bands were visualised under UV light Figure 25. A total of 72 specimens were analysed [180].

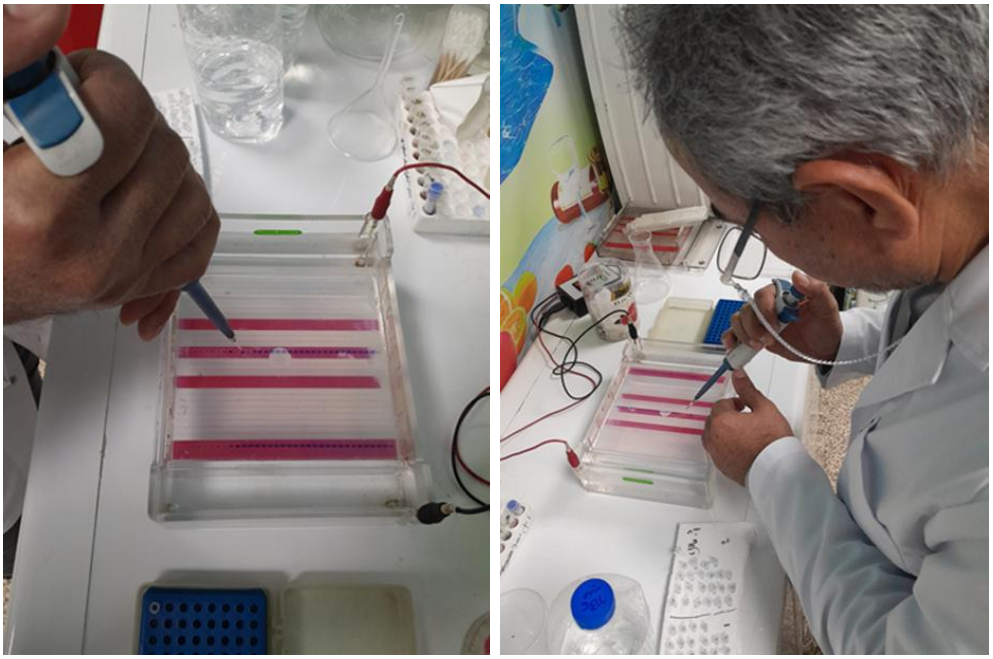


Figure 25. Gel Electrophoresis Test for Detection of PCR Amplification

1.1.47 New ISSR-PCR primers for the Detection of the fingerprint of wheat Genotypes

DNA fragments are amplified using this method, which is PCR. The annealing temperature of the primer to template DNA of each genotype is provided in Table 10. , which details the number of cycles and thermal conditions that are required for each genotype. The products that are produced are fragments that are amplified and contain a lot of sequence. The ISSR-PCR technique was utilised in order to carry out the molecular characterisation of each genotype. An analysis of the population structure was carried out in order to determine the genetic similarities and differences that existed between the 23 genotypes.

In the current investigation, the 20 primers listed in Table 10 were employed for the first time on the wheat genome for molecular characterisation and genetic fingerprinting of the genotypes. Some of these primers had previously been utilised in studies on rice to determine genetic fingerprints. The 20 primers were obtained from Alpha DNA (www.alphadna.com). A 100 micromolar stock solution was prepared for each primer. From this, a 10 micromolar working dilution was prepared by combining

10 microlitres of the stock with 90 microlitres of sterile PCR-grade water in sterile tubes. The ISSR-PCR assay was conducted on a total of 460 samples (Figure 26).

Table 10. Characteristics of the 20 ISSR primers in the study.

N0.	Primers	`Sequences	Length (meres)	Temp
1	ISSR-1	$(AG)_9C$	19	58°C
2	ISSR-2	$(AC)_8G$	17	52°C
3	ISSR-3	$(AG)_8T$	17	50°C
4	ISSR-4	$(TG)_8C$	17	52°C
5	ISSR-5	$(AC)_8Y$	17	48°C
6	ISSR-6	$A(CAG)_5$	16	52°C
7	ISSR-7	$B(CT)_8Y$	18	50°C
8	ISSR-8	$R(ACA)_5$	16	40°C
9	ISSR-9	$(CAC)_7G$	22	74°C
10	ISSR-10	$(CT)_9Y$	19	56°C
11	ISSR-11	$(CA)_8DT$	18	50°C
12	ISSR-12	$(CTC)_6G$	19	64°C
13	ISSR-13	$(GT)_8C$	17	52°C
14	ISSR-14	$G(CA)_8$	17	52°C
15	ISSR-15	$(GAA)_7$	21	56°C
16	ISSR-16	$(GA)_8V$	17	48°C
17	ISSR-17	$(GT)_8C$	17	52°C
18	ISSR-18	$(GA)_8G$	17	52°C
19	ISSR-19	$(GA)_8HC$	18	52°C
20	ISSR-20	$(GACA)_5$	20	60°C
Note: B = C, G, T; D = A, G, T; H = A, C, T; R = A, G; V = A, C, G; Y = C, T				

Figure 26. Preparing the Samples for ISSR-PCR and SSR-PCR Markers Testing.

1.1.48 New SSR-PCR primers (Microsatellite) for detecting salinity- and drought-tolerant wheat genotypes

The aim of the test was to enhance the study results in morphological, physiological and biochemical traits obtained in the field and laboratory, identify tolerant genotypes, and detect salinity- and drought-tolerant genetic loci using molecular markers, clusters (A) and (B), which includes (UD, AB, TB, CL, NF, SA) genotypes, is shown in Figure 37 and Figure 38. This cluster demonstrated tolerance to salinity and drought stress. Additionally, three genotypes were included (LB, PB, JB) genotypes from clusters (C) and (D), which showed sensitivity to salinity and drought stress in Figure 37 and Figure 38.

In this study, new primers (Malik 1, Malik 2) were developed using the *NCBI-Primer BLAST* website with the *Primer3 Plus software* in addition to known primers such as xcfd-18 [181], xgwm-493 [182], Xgwm130 [183], and Xwmc245 [184] to detect salinity- and drought-tolerant genotypes in wheat plants (Table 11). DNA was extracted from fresh leaves of selected genotypes [185,186]. DNA extracted from selected wheat varieties was subjected to SSR analysis using two new primers and four other primers approved in several selective breeding programmes in Table 11 as genetic markers associated with drought and salinity tolerance [182]. The primers were made Alpha ADN, S.E.N.C. (www.alphaadn.com).

The test's templates were prepared; many materials were added according to the maker's instructions for the MasterMax PCR . Specimens were marked before the materials were added. The total reaction mixture (25µl) in Table 8. The reaction mixtures were subjected to a number of cycles at different temperatures in an apparatus (PCR Device – Bio-Rad) as shown in Appendix 0-16. The sum of specimens in the test SSR-PCR (microsatellite) was 72 specimens (Figure 26).

Table 11. Characteristics and features of PCR-SSR primers for salinity and drought tolerance.

Drought					
	Primers	***Sequences***	***Length (meres)***	***Temp.°C***	***Sources***
1	Malek 1	F GGTAGATCGGAAGGACGCTG R CAGGGGGCTCATCACCAAAT	20 20	64 62	NEW
2	Malek 2	F ATTGCAAGGAGCACATCCGA R TCAGCATCATGGAAGGCAGG	20 20	60 62	NEW
3	Xgwm130	F AGCTCTGCTTCACGAGGAAG R CTCCTCTTTATATCGCGTCCC	20 21	62 64	(Haque et al. 2021)[183]
4	Xwmc245	F GCTCAGATCATCCACCAACTTC R AGATGCTCTGGGAGAGTCCTTA	22 22	66 66	(Thungo et al. 2020)[184]
Salinity					
1	Xcfd-18	F CATCCAACAGCACCAAGAGA R GCTACTACTATTTCATTGCGACCA	20 24	60 65	(Hannan et al. 2021)[181]
2	Xgwm-493	F ATCGCATGATGCACGTAGAG R ACATGCATGCCTACCTAATGG	20 21	60 62	(Vaja et al. 2016)[182]

1.1.49 Analysis of Gel Electrophoresis Results for 23 Genotypes Using 20 New Primers

To study the molecular diagnosis of genotypes and evaluate the primers used in the study of molecular variation, it is necessary to analyse the results of gel electrophoresis. Therefore, the gel images were converted into digital data using the Gel Analyser 23.1.1 program to read the presence of fragments or bands (1), and the absence of those bands was set to (0) in Figure 27 and Figure 28.

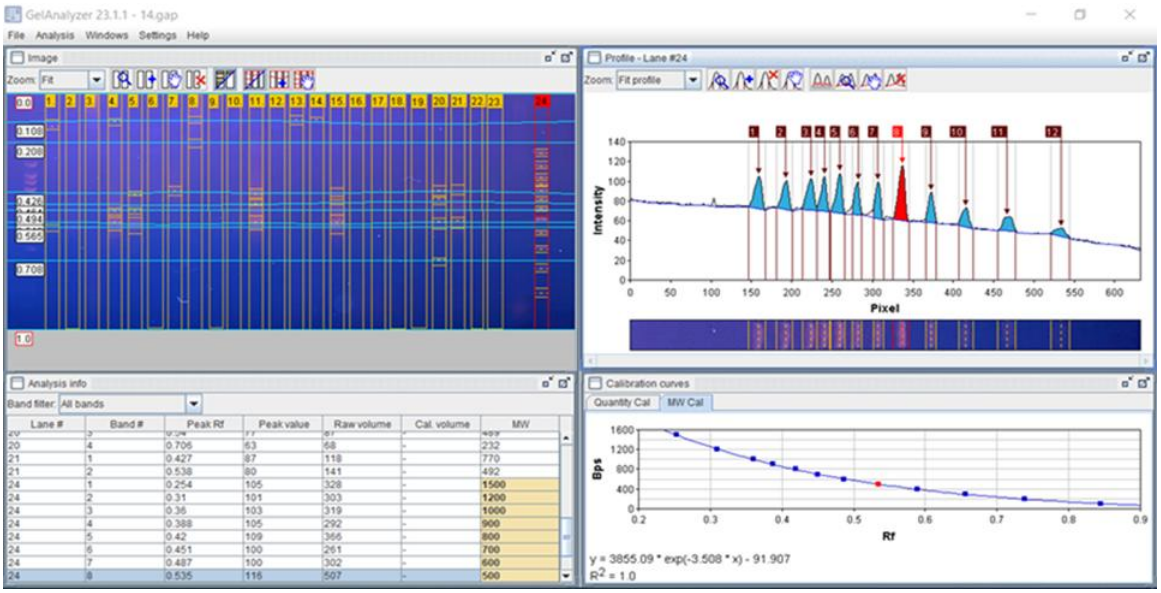
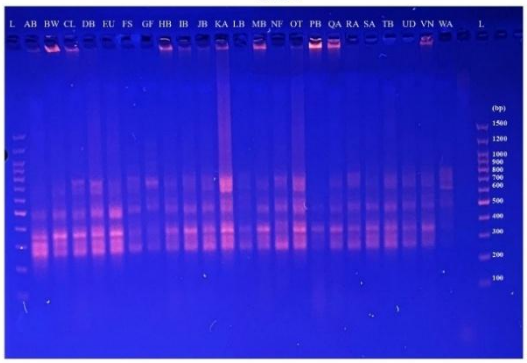
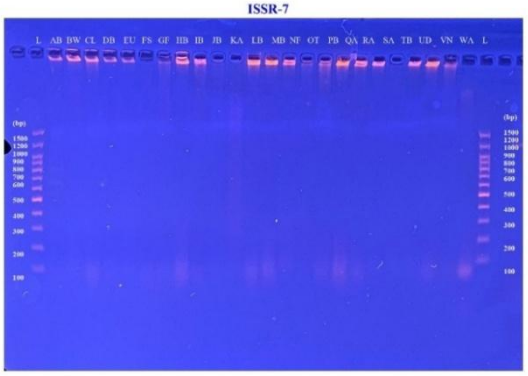


Figure 27. The Gel Analyser 23.1.1 program was used to read the presence of fragments.

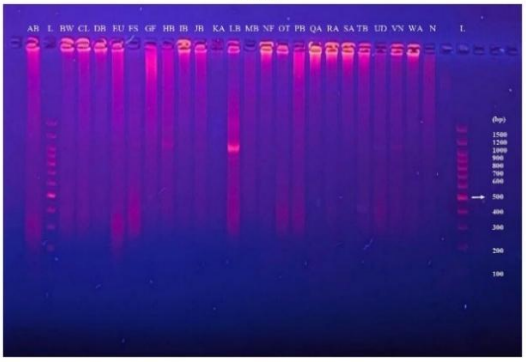
ISSR-1



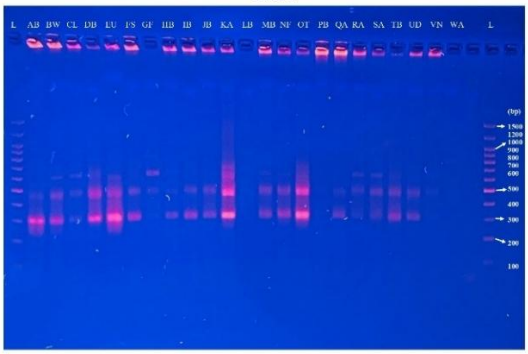
ISSR-7



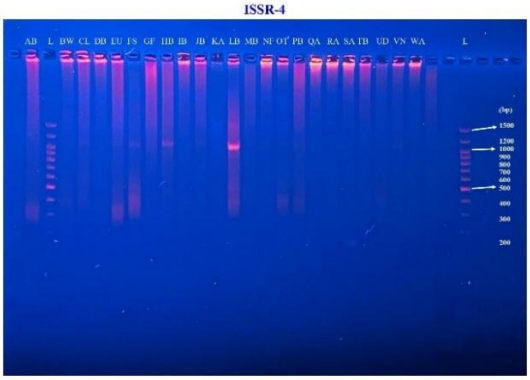
ISSR-6



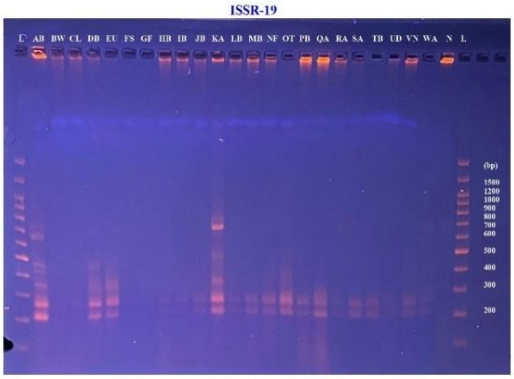
ISSR-5



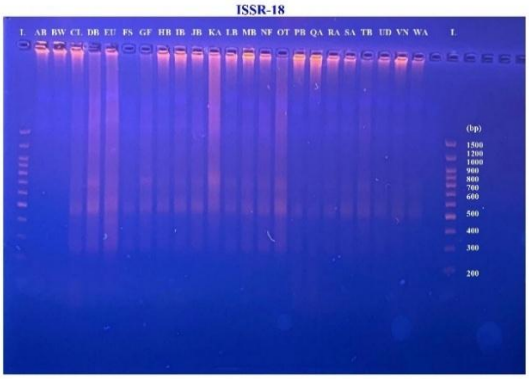
ISSR-4



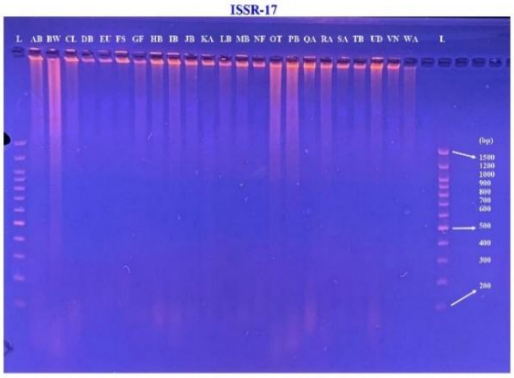
ISSR-19



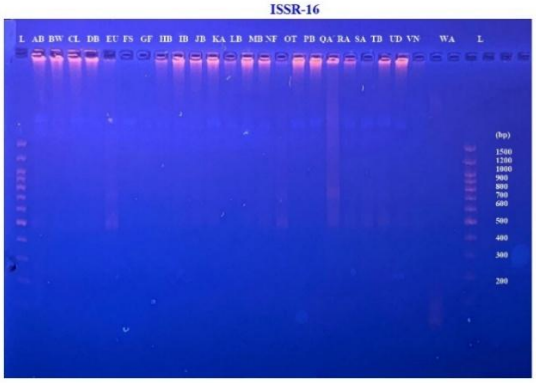
ISSR-18



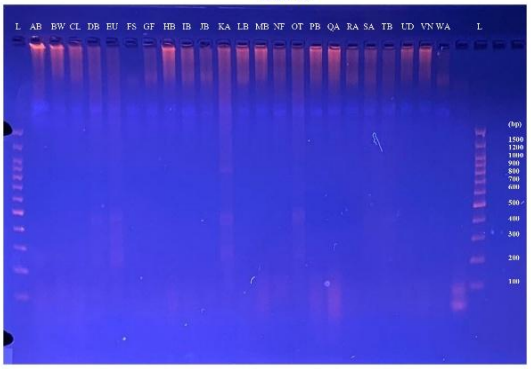
ISSR-17



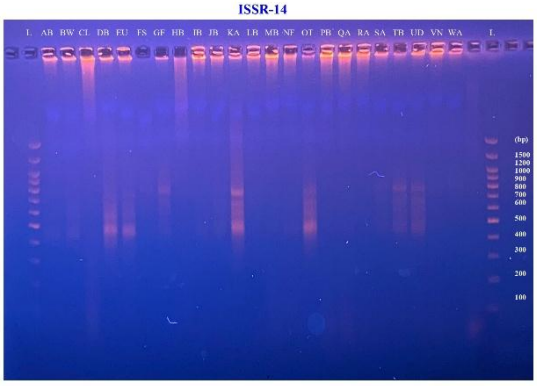
ISSR-16



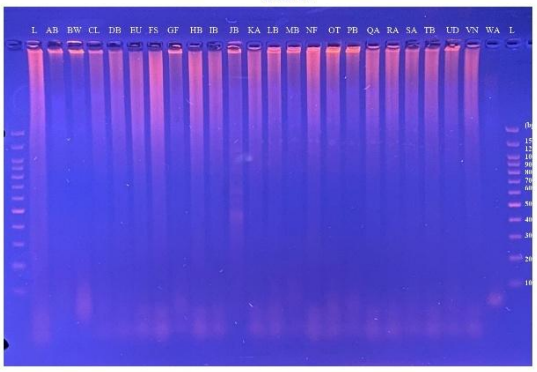
ISSR-15



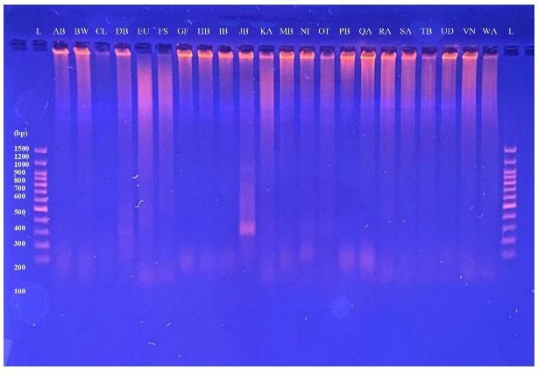
ISSR-14



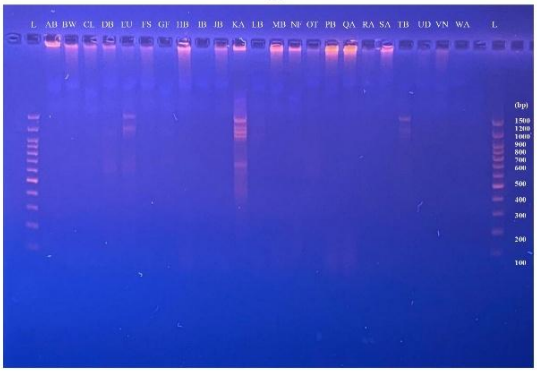
ISSR-13



ISSR-11



ISSR-10



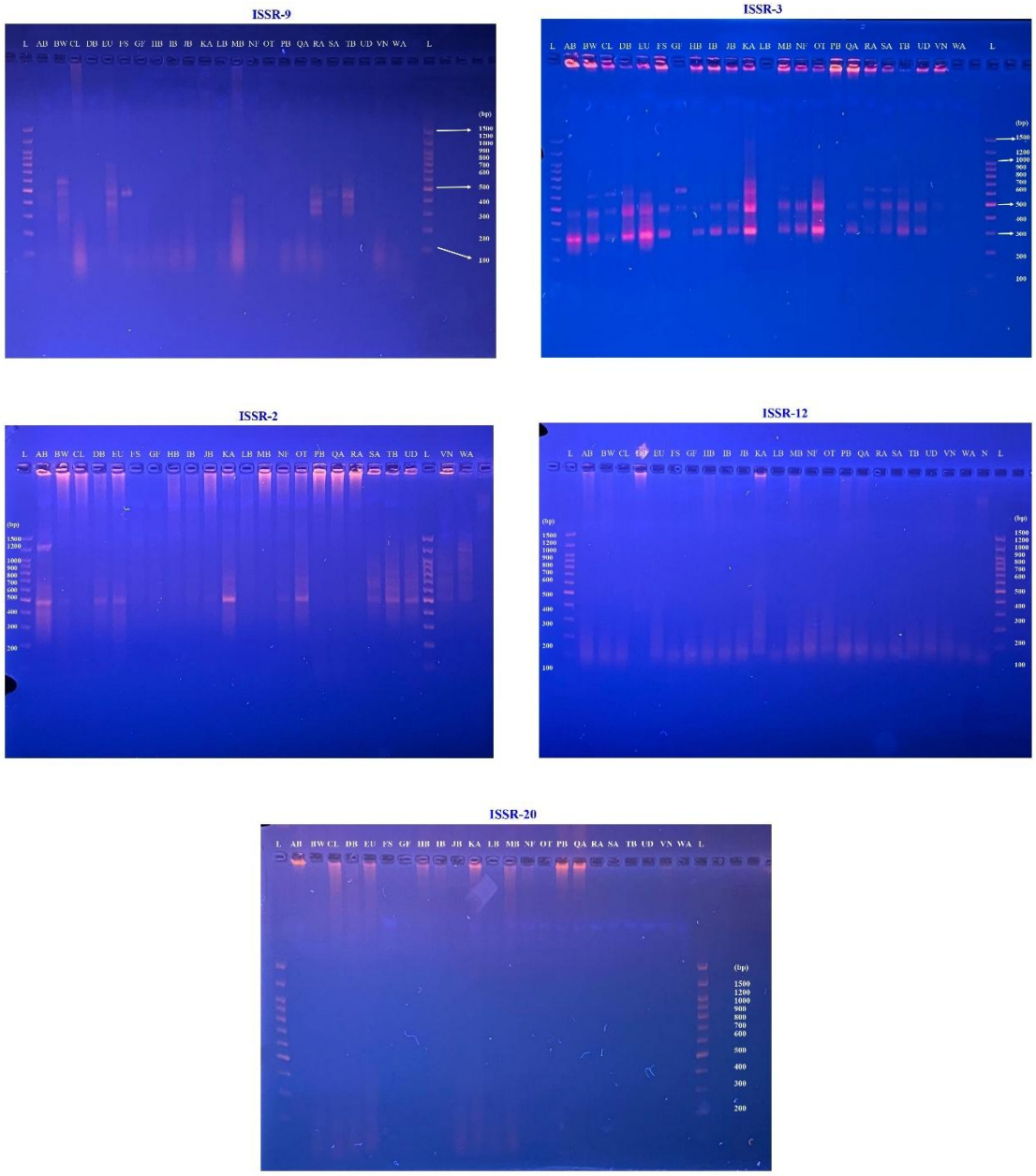


Figure 28. Gel Electrophoresis Analysis for 20 Primers PCR-ISSR

1.1.50 Polymorphisms of 23 Genotypes and 20 New Primers

To evaluate the characteristics of the primers used for the first time with wheat in our study, the polymorphism of the bands extracted from gel electrophoresis analysis was examined to determine the ability of these primers to differentiate

between the genotypes in the study. The polymorphic information content (PIC) was calculated according to [187,188], using the following formula:

PIC=2fi(1-fi).....(21)

Where: fi=frequency of an allele.

Effective Multiplex Ratio (EMR) is the number of polymorphic fragments. The effective multiplex ratio (EMR) and marker index (MI) were calculated according to [188].

EMR=NP/N.....(22)

Where: NP=No. polymorphic loci, and N=Total loci.

MI=EMRx PIC.....(23)

Resolving power (Rp), which shows the ability of primers to identify genetic variation among 23 genotypes was assessed, according to [187,188]:

RP=∑Ib.....(24)

Where: Ib=band informativeness:

Ib=1-[2(0.5-p)].....(25)

Where: p=proportion of clones containing the band.

1.1.51 Genetic Variation Between Genotypes Based On ISSR-PCR Results

The genetic similarity coefficient (GS) among genotypes was calculated using the Dice coefficient based on binary presence (1) and absence (0) matrices, as described by [189], using the formulae:

GSij=2a/(2a+b+c).....(26)

Where: a = shared amplicons; b = bands unique to i; c = bands unique to j.

Then, the matrix obtained was used to perform cluster analysis. In this method, the distance between any two clusters was calculated as the average of the distances between all possible pairs of clusters belonging to the two adjacent clusters, and this process was repeated until all clusters were merged into one hierarchical structure. The

genetic relationship among the wheat genotypes under study was then determined using the software packages SPSS and PAST 4.2 with the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) and the between-groups linkages method [188,189].

1.1.52 Genetic locus sequence

1.1.52.1 Genetic Sequences of PCR-SSR Amplicons

A total of 14 PCR-SSR amplification products were sent to the Canadian facility Alpha (www.alphaadn.com) for commercial sequencing. The resolved amplicons were subjected to bidirectional sequencing utilising the Sanger dideoxy chain-termination method, strictly adhering to the protocols furnished by the sequencing provider (Macrogen Inc., Geumchen, Seoul, South Korea). Only chromatograms of superior clarity, derived from ABI(Applied Biosystems) electrophoretic traces, were retained for subsequent scrutiny, thereby ensuring that the observed nucleotide assignments and polymorphic variations were not attributable to artefacts arising from either PCR amplification or sequencing procedures. Through comparative alignment of the experimentally obtained nucleotide sequences from the local specimens with those retrieved from reference databases, the in silico genomic coordinates and supplementary characteristics of the amplified fragments were unequivocally delineated.

1.1.52.2 Reading of Sequencing Data

The sequencing data obtained from PCR amplicons of the target specimens were carefully edited, aligned using multiple sequence alignment and analysed in detail along with the reference sequences obtained from the genomic database. This analytical procedure was performed using the sequence alignment editor software BioEdit, Version 7.1 (DNASTAR, Madison, WI, USA). All the polymorphic variants found in each sequenced sample were systematically counted for all amplified

fragments and accurately mapped to the corresponding loci in the reference genome. Therefore, the nucleotide designations observed across the PCR amplicons were assigned according to their corresponding coordinates in the reference genomic assembly.

1.1.52.3 Translation of Sequencing into Amino Acid

The deduced amino acid sequences of the target proteins were obtained from the Protein Data Bank (http://www.ncbi.nlm.nih.gov). In order to evaluate the functional consequences of the detected nucleotide substitutions on the resultant polypeptides, all nucleic acid sequences of the investigated genotypes were translated in silico into their corresponding amino acid sequences utilising the Expasy Translate Tool (https://web.expasy.org/translate/).

1.1.52.4 Deposition of Sequences to GenBank

All nucleotide sequences enumerated in Table 12, alongside the primers that yielded interpretable amplicons as presented in Table 11 and Figure 29, were meticulously examined and analysed and subsequently submitted to the NCBI BankIt web-based submission portal. All procedural guidelines stipulated by the submission server were rigorously followed. The deposited sequences were provided to NCBI as nucleic acid sequence records, with the aim of obtaining unique GenBank accession numbers for the sequences in question.

Table 12. Genotype symbols in gene sequencing technology testing.

	Genotypes		Samples
1	Baraka	AB	E1
2	Latifiya	CL	E2
3	Faris	NF	R1
4	Abogurayb	SA	R2
5	Buhuth 22	TB	R3
6	Latifiya	CL	S1
7	Faris	NF	S2
8	Abogurayb	SA	S3
9	Buhuth 22	TB	S4
10	Dujela	UD	S5
11	Latifiya	CL	Q1
12	Dujela	UD	Q2
13	Abogurayb	SA	Q3
14	Buhuth 22	TB	Q4

Figure 29. Genotype symbols and primers.

Statistical Analyses

Morphological and physiological data were collected for 23 genotypes. Due to the different units of measurement used for the studied traits (e.g., height, weight, pigment content), standardisation was necessary before performing cluster analysis to

ensure the accuracy of the results. Raw values for each trait were converted into standardised scores using *SPSS* software.

By using the mean and standard deviation and their conversion to standard scores *(Z-score)*, we were able to assess the genotypes in each trait under stress conditions, as well as create a similarity matrix after cancelling the effect of different units of measurement. The standardisation equation (*Z-score*) was applied [190]:

$$Z = (X - \mu) / \sigma \quad \ldots\ldots\ldots\ldots (27)$$

Where the value of (*X*) for a specific genotype, (μ) Overall average of all values and (σ) Standard Deviation of values. A high positive value (+) indicates the genotype's tolerance to stress for that trait and a negative value (-) indicates the genotype's sensitivity to stress for that trait.

Analysis of hierarchical clusters were achieved using *Ward's method*, which relies on minimising the sum of squared deviations within a group and using the squared Euclidean distance as a measure of variation [191]. A dendrogram was drawn to illustrate the genetic linkage between twenty-three varieties. Based on the dendrogram, the varieties were distributed into four main groups according to the resistance level to the stress (highly tolerant, moderately tolerant, moderately sensitive, and highly sensitive) [192].

The data were statistically analysed using **Statistix 8.1** to determine variance values according to the experimental design of the study. Least Significant Difference (**LSD**) test to compare means at significance 0.05 and 0.01 level according to the type of test and experiment. The results of Pearson's correlation were analysed using **OPSTAT** software. **Gel Analyzer 2.1 software** was used to analyse the gel images from the electrophoresis device.

RESULTS AND DISCUSSION

Effect of Abiotic Stress on the Morphological Traits of Genotypes

1.1.53 Evaluation of Genotypes in Plant Height Trait (P.H)

In Table 13, ANOVA Appendix 0-1, Z-score Appendix 0-18 and LSD test at the significance 0.05 level showed a significant effect among the wheat genotypes, the levels of saline irrigation water treatment and their interaction. The highest treatment (15 $dS.m^{-1}$) significantly reduced P.H and produced the lowest mean value 65.59 cm . In contrast, the control treatment (5 $dS.m^{-1}$) recorded the highest mean value of P.H 97.18 cm. The genotypes chosen for salinity tolerance in this trait were selected based on the lowest standard deviation (SD) values and highest mean performance among the varieties Table 13 along with positive Z-score values Appendix 0-18. Therefore, (NF, CL, AB, SA, UD) genotypes were identified as salt tolerant genotypes with better ability to maintain plant stature under saline conditions. The reduction in P.H may arise from water stress caused by elevated sodium salt concentrations, which obstructed photosynthesis and inhibited nutrition absorption by the cells. Consequently, the plant grew stunted and exhibited insufficient elongation [164,193].

The results of drought stress in Table 13, ANOVA Appendix 0-2, Z-score values in Appendix 0-18 and LSD at a significance (0.05) indicated a significant effect was observed between both drought levels and genotypes, as well as a significant interaction between them. The results in Table 13 showed significant differences in P.H , at the 30% FC showed the lowest average of 56.14 cm for this trait, compared to the 90% of field capacity level, which gave the highest average of 92.82 cm.

The identification of salinity-tolerant genotypes for this trait was based on two complementary criteria: the lowest standard deviation (SD) values associated with the highest mean performance among the varieties Table 13, alongside positive Z-score values Appendix 4-18. Accordingly, genotypes (NF, CL, AB, SA, TB, UD) were selected as exhibiting drought tolerance, as reflected by their capacity to maintain P.H under saline conditions in Figure 30. Drought stress impairs the intake of nutrition by

decreasing the energy required for the conversion of mineral nutrients into organic forms that are utilised in metabolic functions. In addition, phosphorus content is decreased in plant tissues under water stress [81]. There is genetic variation in some growth traits of the variants, especially in the length of the internodes and the spike holder, which constitutes about fifty percent of the P.H in some types. This is consistent with the results of [82].

Table 13. Abiotic Stress on P.H Trait(cm) in Wheat (Average for 2022 - 2024).

	Salinity				**Drought**			
Genotypes	***Control 5 dS/m***	***10 dS/m***	***15 dS/m***	***Means ± SD***	***Control 90% FC***	***60%***	***30%***	***Means ± SD***
Baraka«**AB**»	92.68± 4.4	92.85± 2.96	88.38± 3.54	**91.31± 2.53**	88.28± 8.89	84.67± 6.01	79.04± 7.21	**84±4.66**
Wafea«**BW**»	109.63 ±5.74	63.01± 1.85	54.95± 5.81	75.86± 29.52	105.4± 11.59	54.37± 3.76	44.92± 11.84	68.23± 32.53
Latefiya«**C**L»	116.27 ±3.6	113.08 ±2.73	102.95 ±1.14	**110.77 ±6.96**	112.11 ±7.27	105.21 ±5.55	93.9±2. 33	**103.74 ±9.19**
Binekal«**DB**»	100.32 ±1.9	97.16± 3.42	65.54± 0.85	87.68± 19.23	96±3.8 4	89.05± 6.94	55.73± 1.73	80.26± 21.52
Urok«**EU**»	89.36± 6.99	58.03± 2.15	25.49± 2.69	57.63± 31.94	84.93± 14.11	49.32± 4.37	14.86± 5.49	49.7±3 5.04
Sham«**FS**»	62.79± 3.78	50.74± 4.98	34.1±1. 66	49.21± 14.41	58.08± 7.64	41.92± 10.12	23.64± 3.38	41.21± 17.23
Fateh«**GF**»	95.34± 4.34	92.19± 1.43	72.16± 5.27	86.56± 12.57	90.97± 8.76	84±2.9 1	62.49± 10.75	79.15± 14.85
Buhoth10«**HB**»	78.73± 1.25	70.63± 1.58	69.85± 1.56	73.07± 4.92	74.19± 2.52	62.12± 3.22	60.12± 3.18	65.48± 7.61
Buhoth158«**IB**»	92.68± 4	82.57± 2.15	61.24± 4.54	78.83± 16.05	88.28± 8.08	74.24± 4.36	51.34± 9.26	71.29± 18.65
Babol113«**JB**»	115.61 ±2.06	108.77 ±5.28	87.06± 1.56	103.81 ±14.91	111.44 ±4.16	100.83 ±10.72	77.69± 3.18	96.65± 17.26
Alraq«**KA**»	122.25 ±1.19	79.59± 2.84	77.46± 1.98	93.1±2 5.27	118.15 ±2.4	71.21± 5.77	67.89± 4.04	85.75± 28.11
Bwru«**LB**»	56.14± 0.44	45.43± 0.87	40.38± 0.99	47.32± 8.05	51.37± 0.88	36.53± 1.76	30.06± 2.03	39.32± 10.93
Baghdad«**MB**»	101.65 ±0.86	83.57± 3.45	65.54± 1.58	83.59± 18.06	97.34± 1.73	75.25± 7	55.73± 3.22	76.11± 20.82
Faris«**NF**»	122.58 ±3.18	118.06 ±2.45	111.89 ±3.87	**117.51 ±5.37**	118.48 ±6.43	110.26 ±4.98	103.02 ±7.88	**110.59 ±7.74**
Tamuz«**OT**»	97.67± 0.76	80.58± 4.3	50.65± 1.5	76.3±2 3.8	93.32± 1.53	72.22± 8.72	40.53± 3.06	68.69± 26.57
Buhoth«**PB**»	132.22 ±0.6	78.59± 5.49	62.23± 4.96	91.01± 36.61	128.22 ±1.2	70.2±1 1.14	52.36± 10.11	83.59± 39.66

Abaá95«**QA**»	114.94 ±4.87	85.89± 5.76	67.53± 2.98	89.45± 23.91	110.77 ±9.84	77.6±1 1.7	57.76± 6.08	82.04± 26.78
Abaá99«**RA**»	140.52 ±0.86	92.19± 1.85	51.97± 1.82	94.89± 44.34	136.6± 1.73	84±3.7 6	41.88± 3.71	87.5±4 7.46
AbóGhuriyb «**SA**»	89.69± 2.62	84.89± 2.58	82.09± 1.43	**85.56± 3.84**	85.26± 5.29	76.59± 5.24	72.62± 2.91	**78.16± 6.47**
Buhoth22«**TB** »	95.67± 2.54	86.88± 3.32	80.44± 1.13	87.67± 7.65	91.3±5. 13	81.98± 6.99	77.69± 4.06	**83.66± 6.96**
Dujela«**UD**»	62.79± 5.72	56.04± 1	52.3±2. 44	**57.04± 5.31**	58.08± 11.55	47.3±2. 03	42.22± 4.98	**49.2±8. 1**
Nemichinovka «**VN**»	48.83± 3.43	34.82± 1.42	29.46± 1.31	37.7±1 0	43.99± 6.93	25.76± 2.89	20.6±2. 03	30.12± 12.29
AbóRaghef «**WA**»	96.67± 2.73	86.22± 1.64	74.81± 0.71	85.9±1 0.93	92.31± 5.51	77.94± 3.33	65.19± 1.45	78.48± 13.57
Means	97.18± 23.81	80.08± 21.13	65.59± 21.92	80.95± 19.98	92.82± 24.05	71.85± 21.51	56.14± 22.5	73.61± 20.29
LSD.05	T=0.73	V=2.86	TXV	4.96	T=1.47	V=5.79	TXV	10.03

Figure 30. Tolerant genotypes (NF, UD, CL, and SA) on P.H. trait.

1.1.54 Evaluation of Genotypes in the No. of tillers for plant(N.T.P)

Salinity Stress, the results for the No. of tillers for plantrevealed a significant interaction between irrigation water salinity and wheat genotypes as shown in Table 14, ANOVA Appendix 4-1, , the least significant difference (LSD) test at the 0.05 significance level and the Z-score values Appendix 0-18. The treatment (15 dS/m) had the lowest average No. of tillers for plant(7.56) and the control treatment (5 dS/m) had the highest average value (9.42). Salinity stress severely affected ion homeostasis in plant tissues leading to enhanced sodium and chloride accumulation. However, salinity stress reduced nitrate (NO_3^-) concentrations in leaves. This ionic imbalance subsequently decreased photosynthetic output and nutrient availability at tiller emergence from the main stem [86,194]. The genotypes (UD, SA, NF, CL, TB and AB) were considered salinity tolerant for this trait because the lowest SD values with the highest mean performance among the varieties Table 14, and confirmed by the positive Z-score values in Figure 31, Figure 32. These tolerant cultivars exhibited a relatively lower reduction in tiller number and yield under saline condition as compared to sensitive genotypes, which is in agreement with the earlier findings [85]. Drought Stress, the results of Table 14 and ANOVA (Appendix 0-2), LSD test at 0.05 level, and Z-score values in Appendix 0-18, showed a significant interaction between

genotypes and levels of drought stress on the number of tillers for plant. Mean comparisons with LSD test showed significant differences among drought treatments. The most severe drought level (30% field capacity) had the lowest mean No. of tillers for plant(6.78) as compared to the control (90% field capacity) and moderate stress (60% field capacity) levels which recorded 9.07 and 7.84 tillers for plant respectively. The genotypes (UD, SA, NF, CL, TB and AB) were identified as drought tolerant for this trait based on the lowest SD values associated with the highest mean values across the varieties Table 14, and confirmed by positive Z-score values Appendix 4-18. These findings are in agreement with previous work on wheat [113] that indicated drought stress limits water and nutrient availability, which restricts cell growth and division, thus decreasing tiller production.

Table 14. Abiotic Stress on No. of tillers for plant in Wheat Varieties (Average for 2022-2024).

	Salinity				**Drought**			
Genotypes	***Control 5 dS/m***	***10 dS/m***	***15 dS/m***	***Means ± SD***	***Control 90% FC***	***60%***	***30%***	***Means ± SD***
Baraka«**AB**»	11.53± 0.11	8.29±0. 18	10.03± 0.4	9.95±1. 62	9.32±0. 28	9.91±0. 12	8.81±0. 2	9.35±0. 55
Wafea«**BW**»	8.21±0. 41	7.63±0. 36	6.75±0. 46	7.53±0. 73	7.56±0. 42	6.63±0. 37	5.58±0. 47	6.59±0. 99
Latefiya«**C**L»	11.1±0. 29	10.58± 0.3	9.77±0. 09	10.48± 0.67	10.85± 0.13	11.93± 0.09	8.54±0. 51	10.44± 1.73
Binekal«**DB**»	9.83±0. 23	10.05± 0.03	8.47±0. 55	9.45±0. 85	8.78±0. 34	7.86±0. 53	7.68±0. 51	8.11±0. 59
Urok«**EU**»	7.67±0. 09	6.1±0.2 8	5.66±0. 31	6.48±1. 06	7.02±0. 09	4.89±0. 23	5.1±0.3	5.67±1. 17
Sham«**FS**»	9.37±0. 53	8.09±0. 17	5.93±0. 12	7.79±1. 74	8.74±0. 54	7.11±0. 17	4.69±0. 14	6.85±2. 04
Fateh«**GF**»	9.97±0. 09	8.52±0. 11	7.45±0. 16	8.65±1. 26	9.35±0. 09	7.55±0. 12	6.27±0. 2	7.73±1. 55
Buhoth10«**HB**»	5.55±0. 22	5.84±0. 49	3.74±0. 31	5.04±1. 14	5.49±0. 41	5.5±0.4 1	2.76±0. 23	4.58±1. 58
Buhoth158«**IB**»	5.02±0. 39	3.55±0. 34	3.28±0. 44	3.95±0. 94	10.91± 0.25	7.52±0. 27	6.96±0. 25	8.46±2. 14
Babol113«**JB**»	9.83±0. 06	8.69±0. 16	7.88±0. 46	8.8±0.9 8	9.22±0. 06	7.72±0. 17	6.96±0. 44	7.97±1. 15

Alraq«**KA**»	8.57±0.34	7.69±0.49	7.25±0.33	7.84±0.67	7.93±0.34	6.7±0.5	6.1±0.37	6.91±0.93
Bwru«**LB**»	9.4±0.33	8.82±0.51	8.47±0.55	8.9±0.47	7.93±0.34	7.38±0.34	6.44±0.22	7.25±0.75
Baghdad«**MB**»	9.1±0.46	7.76±0.29	7.58±0.22	8.15±0.83	8.47±0.47	6.25±0.25	6.82±0.3	7.18±1.15
Faris«**NF**»	11.29±0.38	11.18±0.16	10.86±0.62	11.11±0.23	10.95±0.02	10.93±0.19	10.61±0.33	10.83±0.19
Tamuz«**OT**»	9.37±0.22	8.56±0.17	6.32±0.33	8.08±1.58	8.74±0.22	7.59±0.18	5±0.37	7.11±1.92
Buhoth«**PB**»	8.9±0.38	6.57±0.23	5.2±0.33	6.89±1.87	8.27±0.39	5.54±0.23	3.76±0.34	5.85±2.27
Abaá95«**QA**»	5.45±0.39	4.74±0.41	4.3±0.48	4.83±0.58	4.74±0.4	3.66±0.43	2.83±0.5	3.74±0.96
Abaá99«**RA**»	8.27±0.42	7.26±0.25	6.92±0.38	7.48±0.7	7.63±0.43	6.25±0.26	5.55±0.4	6.48±1.06
AbóGhuriyb «**SA**»	14.05±0.28	13.93±0.79	11.55±0.54	13.18±1.41	11.49±0.19	10.93±0.23	10.71±0.24	11.05±0.4
Buhoth22«**TB**»	11.59±0.5	11.44±0.46	10.39±0.32	11.14±0.65	13.05±0.22	10.63±0.36	10.44±0.06	11.37±1.45
Dujela«**UD**»	11.59±0.46	12.24±0.2	10.89±0.21	11.57±0.67	12.51±0.59	11.38±0.18	11.71±0.1	11.87±0.58
Nemichinovka «**VN**»	11.53±0.11	9.72±0.53	8.18±0.16	9.81±1.68	10.95±0.11	8.78±0.54	6.86±0.17	8.86±2.05
AbóRaghef «**WA**»	9.4±0.29	8.56±0.15	7.02±0.06	8.32±1.21	8.78±0.3	7.59±0.16	5.65±0.06	7.34±1.58
Means	9.42±2.17	8.51±2.4	7.56±2.31	8.5±2.24	9.07±2.04	7.84±2.21	6.78±2.45	7.89±2.15
LSD.05	T=0.1806	V=0.3108	TXV	0.5383	T=0.1370	V=0.2780	TXV	0.4815

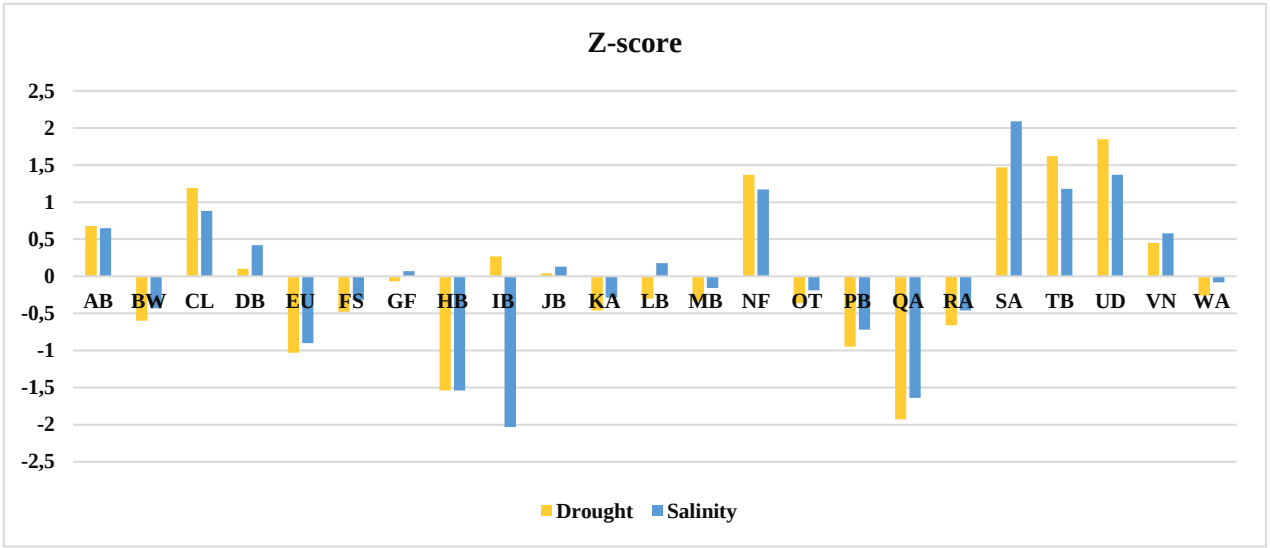


Figure 31. Morphological variation of genotypes in Z-score values on №.T.P.

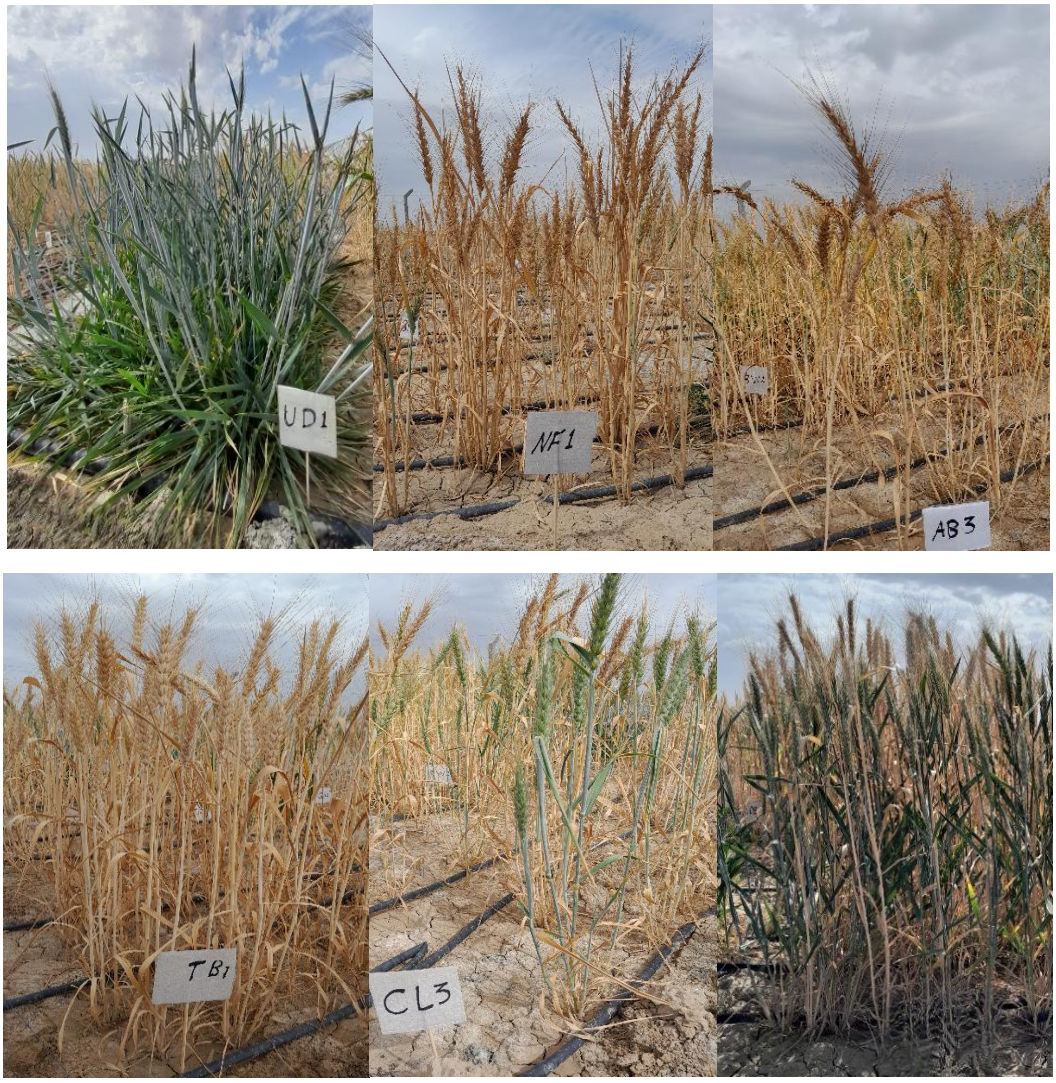


Figure 32. Tolerant genotypes (UD, NF AB, and TB)

1.1.55 Evaluation of Genotypes in the Flag Leaf Area (F.L.A)

Flag leaf area (F.L.A.) was significantly impacted by the salty irrigation water, according to Table 15 and ANOVA (Appendix 4-1). The salinity level of 10 $ds.m^{-1}$ recorded 37.77 cm^2 and the maximum control level of 44.98 cm^2 in the F.L.A trait, while the level of 15 $ds.m^{-1}$ recorded the lowest average of 31.23 cm^2. The difference might be explained by the fact that salt stress during the vegetative stage restricts leaf expansion and photosynthesis [193], and the flag leaf development rate is a significant adaptation feature linked to salinity avoidance [83].

The ANOVA in Appendix 4-2 and Table 15 indicated a significant interaction among varieties and drought treatments, as well as differences in the mean values of the treatments and genotypes based on LSD at the significance level of 0.05. At 30% field capacity level recorded the lowest average value of 29 cm^2 flag leaf area, whereas the control level produced the highest average of 44.12 cm^2 F.L.A., as reported by [113]. Water stress during the vegetative stage limits leaf expansion and photosynthesis [83].

According to the lowest SD value of the highest mean value of the genotypes in Table 15, as well as the positive Z-score values, the genotypes (AB, NF, SA, KA, UD, TB) Figure 34 were selected as salinity and drought-tolerant varieties for that trait.

The Figure 33 indicates that the UD genotype exhibits traits associated with drought resistance, which may be attributed to a waxy film on the leaf surface. The role of wax on the epidermis proved physiologically significant in mitigating water stress [84].

Table 15. Impact of Stress on Flag Leaf Area Trait (cm^2) in Wheat (Average for 2022-2024).

	Salinity				**Drought**			
Genotypes	***control 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means ± SD***	***control 90% FC***	***60%***	***30%***	***Means ± SD***
Baraka«**AB**»	70.47± 4.38	67.89± 0.44	66.31± 0.78	**68.22± 2.1**	69.61± 4.38	66.12± 0.44	63.98± 0.78	**66.57± 2.84**
Wafea«**BW**»	54.2±1. 68	50.46± 0.29	37.03± 0.52	47.23± 9.03	53.34± 1.68	48.69± 0.29	34.69± 0.52	45.58± 9.71
Latefiya«**C**L»	55.39± 3.94	35.6±0. 44	30.82± 0.6	40.6±1 3.02	54.53± 3.94	33.83± 0.44	28.49± 0.6	38.95± 13.75
Binekal«**DB**»	54.71± 5.61	47.39± 0.59	30.82± 0.45	44.31± 12.24	53.85± 5.61	45.62± 0.59	28.49± 0.45	42.66± 12.94
Urok«**EU**»	43.52± 2.84	33.55± 0.29	29.79± 0.45	35.62± 7.1	42.67± 2.84	31.78± 0.29	27.46± 0.45	33.97± 7.84
Sham«**FS**»	37.59± 2.85	26.2±0. 22	23.93± 0.44	29.24± 7.32	36.74± 2.85	24.43± 0.22	21.6±0. 44	27.59± 8.05
Fateh«**GF**»	51.83± 2.77	44.48± 0.61	32.89± 1.18	43.07± 9.55	50.97± 2.77	42.71± 0.61	30.56± 1.18	41.42± 10.27

Buhoth10«**HB**»	53.35± 2.71	45.17± 1.12	44.43± 2.6	47.65± 4.95	52.5±2. 71	43.4±1. 12	42.1±2. 6	46±5.6 6
Buhoth158«**IB**»	50.64± 2.84	43.8±0. 78	28.41± 0.6	40.95± 11.39	49.79± 2.84	42.03± 0.78	26.08± 0.6	39.3±1 2.09
Babol113«**JB**»	57.59± 2.19	37.99± 0.9	27.21± 0.66	40.93± 15.4	56.73± 2.19	36.22± 0.9	24.88± 0.66	39.28± 16.15
Alraq«**KA**»	46.24± 0.45	44.65± 0.69	41.33± 0.6	**44.07± 2.5**	45.38± 0.45	42.89± 0.69	39±0.6	**42.42± 3.21**
Bwru«**LB**»	17.43± 0.53	15.09± 0.44	9.81±0. 9	14.11± 3.9	16.57± 0.53	13.33± 0.44	7.48±0. 9	12.46± 4.61
Baghdad«**MB**»	45.73± 0.51	34.57± 0.39	31.68± 0.88	37.33± 7.42	44.87± 0.51	32.8±0. 39	29.35± 0.88	35.68± 8.15
Faris«**NF**»	61.66± 0.53	60.71± 0.82	58.04± 0.97	**60.14± 1.87**	60.8±0. 53	58.95± 0.82	55.71± 0.97	**58.49± 2.58**
Tamuz«**OT**»	49.46± 0.67	38.33± 0.22	25.14± 0.52	37.64± 12.17	48.6±0. 67	36.56± 0.22	22.81± 0.52	35.99± 12.91
Buhoth«**PB**»	48.95± 0.44	23.81± 0.67	21±0.9	31.25± 15.39	48.09± 0.44	22.04± 0.67	18.67± 0.9	29.6±1 6.1
Abaá95«**QA**»	40.47± 0.73	35.94± 0.88	28.07± 0.64	34.83± 6.28	39.62± 0.73	34.17± 0.88	25.74± 0.64	33.18± 6.99
Abaá99«**RA**»	41.32± 0.91	38.84± 0.69	26.34± 0.66	35.5±8. 03	40.47± 0.91	37.08± 0.69	24.01± 0.66	33.85± 8.69
AbóGhuriyb «**SA**»	47.42± 0.73	45.68± 0.74	42.88± 1.11	**45.33± 2.29**	46.57± 0.73	43.91± 0.74	40.55± 1.11	**43.68± 3.01**
Buhoth22«**TB**»	38.27± 0.39	35.27± 0.54	34.28± 0.52	**35.94± 2.08**	37.42± 0.39	34.17± 0.69	32.63± 0.37	**34.74± 2.44**
Dujela«**UD**»	11.5±1. 11	11.51± 0.14	10.19± 1.03	**11.06± 0.76**	10.64± 1.11	10.08± 0.22	9.54±0. 45	**10.09± 0.55**
Nemichinovka «**VN**»	21.16± 0.37	18.51± 0.22	16.35± 0.23	18.67± 2.41	20.3±0. 37	16.74± 0.22	14.02± 0.23	17.02± 3.15
AbóRaghef «**WA**»	35.56± 0.75	33.38± 0.31	21.52± 0.45	30.15± 7.55	34.7±0. 75	31.61± 0.31	19.19± 0.45	28.5±8. 21
Means	*44.98± 13.88*	*37.77± 13.31*	*31.23± 13.28*	*37.99± 12.87*	*44.12± 13.88*	*36.05± 13.28*	*29±13. 17*	*36.39± 12.8*
LSD.05	*T=0.37 74*	*V=1.36 15*	*TXV*	*2.3581*	*T=0.37 35*	*V=1.35 75*	*TXV*	*2.3513*

Figure 33. The presence of a waxy layer on the surface of the leaves of a tolerant variety

Figure 34. Tolerant genotypes (AB and UD) on F.L.A trait

1.1.56 Evaluation of Genotypes in Grain Weight Per Spike Trait (G.W.S)

The results in Table 16 and ANOVA Appendix 4-1, Z-score values Appendix 4-18 and LSD at the 0.05 level showed a significant interaction between genotypes and

salinity levels on G.W.S., thus indicating a significant effect within salinity levels in G.W.S., where the salinity level of 15 dS m^{-1} recorded the lowest mean value of 2.03 g for this trait, compared with the control salinity level, which recorded a mean value of 2.95 g.

The ANOVA results in Appendix 4-2 and Table 16 showed a significant interaction between varieties and drought treatments. The statistical analysis and LSD at the 5% level demonstrated that the variations between the averages of the varieties and treatments were significant.

The results of the water stress analysis indicated significant differences in the G.W.S. trait, with the 30% field capacity level producing the lowest average of 1.61 g, while the control level at 90% field capacity produced the highest average of 2.76 g.

For the varieties, according to the lowest SD value of the highest average value of the varieties in

Table 16, as well as to the positive Z-score values in Appendix 4-18, the (AB, NF, TB, SA, HB, UD) genotypes were selected as salinity- and drought-tolerant varieties for that trait. Salinity-induced osmotic pressure affected the availability of water and nutrients, particularly during the reproductive and grain-filling stages, resulting in a decrease in grain weight and thus affecting grain yield [195]. [196] reported that grain weight per spike decreased significantly with increasing drought levels from 100% to 25% of field capacity across 24 wheat genotypes. Genetic variation and wheat gene susceptibility to water stress are assessed using the grain yield trait, as shown in Figure 35.

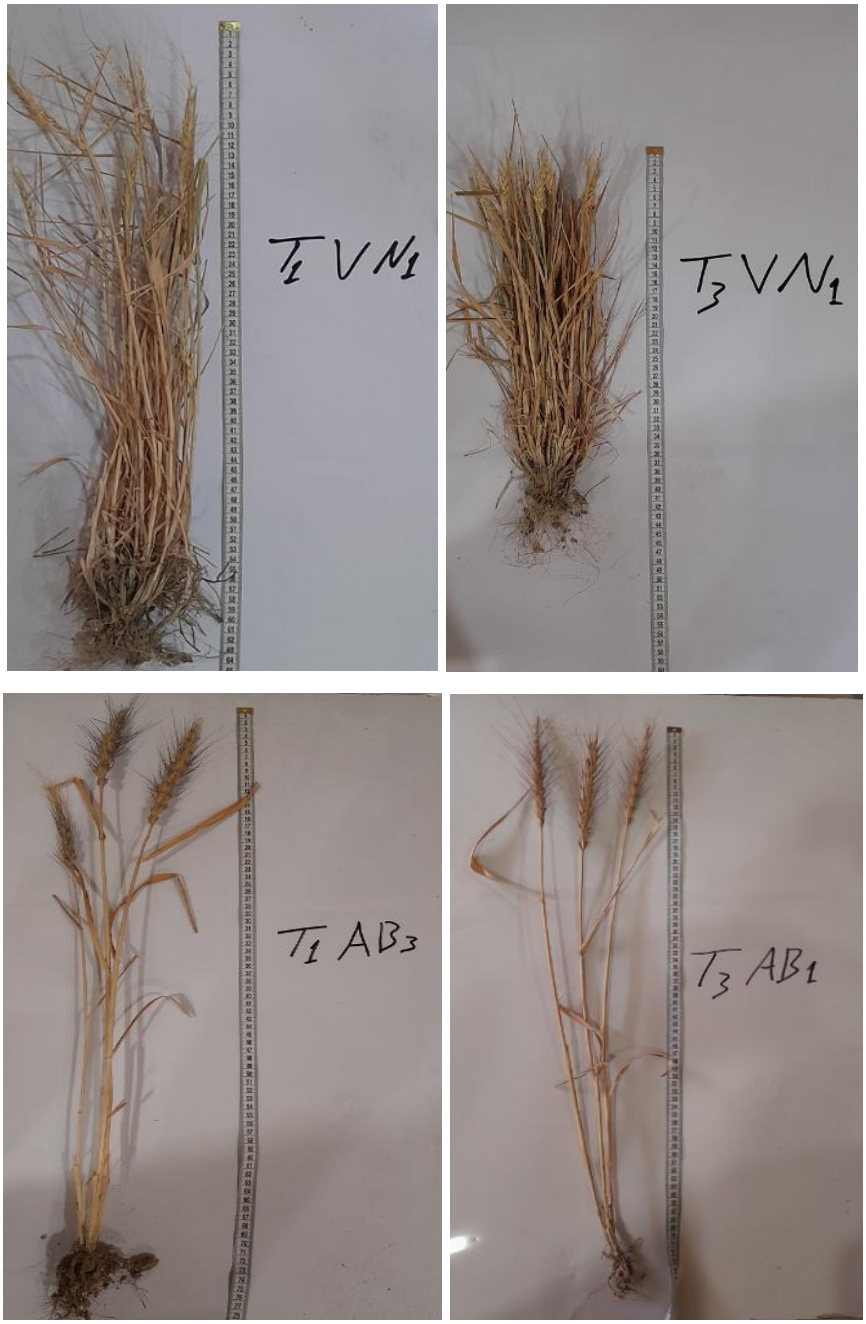


Figure 35. Genetic variation of genotypes (VN and AB) under stress

Table 16. Impact of Stress on Grain Weight (g) Per Spike (Average for 2022-2024).

	Salinity				**Drought**			
Genotypes	***control 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means ± SD***	***control 90% FC***	***60%***	***30%***	***Means ± SD***
Baraka«**AB**»	4.6±0.15	4.88±0.09	3.95±0.07	**4.48±0.48**	4.37±0.08	4.51±0.08	3.54±0.14	**4.14±0.52**
Wafea«**BW**»	3.32±0.29	2.15±0.28	2.68±0.31	2.72±0.59	3.03±0.58	2.32±0.64	1.71±0.58	2.35±0.66
Latefiya«**C**L»	2.8±0.29	2.54±0.28	2.1±0.29	2.48±0.36	2.67±0.46	2.41±0.38	1.99±0.34	2.36±0.34
Binekal«**DB**»	3.48±0.24	1.49±0.19	2.01±0.25	2.33±1.03	3.19±0.48	1.64±0.51	1.04±0.39	1.95±1.11
Urok«**EU**»	3.04±0.29	2.13±0.28	1.68±0.27	2.28±0.69	2.74±0.58	1.76±0.56	1.23±0.55	1.91±0.77
Sham«**FS**»	1.48±0.28	1.93±0.28	1.41±0.43	1.61±0.28	1.63±0.57	1.37±0.46	1.13±0.76	1.38±0.25
Fateh«**GF**»	2.26±0.29	2.72±0.29	1.74±0.29	2.24±0.49	2.42±0.59	1.53±0.29	1.66±0.29	1.87±0.48
Buhoth10«**HB**»	3.59±0.27	2.82±0.28	2.13±0.26	**2.84±0.73**	3.3±0.54	2±0.45	2.14±0.45	**2.48±0.71**
Buhoth158«**IB**»	2.53±0.29	0.98±0.28	1.9±0.29	1.8±0.78	2.23±0.59	1.07±0.48	1.2±0.48	1.5±0.63
Babol113«**JB**»	3.14±0.29	1.3±0.28	1.84±0.27	2.09±0.94	2.84±0.58	1.25±0.44	1.23±0.49	1.78±0.92
Alraq«**KA**»	3.58±0.3	1.29±0.29	2.07±0.27	2.31±1.16	3.29±0.6	1.37±0.44	1.36±0.49	2±1.11
Bwru«**LB**»	1.87±0.17	0.83±0.15	1.39±0.27	1.36±0.52	1.57±0.34	0.7±0.36	0.76±0.38	1.01±0.48
Baghdad«**MB**»	3.18±0.29	1.46±0.23	2.69±0.29	2.44±0.88	2.88±0.59	2.33±0.59	1.01±0.46	2.08±0.96
Faris«**NF**»	3.97±0.29	3.24±0.29	3.59±0.3	**3.6±0.36**	3.68±0.6	3.25±0.6	2.82±0.59	**3.25±0.43**
Tamuz«**OT**»	2.7±0.29	2.19±0.28	1.54±0.24	2.14±0.58	2.4±0.58	1.82±0.58	1.09±0.48	1.77±0.66
Buhoth«**PB**»	2.99±0.29	2.12±0.28	1.29±0.17	2.13±0.85	2.69±0.58	1.23±0.12	1.36±0.12	1.76±0.81
Abaá95«**QA**»	2.89±0.29	2.32±0.28	1.32±0.28	2.18±0.79	2.59±0.59	1.52±0.43	1.49±0.48	1.87±0.63
Abaá99«**RA**»	3.42±0.24	2.61±0.28	1.76±0.3	2.59±0.83	3.13±0.49	2.24±0.58	1.31±0.62	2.23±0.91
AbóGhuriyb «**SA**»	3.27±0.29	3.01±0.29	2.6±0.45	**2.96±0.34**	2.97±0.59	2.35±0.59	2.48±0.59	**2.6±0.33**
Buhoth22«**TB**»	3.65±0.27	3.3±0.22	2.95±0.03	**3.3±0.35**	3.36±0.54	2.94±0.45	2.53±0.07	**2.94±0.41**

Dujela«**UD**»	2.68±0.35	2.35±0.23	1.89±0.15	**2.31±0.4**	2.72±0.44	2.25±0.32	1.93±0.18	**2.3±0.4**
Nemichinovka «**VN**»	1.17±0.05	0.25±0.06	0.74±0.1	0.72±0.46	1.55±0.14	1.68±0.14	0.88±0.02	1.37±0.43
AbóRaghef «**WA**»	2.05±0.29	3.37±0.28	1.54±0.3	2.32±0.95	2.32±0.29	2.45±0.29	1.23±0.5	2±0.67
Means	2.94±0.8	2.23±1.01	2.03±0.75	2.4±0.75	2.76±0.67	2±0.82	1.61±0.7	2.13±0.67
LSD.05	T=0.1142	V=0.2370	TXV	0.4105	T=0.2096	V=0.4190	TXV	0.7257

1.1.57 Evaluation of Genotypes in 1000 Grain- Weight trait (W.1000grs)

The results in Table 17 and ANOVA (Appendix 4-1) based on the LSD at 0.05, showed that there was an interaction between varieties and salinity levels for W.1000grs, where the level (15 $dS.m^{-1}$) recorded the lowest mean value of 33.01 g for this trait, compared with the control salinity level, which recorded a mean value of 51.95 g.

As genotypes, based on the lowest SD values of the highest average in the varieties in Table 17 and the positive Z-score values in Appendix 4-18, the genotypes (UD, TB, SA, NF, HB, CL, AB) Figure 36 that showed tolerance to salinity in that trait were selected. These stresses limit the availability of water and nutrients required for grain filling, resulting in smaller and lighter grains [54,90,92,197].

For drought stress, the analysis of variance (ANOVA) in Appendix 4-2 and the LSD test at 5% in Table 17 showed that there was a significant interaction between the varieties and water stress levels. In Table 17, the 30% field capacity treatment recorded the lowest mean value of 22.41 g, compared with the 60% and 90% field capacity treatments, which recorded mean values of 39.62 g and 45.35 g, respectively. The genotypes (UD, SA, TB, NF, CL and AB) selected as resistant to drought in this attribute were based on the lowest standard deviation values and the highest mean of the varieties in Table 17 and the positive Z-score values in Appendix 4-18. Drought stress significantly reduces grain production by hindering plant growth and disrupting key physiological processes, including photosynthesis [83,142–144].

Table 17. Impact of Stress on 1000-Grain Weight (g) in Genotypes (averages for 2022-2024).

	Salinity				**Drought**			
Genotypes	***control 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means ± SD***	***control 90% FC***	***60%***	***30%***	***Means ± SD***
Baraka«**AB**»	58.47± 0.44	69.14± 1.87	51.14± 1.7	**59.58± 9.05**	51.85± 0.3	62.29± 2.08	42.66± 0.42	**52.27± 9.82**
Wafea«**BW**»	65.28± 2.86	53.72± 3.7	45.52± 2.84	54.84± 9.93	58.26± 2.92	46.13± 3.81	33.94± 2.95	46.11± 12.16
Latefiya«**C**L»	44.68± 1.9	51.73± 2.84	35.75± 1.98	**44.05± 8.01**	44.53± 2.92	36.73± 1.95	27.22± 1.23	**36.16± 8.67**
Binekal«**DB**»	61.29± 5.72	48.25± 4.55	40.22± 4.25	49.92± 10.63	54.19± 5.83	40.49± 4.69	28.42± 4.42	41.04± 12.89
Urok«**EU**»	61.29± 2.86	41.29± 3.41	25.82± 3.11	42.8±17.78	54.19± 2.92	33.32± 3.52	13.44± 3.24	33.65± 20.38
Sham«**FS**»	46.34± 2.86	30.84± 2.84	16.39± 0.42	31.19± 14.98	38.94± 2.92	22.55± 2.93	3.62±0.44	21.7±17.68
Fateh«**GF**»	53.32± 2.29	41.29± 2.84	25.82± 3.11	40.14± 13.78	46.06± 2.33	33.32± 2.93	13.44± 3.24	30.94± 16.44
Buhoth10«**HB**»	55.81± 5.72	48.25± 3.7	43.2±3.4	**49.09± 6.35**	40.16± 3.79	49±5.86	31.52± 3.54	40.23± 8.74
Buhoth158«**IB**»	66.77± 2.86	53.22± 3.84	32.61± 2.63	50.87± 17.2	45.24± 3.94	60.28± 2.93	20.5±2.74	42.01± 20.09
Babol113«**JB**»	55.98± 3.09	48.25± 3.08	29.79± 2.83	44.67± 13.45	40.16± 3.16	49.17± 3.17	17.57± 2.95	35.64± 16.28
Alraq«**KA**»	81.22± 3.14	63.17± 3.41	38.73± 3.4	61.04± 21.33	55.41± 3.5	75.14± 3.22	26.87± 3.54	52.48± 24.27
Bwru«**LB**»	53.65± 4.37	34.82± 3.41	32.77± 3.11	40.41± 11.51	46.4±4.45	26.65± 3.52	20.67± 3.24	31.24± 13.46
Baghdad«**MB**»	64.78± 2.73	52.06± 2.65	37.57± 2.63	51.47± 13.61	57.75± 2.78	44.42± 2.73	25.67± 2.74	42.61± 16.12
Faris«**NF**»	78.07± 2.56	70.8±5.36	62.73± 2.62	**70.53± 7.67**	71.31± 2.61	51.43± 2.71	64.26± 5.55	**62.33± 10.08**
Tamuz«**OT**»	32.39± 3.14	46.26± 2.84	19.36± 1.35	32.67± 13.45	38.94± 2.92	24.09± 3.22	6.72±1.41	23.25± 16.13
Buhoth«**PB**»	37.87± 3.14	51.07± 2.99	19.36± 1.13	36.1±15.93	43.86± 3.07	29.73± 3.22	6.72±1.18	26.77± 18.74
Abaá95«**QA**»	34.38± 2.99	46.43± 2.36	24.33± 2.55	35.05± 11.06	39.11± 2.42	26.14± 3.07	11.89± 2.65	25.71± 13.62
Abaá99«**RA**»	50.33± 2.86	34.82± 2.84	22.34± 2.87	35.83± 14.02	43.01± 2.92	26.65± 2.93	14.99± 1.06	28.22± 14.08
AbóGhuriyb «**SA**»	43.85± 3.14	49.08± 1.64	36.41± 1.66	**43.11± 6.37**	41.82± 1.68	35.88± 3.22	27.91± 0.29	**35.2±6.98**
Buhoth22«**TB**»	42.69± 1.9	49.91± 3.58	36.41± 1.63	**43±6.75**	42.67± 3.67	34.68± 1.95	24.46± 1.7	**33.94± 9.13**

Dujela«**UD**»	37.37±2	42.28±1.42	31.94±2.27	**37.2±5.17**	34.87±1.46	29.22±2.05	19.81±2.36	**27.97±7.61**
Nemichinovka «**VN**»	25.41±0.29	33.33±0.28	15.36±0.07	24.7±9.01	18.81±2.04	24.91±1.47	9.47±2.36	17.73±7.77
AbóRaghef «**WA**»	43.68±3.57	55.71±2.84	35.75±2.83	45.05±10.05	35.42±3.65	49±2.93	23.77±2.95	36.06±12.63
Means	51.95±14.25	48.51±10.32	33.01±11.44	44.49±10.59	45.35±10.47	39.62±13.94	22.41±13.28	35.79±10.72
LSD.05	T=1.6491	V=2.6556	TXV	4.5996	T=1.0616	V=2.7229	TXV	4.7162

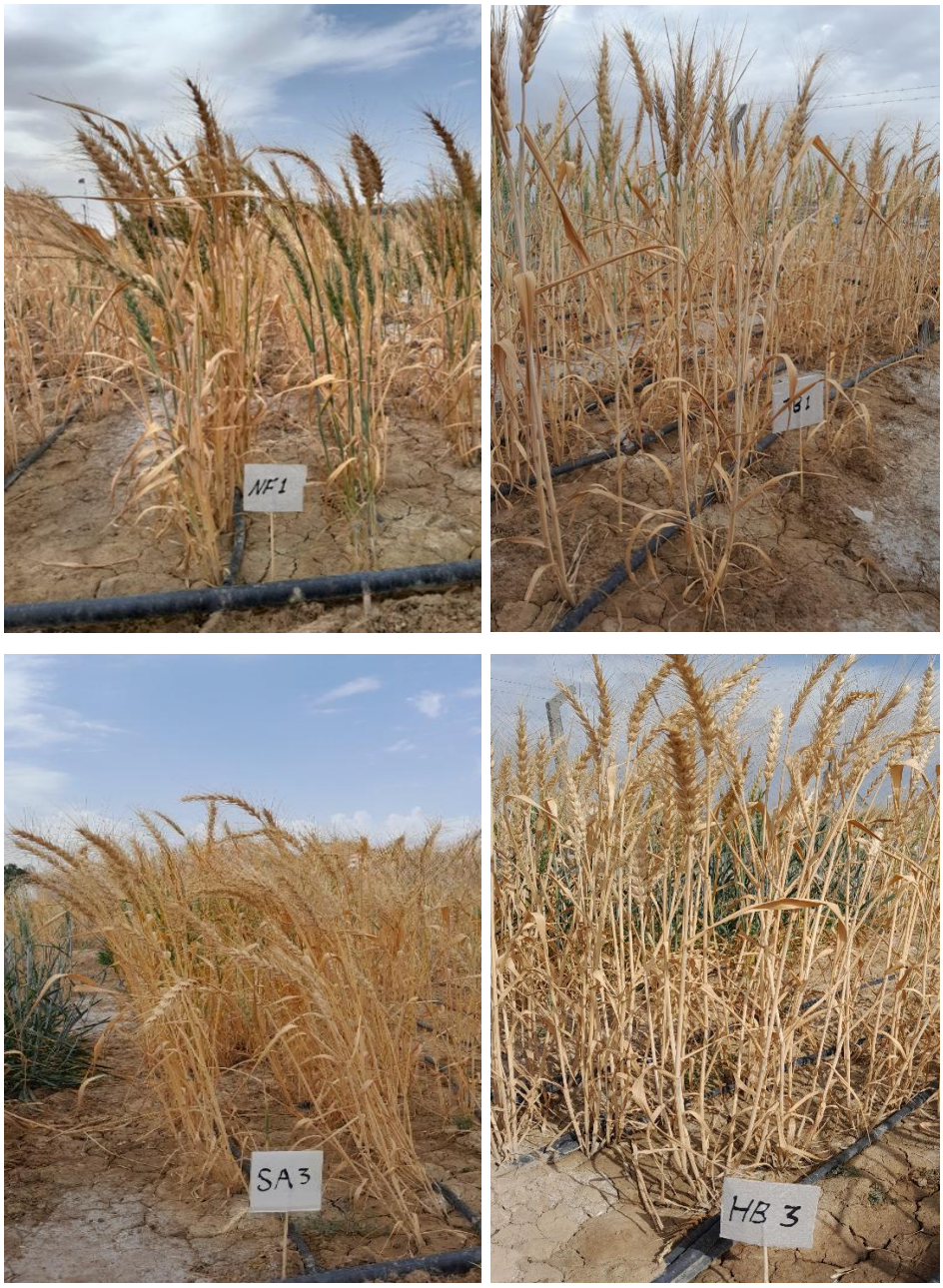


Figure 36. Tolerant genotypes (NF, TB, HB and SA) on W.1000grs trait

1.1.58 Evaluation of Genotypes in Organic mass for planttrait (Bio.Pl)

The ANOVA results in Appendix 4-1 and Table 18 indicated significant variation in organic mass for plant trait (Bio.Pl) at a significance level of 0.05. The 15 $dS.m^{-1}$ level recorded the trait's lowest average (62.81g per plant) compared to the control and 10 $dS.m^{-1}$ levels, where the 5 $dS.m^{-1}$ level produced the highest average of 110.13 g per plant. Salinity affects a number of agronomic characteristics, including flag leaf area, tiller count, and plant height, which together define the biological yield index of the plant [198].

For the varieties in Table 18, the SA variety recorded the maximum average (125.1g), while FS variety had the lowest average of 60 g per plant. The interaction between genotypes and salinity levels of irrigation water was significant at level of 0.05, with SA genotype recording the highest value in interaction (144.7 g) for the Bio. Pl trait.

Through the lowest SD values of the highest mean in the varieties in Table 18 and the positive Z-score values in Appendix 4-18, the genotypes (SA, UD, TB, NF, CL) that showed tolerance to salinity stress in that trait were selected. Studies have reported that wheat genotypes respond differently to salinity, with substantial variations in biomass and grain yield under salt stress [94]. Another study showed that the degree of yield loss varies according to the genotype and plant growth stage [97].

As drought stress, the ANOVA results in Appendix 4-2 and Table 18 revealed that the interaction was significant at a level of 5% for the Bio.Pl trait. The highest value under this interaction was observed for the UD genotype (135.9 g per plant). The LSD test for drought treatments also indicated significant differences in the drought treatments' averages, where 30% of field capacity produced the lowest average biomass (49.68 g per plant) compared with the control (90%) and 60% field capacity levels. The control level recorded the highest average of 102.21 g per plant. Biomass accumulation during early vegetative stages is considered a promising indicator for improving drought tolerance in wheat [96]. According to the lowest SD values of the

highest mean in the genotypes in Table 18 and the positive Z-score values in Appendix 4-18, the genotypes (UD, TB, SA, NF, CL) showed tolerance to salinity stress in this trait.

Table 18. Influence of Stress on Genotypes in Organic mass for plant Trait (g) (Average for 2022-2024).

	Salinity				***Drought***			
Genotypes	***control 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means ± SD***	***control 90% FC***	***60%***	***30%***	***Means ± SD***
Baraka«**AB**»	103.31 ±0.92	82.9±0.43	65.54± 1.23	83.92± 18.91	88.53± 0.35	73.94± 0.78	56.08± 0.54	72.85± 16.25
Wafea«**BW**»	116.93 ±0.33	88.54± 0.85	59.58± 0.75	88.35± 28.68	103.71 ±2.28	79.11± 0.74	59.26± 1.48	80.69± 22.27
Latefiya«**C**L»	135.54 ±0.57	97.5±2.22	91.03± 1.4	**108.02 ±24.05**	116.92 ±0.58	94.83± 4.1	81.65± 5.03	**97.8±17.82**
Binekal«**DB**»	108.63 ±0.57	72.62± 1.24	42.04± 0.71	74.43± 33.33	88.79± 0.34	79.11± 1.95	35.14± 2.57	67.68± 28.59
Urok«**EU**»	105.31 ±0.17	95.51± 2.43	55.28± 1.93	85.36± 26.51	109.81 ±1.05	81.5±0.78	38.24± 1.47	76.52± 36.04
Sham«**FS**»	85.04± 0.72	54.72± 1.3	39.39± 1.73	59.72± 23.23	74.22± 2.39	58.95± 1.06	29.63± 1.03	54.27± 22.66
Fateh«**GF**»	128.89 ±1.44	97.83± 0.43	55.94± 0.82	94.22± 36.61	83.37± 0.58	74.32± 1.06	29.29± 0.9	62.33± 28.97
Buhoth10«**HB**»	126.57 ±0.29	78.59± 1.03	66.2±0.82	90.46± 31.88	92.52± 4.01	68.86± 1.95	31.01± 4.54	64.13± 31.03
Buhoth158«**IB**»	119.59 ±1.31	84.56± 0.57	70.51± 1.13	91.55± 25.28	85.41± 1.05	56.21± 1.18	39.28± 1.35	60.3±23.33
Babol113«**JB**»	94.68± 1.03	66.99± 1.15	51.64± 1.3	71.1±21.81	99.64± 0.58	62.02± 1.28	29.29± 0.74	63.65± 35.21
Alraq«**KA**»	83.71± 0.57	68.64± 1.03	47.01± 0.87	66.45± 18.45	94.56± 0.58	73.98± 0.74	43.41± 0.59	70.65± 25.73
Bwru«**LB**»	113.61 ±0.76	75.94± 1.15	44.03± 0.43	77.86± 34.83	120.31 ±1.47	87.99± 0.45	43.76± 0.85	84.02± 38.43
Baghdad«**MB**»	98±0.33	79.26± 1.89	37.74± 2.47	71.66± 30.84	104.72 ±0.77	65.44± 1.18	31.35± 0.45	67.17± 36.72
Faris«**NF**»	127.56 ±1.03	109.43 ±0.75	95.33± 1.72	**110.78 ±16.16**	118.96 ±1.05	99.95± 0.78	79.59± 1.79	**99.5±19.69**
Tamuz«**OT**»	74.75± 2.34	63.67± 1.03	57.27± 0.99	65.23± 8.84	81±0.89	55.19± 0.85	27.56± 0.9	54.58± 26.72
Buhoth«**PB**»	87.37± 0.87	64±0.82	35.42± 0.87	62.26± 26.02	78.63± 0.73	45.62± 1.34	26.53± 1.8	50.26± 26.36
Abaá95«**QA**»	118.6± 1.03	91.53± 0.75	50.65± 1.42	86.92± 34.21	117.94 ±0.29	68.17± 1.06	54.44± 0.85	80.18± 33.41

Abaá99«**RA**»	97.67± 0.57	80.25± 0.72	60.58± 0.57	79.5±1 8.56	96.25± 0.17	85.6±2. 5	43.07± 2.01	74.97± 28.14
AbóGhuriyb «**SA**»	144.17 ±0.44	122.03 ±4.61	107.25 ±1.86	**124.49 ±18.58**	124.04 ±0.87	96.53± 2.22	78.21± 1.19	**99.6±2 3.07**
Buhoth22«**TB**»	120.26 ±0.87	105.12 ±2.17	86.73± 1.71	104.04 ±16.79	116.59 ±0.89	98.59± 2.24	88.2±1. 78	**101.12 ±14.36**
Dujela«**UD**»	137.53 ±2.54	108.11 ±5.22	99.31± 1.02	**114.98 ±20.02**	135.9± 0.45	127.29 ±4.75	91.3±1. 19	**118.16 ±23.66**
Nemichinovka «**VN**»	112.62 ±2.23	89.2±0. 72	64.22± 3.41	88.68± 24.2	108.11 ±0.34	78.42± 0.88	47.55± 0.78	78.03± 30.29
AbóRaghef «**WA**»	92.68± 3.93	73.29± 0.59	61.9±1. 28	75.96± 15.56	110.82 ±1.34	74.32± 0.59	58.92± 1.18	81.35± 26.66
Means	*110.13 ±18.86*	*84.79± 16.91*	*62.81± 20.45*	*85.91± 17.48*	*102.21 ±16.59*	*77.65± 18.08*	*49.68± 21*	*76.51± 17.36*
LSD.05	*T=0.95*	*V=1.43*	*TXV*	*2.48*	*T=0.82*	*V=1.55*	*TXV*	*2.69*

1.1.59 Evaluation of Genotypes in Yield Trait (Y)

The results of ANOVA (Appendix 4-3 and Table 19) indicated significant variation between treatment levels in grain yield (t/ha) at a significance level of 0.05. The salinity level of 15 dS.m^{-1} produced the lowest average yield (3.86 t.ha^{-1}), while the control (5 dS.m^{-1}) level produced the highest average of 6.86 t.ha^{-1}. For genotypes, in Table 19 the varieties (SA, UD, NF, TB, CL, AB) gave the highest average of 8.32, 8.05, 8.03, 6.72, 6.37, and 6.18 t.ha^{-1}, while the lowest average was 3.25 t.ha^{-1} for the FS variety. Generally, the correlation between yield and salinity concentration follows a negative linear trend, as established by linear regression analysis [95].

The ANOVA results (Appendix 4-3 and Table 19) and LSD test at 0.05 indicated a significant interaction between drought treatments and genotypes. Table 19 further shows significant variation among the varieties affected by irrigation water scarcity. 30% FC treatment produced the lowest average grain yield of 3.48 t.ha^{-1}, compared with the control (90% FC), which recorded the maximum average (6.32 t.ha^{-1}), and the 60% field capacity treatment, which yielded 4.77 t.ha^{-1}. As presented in Table 19, (UD, TB, SA, NF, CL, AB) genotypes yielded the highest average yield of (7.77, 7.5, 7.49, 6.38, 6.06, 5.69 t.ha^{-1}), while the PB genotype recorded the lowest average yield of 2.7 t.ha^{-1}. Table 19 further shows that the SD values for the genotypes

under drought conditions indicated that the FS genotype had the highest SD value (1.7), while the UD genotype had the lowest value (0.91). Yield reductions caused by salinity and drought stress are primarily attributed to a decrease in spike number per plant and decreased grain number per spike [199]. Overall, these stress factors significantly limit wheat productivity by reducing stem growth, development and above-ground dry weight [200]. Tolerant wheat varieties generally show lesser reductions in tiller number and yield [85].

Table 19. Evaluation of Genotypes under the Influence of Stress in the Grain Yield Trait (t/ha) (Average for three years)

	Salinity				***Drought***			
Genotypes	***control 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means ± SD***	***control 90% FC***	***60%***	***30%***	***Means ± SD***
Baraka«**AB**»	7.32±0.06	5.97±0.04	5.25±0.01	**6.18±1.05**	7.21±0.06	5.48±0.04	4.37±0.01	5.69±1.43
Wafea«**BW**»	7.4±0.04	5.03±0.06	3.68±0.05	5.37±1.89	6.52±0.06	5±0.24	3.62±0.08	5.04±1.45
Latefiya«**C**L»	7.58±0.06	6.14±0.23	5.38±0.07	**6.37±1.12**	7.55±0.15	5.81±0.19	4.83±0.1	6.06±1.38
Binekal«**DB**»	6.01±0.06	4.11±0.08	2.39±0.04	4.17±1.81	5.75±0.03	4.2±0.07	2.73±0.02	4.23±1.51
Urok«**EU**»	6.96±0.08	5.05±0.1	3.21±0.06	5.08±1.87	5.97±0.12	4.98±0.06	3.53±0.14	4.82±1.23
Sham«**FS**»	5.26±0.04	2.81±0.06	1.66±0.09	**3.24±1.84**	4.51±0.04	2.73±0.05	1.11±0.08	**2.78±1.7**
Fateh«**GF**»	7.68±0.1	6.15±0.07	4.62±0.04	6.15±1.53	5±0.06	3.65±0.09	1.86±0.04	3.5±1.57
Buhoth10«**HB**»	7.03±0.06	5.47±0.25	4.04±0.09	5.51±1.49	5.33±0.06	3.67±0.08	2.24±0.04	3.75±1.55
Buhoth158«**IB**»	7.6±0.03	5.1±0.07	4.44±0.07	5.72±1.67	5.24±0.04	3.12±0.04	2.07±0.06	3.48±1.61
Babol113«**JB**»	5.49±0.06	4.08±0.09	2.19±0.04	3.92±1.66	5.37±0.08	3.65±0.12	2.21±0.05	3.74±1.58
Alraq«**KA**»	5.74±0.04	3.53±0.04	2.41±0.06	3.89±1.69	5.65±0.06	4.95±0.03	2.57±0.06	4.39±1.62
Bwru«**LB**»	6.38±0.03	4.65±0.07	3±0.02	4.68±1.69	7.05±0.09	5.65±0.07	4.3±0.03	5.66±1.38
Baghdad«**MB**»	6.03±0.06	4.11±0.08	2.36±0.04	4.17±1.84	5.33±0.09	3.84±0.06	2.18±0.06	3.79±1.58
Faris«**NF**»	9.03±0.25	8.02±0.05	7.05±0.06	**8.03±0.99**	7.6±0.06	6.21±0.07	5.32±0.07	**6.38±1.15**

Tamuz«**OT**»	5.19±0.07	3.56±0.04	2.08±0.06	3.61±1.55	4.65±0.07	3.14±0.04	1.81±0.06	3.2±1.42
Buhoth«**PB**»	5.09±0.04	3.14±0.05	1.74±0.09	3.32±1.68	4.48±0.07	2.42±0.06	1.21±0.09	2.7±1.65
Abaá95«**QA**»	6.61±0.12	5.45±0.06	3.8±0.14	5.28±1.41	6.41±0.03	4.95±0.12	3.49±0.05	4.95±1.46
Abaá99«**RA**»	6.4±0.06	5.42±0.03	2.66±0.06	4.83±1.94	6.26±0.08	4.59±0.1	3.03±0.05	4.63±1.61
AbóGhuriyb «**SA**»	9.21±0.05	8.29±0.06	7.45±0.01	**8.32±0.88**	8.51±0.24	7.47±0.05	6.48±0.06	**7.49±1.01**
Buhoth22«**TB**»	7.9±0.05	6.51±0.25	5.75±0.12	**6.72±1.09**	8.56±0.06	7.32±0.14	6.64±0.04	**7.51±0.97**
Dujela«**UD**»	9.1±0.06	7.86±0.14	7.2±0.05	**8.05±0.96**	8.69±0.04	7.73±0.06	6.87±0.01	**7.77±0.91**
Nemichinovka «**VN**»	6.86±0.03	5.42±0.13	3.96±0.05	5.41±1.45	6.69±0.04	4.57±0.06	3.47±0.05	4.91±1.64
AbóRaghef «**WA**»	5.93±0.09	4.28±0.07	2.4±0.06	4.2±1.77	7.07±0.03	4.64±0.07	4.03±0.07	5.25±1.61
Means	*6.86±1.23*	*5.22±1.5*	*3.86±1.78*	*5.31±1.48*	*6.32±1.29*	*4.77±1.46*	*3.48±1.68*	*4.86±1.47*
LSD.05	*T=0.039*	*V=0.0802*	*TXV*	*0.1389*	*T=0.0417*	*V=0.0767*	*TXV*	*0.1328*

1.1.60 Morphological Traits of Genotypes During the 2022-2024 Seasons

The results in the ANOVA tables (Appendix 4-1 and Appendix 4-2) and the results in Table 20 and Table 22 indicated that, at a significance (0.05), there were no varieties between the years of cultivation (2022-2024) for most morphological traits affected by salinity and drought stress. The consistency of the results of the response of the genotypes to salinity and drought stress indicates the genetic stability of the genotypes, and the methods used in the study methodology were of great importance in achieving the study objectives.

This is due to several interconnected reasons. The efficiency of the drip irrigation system method (85%), as mentioned [159], used in the experiment, resulted in an accurate distribution of water. Soil analysis using the pressure plate method before planting contributed to determining soil moisture content and calculating the necessary water requirements in the study of water stress based on irrigation levels. Irrigation was applied when the soil moisture content reached 90%, 60%, and 30% of

field capacity thresholds. At each threshold, water was added to bring the soil moisture to 100% of field capacity in Irrigation was applied when the soil moisture content reached 90%, 60% and 30% of field capacity thresholds. At each threshold, water was added to bring the soil moisture to 100% of field capacity Irrigation was applied when the soil moisture content reached 90%, 60% and 30% of field capacity thresholds. At each threshold, water was added to bring the soil moisture to 100% of field capacity (Table 6). The similarity of climatic conditions during the growing seasons, especially the similarity of rainfall and temperature in Table 4, contributed to reducing the variation in external environmental stress.

In Table 20 , Table 21,

Table 22 and

Table 23 the genotypes SA, NF, UD, TB, CL, and AB had the highest averages and low values in SD and positive Z-score values on morphological traits under salinity and drought stress in the studied traits.

Table 20. Morphological (Biomass per plant, W.1000 and yield) Traits of Genotypes Affected by Drought Stress during the 2022-2024 Seasons

Drought stress												
	Biomass.(g.pl-1)				***W.1000 (g)***				***yield (t/ha)***			
Genotypes	**2022**	**2023**	**2024**	**Mean**	**2022**	**2023**	**2024**	**Mean**	**2022**	**2023**	**2024**	**Mean**
Baraka«**AB**»	74.22	71.8	72.5	72.9	53.3	51.5	52	52.3	5.79	5.56	5.71	5.69
Wafea«**BW**»	82.19	78.8	81.1	80.7	47	45	46.3	46.1	5.14	4.93	5.07	5.04
Latefiya«**C**L»	99.66	95.5	98.3	97.8	36.8	35.3	36.3	36.2	6.18	5.92	6.09	6.06
Binekal«**DB**»	68.9	66.2	68	67.7	41.8	40.1	41.2	41	4.31	4.13	4.25	4.23
Urok«**EU**»	77.87	74.8	76.8	76.5	34.2	32.9	33.8	33.7	4.92	4.71	4.85	4.83
Sham«**FS**»	55.24	53.1	54.5	54.3	22.1	21.3	21.8	21.7	2.83	2.73	2.80	2.79
Fateh«**GF**»	63.44	60.9	62.6	62.3	31.5	30.3	31.1	30.9	3.56	3.42	3.52	3.50

Buhoth10«**HB**»	65.26	62.7	64.4	64.1	41	39.3	40.4	40.2	3.81	3.66	3.76	3.75
Buhoth158«**IB**»	61.39	58.9	60.6	60.3	42.8	41	42.2	42	3.54	3.40	3.49	3.48
Babol113«**JB**»	64.76	62.3	63.9	63.7	36.3	34.8	35.8	35.6	3.81	3.66	3.76	3.74
Alraq«**KA**»	71.94	69.1	71	70.7	53.5	51.3	52.7	52.5	4.47	4.29	4.41	4.39
Bwru«**LB**»	85.52	82.2	84.4	84	31.8	30.5	31.4	31.2	5.77	5.53	5.69	5.67
Baghdad«**MB**»	68.34	65.7	67.5	67.2	43.4	41.7	42.8	42.6	3.85	3.70	3.80	3.79
Faris«**NF**»	101.38	97.2	100	99.5	63.6	60.8	62.6	62.3	6.50	6.23	6.41	6.38
Tamuz«**OT**»	55.55	53.4	54.8	54.6	23.6	22.8	23.3	23.3	3.26	3.13	3.22	3.20
Buhoth«**PB**»	51.14	49.2	50.5	50.3	27.2	26.2	26.9	26.8	2.75	2.64	2.71	2.70
Abaá95«**QA**»	81.63	78.4	80.5	80.2	26.2	25.2	25.8	25.7	5.04	4.84	4.97	4.95
Abaá99«**RA**»	76.34	73.3	75.3	75	28.7	25.9	28.3	27.7	4.71	4.52	4.65	4.63
AbóGhuriyb «**SA**»	101.47	97.3	100	99.6	35.9	34.4	35.4	35.2	7.63	7.31	7.52	7.49
Buhoth22«**TB**»	103.06	98.7	101.6	101.1	34.6	33.2	34.1	33.9	7.65	7.33	7.54	7.51
Dujela«**UD**»	120.41	115.4	118.7	118.2	28.5	27.3	28.1	28	7.92	7.58	7.80	7.77
Nemichinovka «**VN**»	79.44	76.3	78.4	78	18.1	17.3	17.8	17.7	5.00	4.80	4.93	4.91
AbóRaghef «**WA**»	82.85	79.5	81.7	81.4	36.8	35.2	36.2	36.1	5.34	5.13	5.27	5.25
Means	*77.91*	*74.8*	*76.8*	*76.5*	*36.5*	*34.9*	*35.9*	*35.8*	*4.95*	*4.75*	*4.88*	*4.86*
LSD.05	*2.77*	*5.28*	*5.46*	*1.55*	*1.92*	*9.4*	*9.6*	*2.72*	*0.07*	*0.26*	*0.27*	*0.08*

Table 21. Morphological (Flag leaf area, plant height and Tillers) Traits of Genotypes Affected by Drought Stress during the 2022-2024 Seasons

Drought stress												
	Flag leaf (cm2)				***P.H (cm)***				***Tillers (N0.Pl-1)***			
Genotypes	**2022**	**2023**	**2024**	**Mean**	**2022**	**2023**	**2024**	**Mean**	**2022**	**2023**	**2024**	**Mean**
Baraka«**AB**»	67.9	65	66.9	66.6	85.6	84.7	83.2	84.5	9.5	9.2	9.3	9.3
Wafea«**BW**»	46.4	44.5	45.8	45.6	69.5	67.6	67.6	68.2	6.7	6.4	6.6	6.6
Latefiya«**C**L»	39.7	38.1	39.1	39	105.8	102.7	102.7	103.7	10.6	10.2	10.5	10.4
Binekal«**DB**»	43.4	41.7	42.8	42.7	81.8	78	79.5	79.7	8.3	7.9	8.1	8.1
Urok«**EU**»	34.6	33.2	34.1	34	50.5	49.3	49.3	49.7	5.8	5.5	5.7	5.7
Sham«**FS**»	28.1	27	27.7	27.6	42	40.8	40.8	41.2	7	6.7	6.9	6.8
Fateh«**GF**»	42.2	40.5	41.6	41.4	80.7	78.4	78.4	79.2	7.9	7.5	7.8	7.7
Buhoth10«**HB**»	46.9	44.9	46.2	46	66.7	64.8	64.8	65.5	4.7	4.5	4.6	4.6
Buhoth158«**IB**»	40	38.4	39.5	39.3	72.6	70.6	70.6	71.3	8.6	8.3	8.5	8.5
Babol113«**JB**»	40	38.4	39.5	39.3	98.5	95.7	95.7	96.7	8.1	7.8	8	8
Alraq«**KA**»	43.3	41.4	42.6	42.4	87.3	85	85	85.8	7	6.7	6.9	6.9
Bwru«**LB**»	12.7	12.2	12.5	12.5	40.1	39	39	39.3	7.4	7.1	7.3	7.3
Baghdad«**MB**»	36.4	34.8	35.8	35.7	77.5	75.4	75.4	76.1	7.3	7	7.2	7.2
Faris«**NF**»	59.6	57.1	58.8	58.5	112.7	109.5	109.5	110.6	11	10.6	10.9	10.8
Tamuz«**OT**»	36.7	35.2	36.2	36	69.9	68.1	68.1	68.7	7.2	6.9	7.1	7.1
Buhoth«**PB**»	30.1	29	29.7	29.6	85.1	82.8	82.8	83.6	6	5.7	5.9	5.9
Abaá95«**QA**»	33.8	32.4	33.3	33.2	83.6	81.3	81.3	82	3.8	3.7	3.8	3.7
Abaá99«**RA**»	34.5	33.1	34	33.9	89	86.7	86.7	87.5	6.6	6.3	6.5	6.5
AbóGhuriyb «**SA**»	44.5	42.6	43.9	43.7	79.7	77.4	77.4	78.2	11.3	10.8	11.1	11
Buhoth22«**TB**»	35.4	33.9	34.9	34.7	85.3	82.8	82.8	83.7	11.6	11.1	11.4	11.4
Dujela«**UD**»	10.3	9.8	10.1	10.1	50.1	48.7	48.7	49.2	12.1	11.6	11.9	11.9
Nemichinovka «**VN**»	17.4	16.6	17.1	17	30.7	31.1	28.6	30.1	9	8.7	8.9	8.9

AbóRaghef «**WA**»	29	27.8	28.6	28.5	80	77.7	77.7	78.5	7.5	7.2	7.4	7.3
Means	*37.1*	*35.5*	*36.6*	*36.4*	*75*	*73*	*72.9*	*73.6*	*8.1*	*7.7*	*7.9*	*7.9*
LSD.05	*0.65*	*4.6*	*4.75*	*1.36*	*2.73*	*10*	*10.04*	*5.79*	*0.24*	*0.9*	*0.98*	*0.28*

Table 22. Morphological (Biomass per plant, W.1000 and yield) Traits of Genotypes Affected by Salinity Stress for the 2022-2024 Seasons

Salinity stress												
	Biomass.(g.pl-1)				***W.1000 (g)***				***yield (t/ha)***			
Genotypes	**2022**	**2023**	**2024**	**Mean**	**2022**	**2023**	**2024**	**Mean**	**2022**	**2023**	**2024**	**Mean**
Baraka«**AB**»	85.5	84.3	81.9	83.9	60.8	59.9	58.1	59.6	6.30	6.03	6.21	6.18
Wafea«**BW**»	89.98	88.8	86.3	88.4	55.9	55.1	53.5	54.8	5.47	5.25	5.40	5.37
Latefiya«**C**L»	110.06	108.6	105.5	108	44.9	44.3	43	44.1	6.49	6.40	6.21	6.37
Binekal«**DB**»	75.76	74.8	72.8	74.4	50.9	50.2	48.7	49.9	4.24	4.07	4.19	4.17
Urok«**EU**»	86.94	85.8	83.4	85.4	43.6	43	41.8	42.8	5.17	4.96	5.10	5.08
Sham«**FS**»	60.8	60	58.4	59.7	31.7	31.3	30.5	31.2	3.30	3.09	3.34	3.25
Fateh«**GF**»	95.93	94.7	92.1	94.2	40.9	40.3	39.2	40.1	6.27	6.00	6.18	6.15
Buhoth10«**HB**»	92.11	90.9	88.4	90.5	50	49.3	47.9	49.1	5.62	5.38	5.54	5.51
Buhoth158«**IB**»	93.26	92	89.4	91.6	51.8	51.1	49.7	50.9	5.82	5.58	5.75	5.72
Babol113«**JB**»	72.41	71.4	69.4	71.1	45.5	44.9	43.6	44.7	3.99	3.83	3.94	3.92
Alraq«**KA**»	67.69	66.8	64.9	66.5	62.2	61.3	59.6	61	3.96	3.80	3.91	3.89
Bwru«**LB**»	79.25	78.2	76.1	77.9	41.2	40.6	39.5	40.4	4.76	4.57	4.70	4.68
Baghdad«**MB**»	72.95	72	70	71.7	52.4	51.7	50.3	51.5	4.24	4.07	4.19	4.17
Faris«**NF**»	112.9	111.3	108.1	110.8	71.9	70.9	68.8	70.5	8.19	7.84	8.08	8.03
Tamuz«**OT**»	66.48	65.6	63.7	65.2	33.3	32.8	31.9	32.7	3.68	3.53	3.63	3.61
Buhoth«**PB**»	63.38	62.6	60.9	62.3	36.8	36.3	35.3	36.1	3.38	3.25	3.34	3.32
Abaá95«**QA**»	88.49	87.3	84.9	86.9	35.7	35.2	34.2	35	5.38	5.16	5.31	5.29
Abaá99«**RA**»	80.99	79.9	77.6	79.5	36.5	36	35	35.8	4.92	4.72	4.85	4.83
AbóGhuriyb «**SA**»	126.87	125.1	121.5	124.5	44	43.3	42.1	43.1	8.48	8.12	8.36	8.32
Buhoth22«**TB**»	106.02	104.6	101.5	104	43.8	43.2	42	43	6.85	6.72	6.59	6.72

Dujela«**UD**»	117.17	115.6	112.2	115	37.9	37.4	36.3	37.2	8.21	7.86	8.10	8.05
Nemichinovka «**VN**»	90.33	89.1	86.6	88.7	25.2	24.8	24.1	24.7	5.51	5.29	5.44	5.41
AbóRaghef «**WA**»	77.39	76.3	74.2	76	45.9	45.3	44	45.1	4.28	4.11	4.22	4.20
Means	*87.51*	*86.3*	*83.9*	*85.9*	*45.3*	*44.7*	*43.4*	*44.5*	*5.41*	*5.20*	*5.33*	*5.31*
LSD.05	*2.57*	*5.05*	*4.9*	*1.43*	*4.73*	*9.33*	*9.06*	*2.66*	*0.144*	*0.257*	*0.261*	*0.081*

Table 23. Morphological (Flag leaf area, P.H and Tillers) Traits of Genotypes Affected by Salinity Stress for the 2022-2024 Seasons

Salinity stress												
	Flag leaf (cm2)				***P.H (cm)***				***Tillers (N0.Pl^{-1})***			
Genotypes	***2022***	***2023***	***2024***	***Mean***	***2022***	***2023***	***2024***	***Mean***	***2022***	***2023***	***2024***	***Mean***
Baraka«**AB**»	69.6	68.2	66.9	68.2	93.1	91.8	89	91.3	10.1	10	9.7	9.9
Wafea«**BW**»	48.1	47.8	45.8	47.2	77.2	76.2	74.1	75.9	7.7	7.6	7.3	7.5
Latefiya«**C**L»	41.4	41.3	39.1	40.6	112.9	111.3	108	110.8	10.7	10.5	10.2	10.5
Binekal«**DB**»	45.1	44.9	42.8	44.3	89.3	88.1	85.6	87.7	9.6	9.5	9.2	9.5
Urok«**EU**»	36.3	36.4	34.1	35.6	58.6	57.9	56.4	57.6	6.6	6.5	6.3	6.5
Sham«**FS**»	29.8	30.2	27.7	29.2	50.1	49.4	48.1	49.2	7.9	7.8	7.6	7.8
Fateh«**GF**»	43.9	43.7	41.6	43.1	88.2	87	84.5	86.6	8.8	8.7	8.4	8.6
Buhoth10«**HB**»	48.6	48.2	46.2	47.7	74.5	73.4	71.3	73.1	5.1	5.1	4.9	5
Buhoth158«**IB**»	41.7	41.7	39.5	41	80.3	79.2	77	78.8	4	4	3.9	3.9
Babol113«**JB**»	41.7	41.7	39.5	40.9	105.8	104.3	101.3	103.8	9	8.8	8.6	8.8
Alraq«**KA**»	44.9	44.7	42.6	44.1	94.8	93.6	90.9	93.1	8	7.9	7.7	7.8
Bwru«**LB**»	14.4	15.4	12.5	14.1	48.2	47.6	46.2	47.3	9.1	8.9	8.7	8.9
Baghdad«**MB**»	38	38.1	35.8	37.3	85.2	84	81.6	83.6	8.3	8.2	8	8.2
Faris«**NF**»	61.3	60.3	58.8	60.1	119.8	118.1	114.6	117.5	11.3	11.2	10.8	11.1
Tamuz«**OT**»	38.3	38.4	36.2	37.6	77.7	76.7	74.5	76.3	8.2	8.1	7.9	8.1
Buhoth«**PB**»	31.8	32.2	29.7	31.3	92.7	91.4	88.9	91	7	6.9	6.7	6.9
Abaá95«**QA**»	35.5	35.7	33.3	34.8	91.1	89.9	87.4	89.5	4.9	4.9	4.7	4.8

Abaá99«**RA**»	36.2	36.3	34	35.5	96.6	95.3	92.8	94.9	7.6	7.5	7.3	7.5
AbóGhuriyb «**SA**»	46.2	45.9	43.9	45.3	87.2	86	83.4	85.6	13.4	13.2	12.9	13.2
Buhoth22«**TB**»	36.6	36.3	34.9	35.9	89.4	88.1	85.5	87.7	11.4	11.2	10.9	11.1
Dujela«**UD**»	11.3	11.8	10.1	11.1	58.2	57.3	55.7	57	11.8	11.6	11.3	11.6
Nemichinovka «**VN**»	19	19.9	17.1	18.7	38.4	37.9	36.8	37.7	10	9.9	9.6	9.8
AbóRaghef «**WA**»	30.7	31.1	28.6	30.2	87.6	86.3	83.8	85.9	8.5	8.4	8.1	8.3
Means	*38.7*	*38.7*	*36.6*	*38*	*82.5*	*81.4*	*79*	*80.9*	*8.7*	*8.5*	*8.3*	*8.5*
LSD.05	*2.41*	*4.66*	*4.75*	*1.36*	*5.1*	*10.1*	*9.77*	*2.86*	*0.55*	*1.09*	*1.06*	*0.31*

1.1.61 Sensitivity of Genotypes to Salinity and Drought Stress Based on Yield Traits

1.1.61.1 Evaluation of Genotypes Based in Yield Index (YI)

In the ANOVA table (Appendix 4-3 and Table 24), comparison of genotype means using the LSD test (0.05) indicated that the effect of irrigation salinity level on the yield index (YI) was not significant. The SA genotype recorded the highest YI value (1.62) and also produced the highest values at all salinity levels, compared with (FS, PB) genotypes, which recorded the minimum mean YI values (0.58, 0.6), respectively. For drought stress treatment on YI in the ANOVA (Appendix 4-3 and Table 24), the differences were also not significant. However, the comparison between the genotype means using the LSD in Table 24 indicated that UD variety recorded the highest YI value (1.66), whereas the PB and FS genotypes exhibited the lowest values (0.54 and 0.52), respectively. According to the criteria for evaluating stress-tolerant and stress-sensitive genotypes, genotypes with the highest yield index values are

considered stress-tolerant, while the genotypes with the lowest yield index values are classified as stress-sensitive, as indicated by [167].

Table 24. Evaluation of Genotypes under Salinity and Drought Stress for the Yield Index (YI) Trait

Salinity					**Drought**			
Genotypes	***(control) 5ds/m***	***10ds/m***	***15ds/m***	***Means***	***(control) 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	1.07	1.14	1.36	**1.19**	1.14	1.15	1.26	1.18
Wafea«**BW**»	1.08	0.96	0.95	1	1.03	1.05	1.04	1.04
Latefiya«**C**L»	1.11	1.18	1.39	**1.23**	1.19	1.22	1.39	**1.27**
Binekal«**DB**»	0.88	0.79	0.62	0.76	0.91	0.88	0.79	0.86
Urok«**EU**»	1.01	0.97	0.83	0.94	0.94	1.04	1.01	1
Sham«**FS**»	0.77	0.54	0.43	**0.58**	0.71	0.57	0.32	**0.54**
Fateh«**GF**»	1.12	1.18	1.2	1.16	0.79	0.76	0.53	0.7
Buhoth10«**HB**»	1.02	1.05	1.05	1.04	0.84	0.77	0.64	0.75
Buhoth158«**IB**»	1.11	0.98	1.15	1.08	0.83	0.65	0.6	0.69
Babol113«**JB**»	0.8	0.78	0.57	0.72	0.85	0.76	0.64	0.75
Alraq«**KA**»	0.84	0.68	0.62	0.71	0.89	1.04	0.74	0.89
Bwru«**LB**»	0.93	0.89	0.78	0.87	1.11	1.18	1.24	1.18
Baghdad«**MB**»	0.88	0.79	0.61	0.76	0.84	0.81	0.63	0.76
Faris«**NF**»	1.32	1.53	1.83	**1.56**	1.2	1.3	1.53	**1.34**
Tamuz«**OT**»	0.76	0.68	0.54	0.66	0.74	0.66	0.52	0.64
Buhoth«**PB**»	0.74	0.6	0.45	**0.6**	0.71	0.51	0.35	**0.52**
Abaá95«**QA**»	0.96	1.04	0.98	1	1.01	1.04	1	1.02
Abaá99«**RA**»	0.93	1.04	0.69	0.89	0.99	0.96	0.87	0.94
AbóGhuriyb «**SA**»	1.34	1.59	1.93	**1.62**	1.35	1.56	1.86	**1.59**
Buhoth22«**TB**»	1.15	1.25	1.49	**1.3**	1.35	1.53	1.91	**1.6**
Dujela«**UD**»	1.33	1.5	1.87	**1.57**	1.37	1.62	1.98	**1.66**
Nemichinovka «**VN**»	1	1.04	1.03	1.02	1.06	0.96	1	1.01
AbóRaghef «**WA**»	0.86	0.82	0.62	0.77	1.12	0.97	1.16	1.08
Means	*1*	*1*	*1*	*1*	*1*	*1*	*1*	*1*
LSD.05	*T=8.66*	*V=0.016*	*TXV*	*0.028*	*T=7.9*	*V=0.017*	*TXV*	*0.029*

1.1.61.2 Evaluation of Genotypes in Yield Stability Index (YSI)

Table 25 and the ANOVA table in Appendix 4-3 indicate that, under salinity stress conditions, analysis of means using the least significant difference test at a significance (0.05) revealed that (SA, NF, UD, CL, AB) genotypes exhibited the highest yield stability index (YSI) values (0.90, 0.89, and 0.84), respectively, with no significant differences among them. In contrast, the FS genotype recorded the lowest YSI value of 0.62. The ANOVA results (Appendix 4-3 and Table 25) of the effect of drought stress levels on the varieties in this study trait indicated that the (UD, SA, TB, NF, CL, AB) genotypes recorded the maximum values of YSI (0.89, 0.88, 0.84, 0.80 and 0.79), respectively, compared to the PB and FS genotypes, which exhibited the lowest values (0.60 and 0.62). Genotypes with high YSI values demonstrated stress tolerance traits and often indicated positive correlations with other traits like chlorophyll content, seed weight, number of spikes, and shoots, consistent with the findings reported by [167].

Table 25. Evaluation of Genotypes under Salinity and Drought Stress for the Yield Stability Index (YSI)

Salinity					**Drought**			
Genotypes	***(control) 5ds/m***	***10ds/m***	***15ds/m***	***Means***	***(control) 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	1	0.82	0.72	**0.84**	1	0.76	0.61	**0.79**
Wafea«**BW**»	1	0.68	0.5	0.73	1	0.77	0.56	0.77
Latefiya«**C**L»	1	0.81	0.71	**0.84**	1	0.77	0.64	**0.8**
Binekal«**DB**»	1	0.68	0.4	0.69	1	0.73	0.48	0.74
Urok«**EU**»	1	0.73	0.46	0.73	1	0.83	0.59	0.81
Sham«**FS**»	1	0.53	0.32	**0.62**	1	0.61	0.25	**0.62**
Fateh«**GF**»	1	0.8	0.6	0.8	1	0.73	0.37	0.7
Buhoth10«**HB**»	1	0.78	0.58	0.78	1	0.69	0.42	0.7
Buhoth158«**IB**»	1	0.67	0.58	0.75	1	0.59	0.4	0.66
Babol113«**JB**»	1	0.74	0.4	0.71	1	0.68	0.41	0.7
Alraq«**KA**»	1	0.62	0.42	0.68	1	0.88	0.45	0.78
Bwru«**LB**»	1	0.73	0.47	0.73	1	0.8	0.61	0.8

Baghdad«**MB**»	1	0.68	0.39	0.69	1	0.72	0.41	0.71
Faris«**NF**»	1	0.89	0.78	**0.89**	1	0.82	0.7	**0.84**
Tamuz«**OT**»	1	0.69	0.4	0.7	1	0.68	0.39	0.69
Buhoth«**PB**»	1	0.62	0.34	0.65	1	0.54	0.27	**0.6**
Abaá95«**QA**»	1	0.82	0.57	0.8	1	0.77	0.54	0.77
Abaá99«**RA**»	1	0.85	0.42	0.75	1	0.73	0.48	0.74
AbóGhuriyb «**SA**»	1	0.9	0.81	**0.9**	1	0.88	0.76	**0.88**
Buhoth22«**TB**»	1	0.82	0.73	**0.85**	1	0.85	0.78	**0.88**
Dujela«**UD**»	1	0.86	0.79	**0.89**	1	0.89	0.79	**0.89**
Nemichinovka «**VN**»	1	0.79	0.58	0.79	1	0.68	0.52	0.73
AbóRaghef «**WA**»	1	0.72	0.4	0.71	1	0.66	0.57	0.74
Means	*1*	*0.75*	*0.54*	*0.76*	*1*	*0.74*	*0.52*	*0.75*
LSD.05	*T=5.29*	*V=0.01*	*TXV*	*0.02*	*T=6.52*	*V=0.02*	*TXV*	*0.021*

1.1.61.3 Estimation of Stress Tolerance Index (STI) for Genotypes

In Table 26 and the ANOVA (Appendix 4-3), analysis of means using the LSD test at (0.05), showed that the SA genotype exhibited the highest salinity stress tolerance index (STI) value (1.63) among the genotype means, compared with the (FS, PB) genotypes, which recorded the minimum value (0.36). The interaction was no significant at level of 0.05 between genotype and salinity levels, which indicated that the (SA, UD, NF, TB and CL) genotypes produced the highest STI values under salinity stress (1.63, 1.56, 1.54, 1.13, 1.03), respectively. Therefore, the SA, UD, NF, TB and CL genotypes were considered salinity-tolerant, whereas the FS and PB genotypes are considered sensitive to salinity based on this index.

Table 26 and the ANOVA (Appendix 4-3) also present the tolerance indices of genotypes under drought stress, with (UD, TB, SA, NF, CL and AB genotypes exhibiting the highest STI values (1.69, 1.61, 1.59, 1.21, 1.15 and 1.03), respectively. This genotype recorded the highest STI values across all treatment levels, in contrast to the (FS, PB) genotypes, which yielded the lowest values of (0.31,0.30), respectively, indicating drought sensitivity. Genotypes with the highest STI values are classified as

stress-tolerant, whereas those with the lowest values are deemed stress-sensitive, as reported by [166].

Table 26. Estimation of Salinity and Drought Stress Tolerance Index (STI) for Varieties

	Salinity				**Drought**			
Genotypes	***control 5ds/m***	***10 ds/m***	***15 ds/m***	***Means***	***control 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	1.14	0.93	0.82	**0.96**	1.3	0.99	0.79	**1.03**
Wafea«**BW**»	1.16	0.79	0.58	0.84	1.06	0.82	0.59	0.82
Latefiya«**C**L»	1.22	0.99	0.87	**1.03**	1.43	1.1	0.91	**1.15**
Binekal«**DB**»	0.77	0.52	0.3	0.53	0.83	0.6	0.39	0.61
Urok«**EU**»	1.03	0.75	0.48	0.75	0.89	0.74	0.53	0.72
Sham«**FS**»	0.59	0.31	0.19	**0.36**	0.51	0.31	0.13	0.31
Fateh«**GF**»	1.25	1	0.75	1	0.62	0.46	0.23	0.44
Buhoth10«**HB**»	1.05	0.82	0.6	0.82	0.71	0.49	0.3	0.5
Buhoth158«**IB**»	1.23	0.82	0.72	0.92	0.69	0.41	0.27	0.46
Babol113«**JB**»	0.64	0.48	0.25	0.46	0.72	0.49	0.3	0.5
Alraq«**KA**»	0.7	0.43	0.29	0.47	0.8	0.7	0.36	0.62
Bwru«**LB**»	0.86	0.63	0.41	0.63	1.24	1	0.76	1
Baghdad«**MB**»	0.77	0.53	0.3	0.53	0.71	0.51	0.29	0.51
Faris«**NF**»	**1.73**	**1.54**	**1.35**	**1.54**	**1.45**	**1.18**	**1.01**	**1.21**
Tamuz«**OT**»	0.57	0.39	0.23	0.4	0.54	0.37	0.21	0.37
Buhoth«**PB**»	0.55	0.34	0.19	**0.36**	0.5	0.27	0.14	0.3
Abaá95«**QA**»	0.93	0.77	0.53	0.74	1.03	0.79	0.56	0.79
Abaá99«**RA**»	0.87	0.74	0.36	0.66	0.98	0.72	0.48	0.73
AbóGhuriyb«**SA**»	**1.8**	**1.62**	**1.46**	**1.63**	**1.81**	**1.59**	**1.38**	**1.59**
Buhoth22«**TB**»	**1.33**	**1.09**	**0.96**	**1.13**	**1.83**	**1.57**	**1.42**	**1.61**
Dujela«**UD**»	**1.76**	**1.52**	**1.39**	**1.56**	**1.89**	**1.68**	**1.49**	**1.69**
Nemichinovka«**VN**»	1	0.79	0.58	0.79	1.12	0.77	0.58	0.82
AbóRaghef «**WA**»	0.75	0.54	0.3	0.53	1.25	0.82	0.71	0.93
Means	*1.03*	*0.8*	*0.61*	*0.81*	*1.04*	*0.8*	*0.6*	*0.81*
LSD.05	*T=5.63*	*V=0.02*	*TXV*	*0.035*	*T=6.26*	*V=0.02*	*TXV*	*0.04*

1.1.61.4 Estimation of Stress Susceptibility Index (SSI) 0f genotypes

In the ANOVA (Appendix 4-3) and Table 27, SSI based on the grain yield (t/ha) of different wheat genotypes, indicated wide variation in susceptibility to irrigation water salinity levels and soil water availability levels from field capacity. The SA, NF and UD genotypes recorded the lowest values for the salinity stress susceptibility index (0.28, 0.32 and 0.35) respectively, with no significant difference between them at the significance level of 0.05. Lower SSI values indicate greater genotype resistance to stress [168,193]; In contrast, the FS genotype recorded the highest salt stress sensitivity index value (1.17). Regarding the values of the sensitivity indices of genotypes under water stress in Table 27 and ANOVA (Appendix 4-3), the UD, SA and TB genotypes had the lowest values across drought stress treatments (0.3, 0.34 and 0,36), while the PB and FS genotypes recorded the highest values (1.17 and 1.09), respectively. Thus, the genotype UD is considered drought tolerant, as reported by [168].

Table 27. Salinity and Drought Stress Susceptibility Index (SSI) for Genotypes

	Salinity				**Drought**			
Genotypes	***(control) 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means***	***(control) 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	0	0.77	0.65	0.47	0	0.98	0.88	0.62
Wafea«**BW**»	0	1.35	1.15	0.83	0	0.95	0.99	0.65
Latefiya«**C**L»	0	0.8	0.66	0.49	0	0.94	0.8	0.58
Binekal«**DB**»	0	1.33	1.38	0.9	0	1.1	1.17	0.75
Urok«**EU**»	0	1.15	1.23	0.79	0	0.68	0.91	0.53
Sham«**FS**»	0	1.95	1.56	**1.17**	0	1.61	1.67	**1.09**
Fateh«**GF**»	0	0.84	0.91	0.58	0	1.1	1.4	0.83
Buhoth10«**HB**»	0	0.93	0.97	0.63	0	1.27	1.29	0.85
Buhoth158«**IB**»	0	1.38	0.95	0.78	0	1.65	1.34	1
Babol113«**JB**»	0	1.07	1.37	0.82	0	1.31	1.31	0.87
Alraq«**KA**»	0	1.61	1.32	0.98	0	0.5	1.21	0.57
Bwru«**LB**»	0	1.13	1.21	0.78	0	0.81	0.87	0.56
Baghdad«**MB**»	0	1.34	1.39	0.91	0	1.14	1.31	0.82
Faris«**NF**»	0	0.47	0.5	**0.32**	0	0.75	0.67	0.47
Tamuz«**OT**»	0	1.32	1.37	0.89	0	1.33	1.36	0.89
Buhoth«**PB**»	0	1.61	1.5	1.04	0	1.87	1.62	**1.17**
Abaá95«**QA**»	0	0.73	0.97	0.57	0	0.93	1.01	0.65

Abaá99«**RA**»	0	0.64	1.33	0.66	0	1.09	1.15	0.74
AbóGhuriyb «**SA**»	0	0.42	0.44	**0.28**	0	0.5	0.53	**0.34**
Buhoth22«**TB**»	0	0.74	0.62	0.45	0	0.59	0.5	**0.36**
Dujela«**UD**»	0	0.57	0.48	**0.35**	0	0.45	0.46	**0.3**
Nemichinovka«**VN**»	0	0.88	0.97	0.61	0	1.3	1.07	0.79
AbóRaghef«**WA**»	0	1.17	1.36	0.84	0	1.4	0.96	0.79
Means	0	1.05	1.06	0.7	0	1.05	1.06	0.71
LSD.05	T=0.024	V=0.04	TXV	0.069	T=0.028	V=0.037	TXV	0.065

Evaluation of the Effects of Salinity and Drought Stress on Grain Content

1.1.62 Evaluation of Protein Content in Wheat Grains

From the results of the ANOVA table Appendix 4-6 and Table 28), and comparing the averages using the least significant difference test at ($p > 0.05$), the effect of salinity stress showed the lowest protein content of 11.62% at the control level (5 ds m^{-1}). The protein content increased at the 10 ds m^{-1} level (12.97%) and the 15 ds m^{-1} level (14.59%). The grain protein content was significantly affected by the interaction between salinity levels and genotypes. The highest protein percentages were observed in the highest salinity treatment (15 dS m^{-1}). The highest protein percentage was recorded in genotypes BW, AB, CL and IB with 15.37%, 15.36%, 15.35% and 15.35%, respectively. The close clustering of the values suggests the relative stability of protein accumulation in these specific genotypes under severe saline conditions. Increase in protein content of wheat flour is well established to result in higher dough stiffness and improved rheological strength which in turn has a positive impact on the bread making quality and processing characteristics. The results of protein content in grains under water stress in Table 28 and the ANOVA table, Appendix 4-6 indicate that the highest protein content was found in UD (11.73%), while the lowest protein content was in FS (10.68%). At the control level (90% of field capacity), the lowest protein content was 9.9%, and the protein content increased at the 60% of field capacity level (10.98%) and the 30% of field capacity (12.78%). These results are in good agreement with the previous reports [100,101,201] showing that salinity and drought stresses could promote grain protein accumulation. This

phenomenon is explained by the inhibition of carbohydrate assimilation under stress conditions and the relative increase of the nitrogenous components. Also, genotypic constitution markedly influences the magnitude of protein enhancement, suggesting divergent mechanisms for stress tolerance. Statistical analyses, including the LSD test, revealed significant genotypic variation under both stress regimes, confirming the role of genetic background in modulating physiological responses to osmotic and ionic stresses.

Table 28. Effect of Salinity and Drought Stress on Wheat Grain Protein Content

	Salinity				**Drought**			
Genotypes	***(control) 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means***	***(control) 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	12	12.66	15.36	13.34	11.17	10.05	13.16	11.46
Wafea«**BW**»	12.03	12.33	15.37	13.24	10.35	10.76	12.99	11.37
Latefiya«**C**L»	11.26	13.48	15.35	13.36	10.58	10.84	13.17	11.53
Binekal«**DB**»	11.53	12.53	14.25	12.77	9.78	11.13	12.37	11.09
Urok«**EU**»	11.87	12.88	14.47	13.07	9.93	11.18	12.74	11.28
Sham«**FS**»	11.33	11.96	13.17	12.15	8.88	10.44	12.72	10.68
Fateh«**GF**»	11.3	13.75	14.94	13.33	9.48	10.04	12.96	10.83
Buhoth10«**HB**»	11.23	13.65	14.9	13.26	9.33	11.09	12.71	11.04
Buhoth158«**IB**»	11.99	12.65	15.35	13.33	9.58	10.54	12.3	10.81
Babol113«**JB**»	11.33	11.98	14.67	12.66	9.35	10.94	12.57	10.95
Alraq«**KA**»	11.3	12.53	14.12	12.65	9.92	10.89	12.52	11.11
Bwru«**LB**»	11.83	12.81	14.42	13.02	10.04	11.16	13.15	11.45
Baghdad«**MB**»	11.15	12.83	14.18	12.72	9.88	10.82	12.47	11.06
Faris«**NF**»	11.76	13.98	14.86	13.53	10.13	12.39	12.17	11.56
Tamuz«**OT**»	11.43	12.13	14.01	12.52	9.2	10.84	12.23	10.76
Buhoth«**PB**»	11.33	12.44	12.96	12.24	8.88	10.49	12.72	10.7
Abaá95«**QA**»	11.17	13.63	14.86	13.22	9.85	11.63	12.6	11.36
Abaá99«**RA**»	11.73	13.12	14.32	13.05	9.22	11.64	12.91	11.26
AbóGhuriyb «**SA**»	11.8	14.37	14.55	13.57	10.81	10.99	12.91	11.57
Buhoth22«**TB**»	12.08	13.38	15.12	13.53	11.31	10.67	13.16	11.71
Dujela«**UD**»	12.62	12.97	15.11	13.56	11.31	10.49	13.4	11.73
Nemichinovka «**VN**»	11.88	13.17	14.69	13.25	9.28	11.66	12.95	11.3

AbóRaghef «**WA**»	11.28	13.08	14.66	13.01	9.38	11.78	13.01	11.39
Means	11.62	12.97	14.59	13.06	9.9	10.98	12.78	11.22
LSD.05	T=0.082	V=0.185	TXV	0.32	T=0.087	V=0.148	TXV	0.256

1.1.63 Evaluation of Moisture Content in Wheat Grains

The results from the ANOVA table Appendix 4-6 and Table 29 indicate that the seed moisture content under salinity stress at the control level (5 $dS.m^{-1}$) was 10.34%, then decreased with increasing stress intensity at the levels of 10 $dS.m^{-1}$ (8.93%) and 15 $dS.m^{-1}$ (7.14%) at ($P > 0.05$). As genotypes, the variety FS had the highest value (11.73%), while UD, NF, TB, CL, AB, and SA had the lowest moisture content (6.14%, 6.45%, 6.53%, 6.59%, 6.89%, and 7.08%), respectively, under salinity stress.

Under drought stress (ANOVA table, Appendix 4-6 and Table 29), at the control level (9.77%), while at the 60% field capacity level (8.15%) and the 30% field capacity level (6.32%). As genotypes, (UD, TB, SA, NF, CL, AB) showed the lowest moisture contents (4.35%, 4.65%, 4.89%, 4.92%, 5.21%, and 5.28%), respectively, under drought stress. While FS (11.49%) and PB (10.78%) had the highest seed moisture content. These results align with the findings in [91,202], where it was shown that the intensity and duration of environmental stress greatly influence seed quality attributes and compositional profiles. In line with the above-mentioned studies, the present study indicated that the studied genotypes experienced a significant reduction in grain moisture content under salinity and drought stress conditions. The reduction in hydration status reflects the changes in water relations and assimilate partitioning that occur under stress during grain filling and again shows the multifaceted effect of abiotic stressors on the ultimate seed quality parameters.

Table 29. Effect of Salinity and Drought on the Moisture Content of Grains

Salinity	**Drought**

Genotype	***(control) 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means***	***(control) 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	7.46	7.61	5.61	6.89	5.83	6.28	3.73	5.28
Wafea«**BW**»	10.63	7.98	6.74	8.45	10.05	7.63	5.47	7.72
Latefiya«**C**L»	6.98	7.3	5.51	6.59	5.27	6.52	3.83	5.21
Binekal«**DB**»	12.43	10.34	8.8	10.52	10.98	9.03	7.17	9.06
Urok«**EU**»	10.93	8.68	7.21	8.94	10.78	8.13	6.8	8.57
Sham«**FS**»	13.63	11.57	10	11.73	13.38	11.33	9.77	11.49
Fateh«**GF**»	10.3	7.61	5.61	7.84	12.98	10	8.13	10.37
Buhoth10«**HB**»	10.2	7.54	6.37	8.04	11.82	9.27	7.73	9.61
Buhoth158«**IB**»	10.3	7.88	5.71	7.96	12.22	10.37	8.8	10.46
Babol113«**JB**»	11.46	11.61	9.04	10.7	12.45	9.1	7.47	9.67
Alraq«**KA**»	11.59	11.91	9.2	10.9	11.05	8.57	7.1	8.91
Bwru«**LB**»	11.9	9.34	8.1	9.78	9.95	7.3	5.13	7.46
Baghdad«**MB**»	13.23	10.24	8.37	10.61	11.65	9.1	7.87	9.54
Faris«**NF**»	7.51	6.76	5.08	6.45	5.07	5.7	4	4.92
Tamuz«**OT**»	13.23	11.27	9.4	11.3	12.35	10.67	8.97	10.66
Buhoth«**PB**»	12.69	11.04	10.7	11.48	12.68	10.6	9.07	10.78
Abaá95«**QA**»	11.03	8.38	7.04	8.81	10.18	7.67	5.37	7.74
Abaá99«**RA**»	11.3	8.81	7.34	9.15	10.68	8.43	6.97	8.69
AbóGhuriyb«**SA**»	7.04	7.95	6.24	7.08	5.8	5.48	3.4	4.89
Buhoth22«**TB**»	6.68	7.93	4.98	6.53	4.97	5.62	3.37	4.65
Dujela«**UD**»	6.04	7.73	4.64	6.14	4.43	5.35	3.27	4.35
Nemichinovka«**VN**»	10.3	7.61	5.61	7.84	10.17	7.95	6.5	8.21
AbóRaghef«**WA**»	11.03	8.38	7.04	8.81	10.05	7.37	5.37	7.59
Means	10.34	8.93	7.14	8.81	9.77	8.15	6.32	8.08
LSD.05	T=0.201	V=0.685	TXV	1.186	T=0.227	V=0.725	TXV	1.256

1.1.64 Evaluation of Gluten Percentage in Wheat Grains

In the ANOVA table Appendix 4-6 and Table 30, the comparison among genotypes showed a high significance at the 0.05 level under salinity stress, where genotypes UD, SA, and NF showed the highest gluten percentages (27.32%, 27.12%, and 26.78%, respectively), while genotypes PB and FS showed the lowest gluten percentages (20.23% and 20.65%). For salinity treatment, the 15 dS m^{-1} level (26.64%) was higher than the control level (20.94%). The highest interaction between genotype and salinity was observed in the NF variety (31.74% gluten). Salinity stress increases protein content and both wet and dry gluten content in wheat grains, with studies indicating increased gluten content at higher salinity levels [91,203]. Drought stress

also increases gluten content in wheat grains. The highest gluten content in the genotype and drought interaction was observed in the QA genotype (30.47%). For drought treatment, the highest gluten content was at 30% of field capacity (28.18%) compared to the control level (18.25%) and 60% of field capacity (22.65%). Many researchers report that the intensity and duration of exposure to salinity and drought stress affect gluten content in grains. In this study, both stresses led to an increase in gluten percentage in the genotypes, which is consistent with the results of [91,92,204].

Table 30. Effect of Salinity and Drought Stress on the Gluten Content of Wheat Grains

	Salinity				**Drought**			
Genotypes	***(control) 5 ds/m***	***10 ds/m***	***15 ds/m***	***Mean***	***(control) 90% FC***	***60%***	***30%***	***Mean***
Baraka«**AB**»	23.57	26.59	28.13	26.1	21.19	27.35	26.54	25.03
Wafea«**BW**»	21.78	25.97	23.27	23.68	20.28	22.09	29.72	24.03
Latefiya«**C**L»	23.53	26.9	28.57	26.33	20.92	26.79	28.02	25.24
Binekal«**DB**»	19.68	24.02	24.7	22.8	16.65	21.57	28.75	22.32
Urok«**EU**»	20.01	25.01	25.23	23.42	17.04	22.41	29.54	23
Sham«**FS**»	17.78	22.52	21.65	20.65	15.13	16.54	26.97	19.55
Fateh«**GF**»	22.59	26.36	28.96	25.97	16.15	18.26	27.54	20.65
Buhoth10«**HB**»	21.22	27.35	25.26	24.61	16.72	19.13	28.15	21.34
Buhoth158«**IB**»	20.47	25.09	29.74	25.1	16.15	17.95	27.46	20.52
Babol113«**JB**»	18.81	23.09	25.59	22.5	16.42	18.98	27.73	21.04
Alraq«**KA**»	19.53	22.54	22.62	21.56	16.65	21.65	29.46	22.59
Bwru«**LB**»	20.2	23.28	26.35	23.28	20.92	23.73	29.04	24.57
Baghdad«**MB**»	18.5	24.9	24.97	22.79	15.78	21.46	28.6	21.95
Faris«**NF**»	22.83	25.77	31.74	26.78	21.58	26.98	27.58	25.38
Tamuz«**OT**»	18.09	22.15	24.68	21.64	14.07	19.23	26.99	20.1
Buhoth«**PB**»	16.9	18.08	25.7	20.23	15.1	17.35	23.53	18.66
Abaá95«**QA**»	21.26	23.03	26.33	23.54	17.8	22.71	30.47	23.66
Abaá99«**RA**»	20.96	21.7	27.2	23.29	16.71	22.38	29.48	22.85
AbóGhuriyb «**SA**»	24.12	27.99	29.24	27.12	23.14	28.58	28.69	26.8
Buhoth22«**TB**»	23.51	26.24	29.42	26.39	22.69	28.28	28.44	26.47
Dujela«**UD**»	25.13	27.13	29.69	27.32	22.02	27.57	28.22	25.93

Nemichinovka «**VN**»	20.93	24.3	27.97	24.4	17.21	24.67	28.42	23.44
AbóRaghef «**WA**»	20.12	23.01	25.76	22.96	19.37	25.19	28.81	24.46
Means	20.94	24.48	26.64	24.02	18.25	22.65	28.18	23.02
LSD.05	T=0.201	V=0.69	TXV	1.186	T=0.227	V=0.725	TXV	1.256

1.1.65 Evaluation of Starch Percentage in Wheat Grains

In the ANOVA table Appendix 4-6 and Table 31, the starch content in grains was highest at the control level of 5 dS m^{-1} (58.43%), then decreased at level of 10 dS m^{-1} (49.5%) and level of 15 dS m^{-1} (36.05%). These results support researchers' findings that salinity stress often lowers starch content, although the extent varies with stress intensity and timing [99]. For genotypes, starch content differed under salinity stress [100]. In this study, the SA variety had the highest grain starch content of 59.5%.

In the present study, drought stress exerted a pronounced effect on grain starch content. The average starch content was 57.43% under well-watered control conditions (90% FC). However, a progressive water deficit led to a significant decrease, and the values dropped to 47.22% for 60% FC and 34.88% for 30% FC. This slow decrease is consistent with earlier findings [102,205], which indicated that drought stress generally leads to reduction of starch content in grains, mainly through reduction in the size of starch granules and overall starch synthesis. Physiological impairment is due to limited carbon assimilation and reduced nitrogen supply to the developing grains under water-limited conditions. It is important to point out that the response to drought was genotypic and that the UD variety was the one that presented the highest starch content (58.62%) under stress, with greater starch retention capacity and greater tolerance to water deficit than the other genotypes evaluated.

Table 31. Effect of Salinity and Drought on the Starch Content of Wheat Grains

Salinity					Drought			
Genotypes	***(control) 5 ds/m***	***10 ds/m***	***15 ds/m***	***Mean***	***(control) 90% FC***	***60%***	***30%***	***Mean***
Baraka«**AB**»	57.5	52.54	44.04	51.36	59.23	48.02	42.44	49.9
Wafea«**BW**»	59.33	47.54	34.24	47.04	59.49	46.79	33.64	46.64
Latefiya«**C**L»	58.5	55.04	45.21	52.92	57.21	53.45	43.56	51.41
Binekal«**DB**»	57.4	45.54	31.24	44.73	56.84	44.08	30.66	43.86
Urok«**EU**»	58.4	46.94	33.04	46.13	57.62	45.63	32.1	45.12
Sham«**FS**»	55	42.34	29.14	42.16	51.65	39.71	25.67	39.01
Fateh«**GF**»	61.5	48.34	35.64	48.49	55.37	42.72	30.28	42.79
Buhoth10«**HB**»	60.7	48.24	35.04	47.99	56.25	44.17	29.99	43.47
Buhoth158«**IB**»	60.9	48.34	35.24	48.16	56.15	41.36	29.09	42.2
Babol113«**JB**»	56.5	44.04	31.54	44.03	56.74	38.25	34.91	43.3
Alraq«**KA**»	52.3	47.64	30.31	43.42	58.51	46.6	28.36	44.49
Bwru«**LB**»	58	45.44	31.94	45.13	60.27	46.89	34.21	47.12
Baghdad«**MB**»	57.9	44.84	30.91	44.55	56.84	43.79	30.18	43.6
Faris«**NF**»	60.6	57.44	48.71	55.58	58.66	56.58	46.25	53.83
Tamuz«**OT**»	57.9	45.14	26.87	43.3	56.74	43.79	25.8	42.11
Buhoth«**PB**»	51.81	50.7	26.74	43.08	53.9	41.07	27.97	40.98
Abaá95«**QA**»	58.8	47.04	33.44	46.43	59.39	46.6	33.54	46.51
Abaá99«**RA**»	59.7	48.04	29.54	45.76	57.23	45.53	31.72	44.83
AbóGhuriyb «**SA**»	60	64.77	53.71	59.49	59.27	55.78	46.92	53.99
Buhoth22«**TB**»	61	57.24	48.01	55.42	60.15	56.36	46.44	54.32
Dujela«**UD**»	61.5	58.04	48.21	55.92	58.62	62.98	51.72	57.77
Nemichinovka «**VN**»	60.6	48.04	34.94	47.86	58.15	46.11	32.87	45.71
AbóRaghef «**WA**»	58	45.14	31.44	44.86	56.68	49.89	33.83	46.8
Means	58.43	49.5	36.05	47.99	57.43	47.22	34.88	46.51
LSD.05	T=1.475	V=2.146	TXV	3.716	T=1.653	V=2.311	TXV	4.002

Effect of Abiotic stress on physiological traits of genotypes

1.1.66 Results of non-enzymatic physiological parameters

1.1.66.1 Evaluation of genotypes in the chlorophyll content

As shown in Table 32 and ANOVA in Appendix 4-4, the chlorophyll content in SPAD units decreased gradually with the increase of salinity levels. The average chlorophyll content was found to be 49.15 SPAD units under control conditions (5 $dS.m^{-1}$). This value was significantly decreased to 42.71 SPAD units in salinity treatment 10 $dS.m^{-1}$ and to 36.82 SPAD units in the maximum salinity level (15 $dS.m^{-1}$). The sharp decline is attributed to the detrimental effects of high salt concentrations, which are known to cause ionic toxicity and osmotic stress, resulting in the acceleration of chlorophyll degradation and decrease of the stability of the photosynthetic pigments [52]. Chlorophyll content was a good indicator of the magnitude of salt stress and decreased in a dose-dependent manner, thereby showing the sensitivity of the photosynthetic apparatus to salinity. As the genotypes, the SA genotype differed significantly from all other genotypes, achieving 50.04 SPAD units, while the second group of genotypes (UD, NF, TB, CL, AB) recorded the highest chlorophyll content, ranging from 47.7 to 46.6 SPAD units. Salinity stress thus reduces chloroplast pigment content, which in turn lowers the efficiency of photosynthesis and decreases productivity, in agreement with previous findings [110].

The levels of drought stress significantly affected chlorophyll content in Table 32 and the ANOVA in Appendix 4-4, The chlorophyll content showed a gradual decline from 47.65 SPAD units in the well-watered control to 26.11 SPAD units at the highest level of drought stress. Under such conditions, there was significant genotypic variation, and the high chlorophyll content (45.53 SPAD units) was recorded for UD variety with superior stress tolerance, while the lowest value (32.66 SPAD units) was observed for FS variety, indicating the greatest susceptibility to abiotic stress. The combined results confirm that chlorophyll content of plants is reduced consistently by salinity and drought stress at all levels tested. Such reductions are inherently associated with the reduction in photosynthetic efficiency, which is a major factor in wheat growth, biomass accumulation and ultimately grain yield [111].

Table 32. Effect of Salinity and Drought Stress on Chlorophyll Content (SPAD) in Flag Leaves of Genotypes

	Salinity				Drought			
Genotypes	***(control) 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means***	***(control) 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	51.9	47.1	40.8	46.6	51.5	41.3	28.9	40.57
Wafea«**BW**»	48.9	44.5	38	43.8	45	38.6	28.63	37.41
Latefiya«**C**L»	53.7	46.3	39.9	46.63	50.5	41.6	29.8	40.63
Binekal«**DB**»	48.7	41.4	30.7	40.27	48.6	37.4	24	36.67
Urok«**EU**»	48.8	40.4	33	40.73	45.4	35.7	20.8	33.97
Sham«**FS**»	45.83	37.33	31	38.06	44.3	33	20.67	32.66
Fateh«**GF**»	41.9	46.1	35.3	41.1	47.6	37.9	22.8	36.1
Buhoth10«**HB**»	47.2	39.7	33.3	40.07	46.33	38.4	24.3	36.34
Buhoth158«**IB**»	48.2	40.4	32.4	40.33	45	35.8	24.7	35.17
Babol113«**JB**»	47.2	41.6	35.3	41.37	48.5	38.4	21.7	36.2
Alraq«**KA**»	47.2	40.8	35.7	41.23	47.7	38.7	25	37.13
Bwru«**LB**»	43.4	48.53	35.3	42.41	44.9	38.9	27.97	37.26
Baghdad«**MB**»	49.8	42.9	33.8	42.17	48.9	37.3	23.2	36.47
Faris«**NF**»	52.7	40.9	48.4	47.33	50.5	43.4	29.9	41.27
Tamuz«**OT**»	47.6	40.2	32.2	40	45.4	35.2	21.2	33.93
Buhoth«**PB**»	48	40.5	31.07	39.86	45.8	35.5	20.07	33.79
Abaá95«**QA**»	49.9	43.7	36	43.2	48	37.4	23.4	36.27
Abaá99«**RA**»	51.1	42.3	34.2	42.53	45	38.6	28.63	37.41
AbóGhuriyb «**SA**»	55.2	50.8	44.13	50.04	50.5	41.6	29.8	40.63
Buhoth22«**TB**»	52.7	40.8	46.6	46.7	49.7	43.1	32.47	41.76
Dujela«**UD**»	53.8	40.5	48.8	47.7	53	47.13	36.47	45.53
Nemichinovka «**VN**»	49.6	42.7	33.8	42.03	49	38.7	26.3	38
AbóRaghef «**WA**»	47.1	42.9	37.1	42.37	44.9	40.9	29.77	38.52
Means	49.15	42.71	36.82	42.89	47.65	38.89	26.11	37.55
LSD.05	T=1.245	V=1.806	TXV	3.128	T=0.816	V=1.695	TXV	2.937

1.1.66.2 Evaluation of Genotypes for Proline Acid Content

In the ANOVA Appendix 0-4 and Table 33, salinity and drought stresses significantly affected the proline accumulation in plants with increasing stress intensity. Under salinity conditions, proline concentration at level 15 $ds.m^{-1}$ averaged 0.82 µg/g DW , which was significantly higher than those at level 10 $ds.m^{-1}$ and the control level. Comparison of genotype means revealed that the SA, UD, NF, TB, and CL genotypes exhibited significantly higher values (0.59, 0.57, 0.57, 0.56, and 0.5 µg/g DW), respectively, than all other genotypes; these genotypes can thus be classified as salinity-tolerant, as reported by [52,170], which indicates that proline concentration rises in salinity-tolerant genotypes but falls in sensitive ones relative to the control.

ANOVA results shown in Appendix 4-4 and presented in Table 33 indicated that drought stress significantly increased proline content, with the maximum value (0.90 µg g^{-1} DW) recorded at the highest level of water deficit (30% field capacity) at $p < 0.05$. Five genotypes (UD, TB, SA, NF and CL) had significantly higher proline concentrations (0.64, 0.63, 0.63, 0.62 and 0.58 µg g^{-1} DW, respectively) than the other genotypes as determined by the least significant difference (LSD) test. These results are in agreement with previous studies on the water stress response in wheat [116], which also reported increased proline biosynthesis under drought conditions. These results taken together confirm the proline accumulation as a valid physiological parameter for assessing genotypic tolerance to salinity and drought stresses and reflect the adaptive capacity of plants to cope with osmotic and oxidative stresses [103].

Table 33. Evaluation Of Genotypes under Salinity and Drought Stresses for Proline Content in Leaves (µg. g^{-1}.DW)

Salinity	Drought

Genotypes	***(control) 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means***	***(control) 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	0.15	0.44	0.83	0.47	0.15	0.5	0.87	0.51
Wafea«**BW**»	0.1	0.27	0.82	0.4	0.11	0.34	0.96	0.47
Latefiya«**C**L»	0.24	0.38	1.02	0.55	0.25	0.37	1.12	0.58
Binekal«**DB**»	0.09	0.24	0.67	0.34	0.1	0.33	0.81	0.41
Urok«**EU**»	0.14	0.24	0.68	0.36	0.1	0.35	0.88	0.44
Sham«**FS**»	0.06	0.22	0.58	0.29	0.13	0.12	0.63	0.29
Fateh«**GF**»	0.09	0.31	0.85	0.42	0.11	0.36	0.86	0.44
Buhoth10«**HB**»	0.06	0.32	0.92	0.43	0.11	0.35	0.96	0.47
Buhoth158«**IB** »	0.1	0.3	0.81	0.4	0.1	0.3	0.92	0.44
Babol113«**JB**»	0.09	0.24	0.58	0.3	0.1	0.27	0.8	0.39
Alraq«**KA**»	0.04	0.24	0.74	0.34	0.06	0.24	0.79	0.37
Bwru«**LB**»	0.09	0.26	0.75	0.37	0.1	0.32	0.84	0.42
Baghdad«**MB**»	0.03	0.28	0.76	0.36	0.09	0.27	0.84	0.4
Faris«**NF**»	0.21	0.44	1.04	0.57	0.24	0.49	1.15	0.62
Tamuz«**OT**»	0.09	0.22	0.54	0.29	0.07	0.27	0.71	0.35
Buhoth«**PB**»	0.07	0.22	0.58	0.29	0.07	0.26	0.62	0.32
Abaá95«**QA**»	0.09	0.25	0.88	0.41	0.11	0.32	0.94	0.46
Abaá99«**RA**»	0.09	0.29	0.77	0.38	0.1	0.32	0.92	0.45
AbóGhuriyb «**SA**»	0.15	0.49	1.13	0.59	0.23	0.5	1.14	0.63
Buhoth22«**TB**»	0.18	0.43	1.07	0.56	0.23	0.49	1.16	0.63
Dujela«**UD**»	0.19	0.45	1.08	0.57	0.23	0.51	1.17	0.64
Nemichinovka «**VN**»	0.1	0.27	0.85	0.41	0.1	0.32	0.84	0.42
AbóRaghef «**WA**»	0.05	0.29	0.83	0.39	0.11	0.35	0.85	0.44
Means	0.11	0.31	0.82	0.41	0.13	0.35	0.9	0.46
LSD.05	T=0.028	V=0.045	TXV	0.078	T=0.029	V=0.04	TXV	0.073

1.1.66.3 Evaluation of Genotypes for Relative Water Content (RWC)

The results of ANOVA Appendix 4-4 and Table 34 highly significant ($p< 0.05$) effects of salinity, drought stress and genotype on relative water content (RWC) and

their interactive effects as well. Average RWC decreased gradually and significantly under drought stress, being 83.45% in well-watered control conditions (90% FC) and 50.01% at the most severe drought level (30% FC). This decrease means that water uptake is impaired and water loss by transpiration is increased. The genotype UD was significantly superior to all other genotypes under stress conditions with an RWC value of 84.58%. In the interaction effect, it was also superior, with a value of 94.80% showing the ability to maintain cellular hydration to a high degree.

Likewise, salinity stress greatly reduced the RWC from 83.97% under control conditions to 55.19% at the highest salinity level (15 $dS.m^{-1}$). The decrease is mainly due to osmotic stress that limits the water uptake by the roots and modifies the water relations in plants. Maximum mean RWC was obtained for SA and UD genotypes for water uptake and retention capacity (86.03% and 85.09%, respectively), depicting their superior water retention capacity.

Genotypes that minimise water loss from leaves are generally considered to be more drought tolerant because they are less affected by evaporative and transpirational demands and therefore maintain favourable internal water status [103]. In this regard, earlier studies [109] have indicated that the deposition of epicuticular wax on the leaf surfaces can be an important adaptive trait in drought-tolerant genotypes, as the increased wax load effectively reduces the cuticular transpiration and mitigates the water loss from the plant tissues.

Table 34. Evaluation of Genotypes Affected by Salinity and Drought Stress for Relative Water Content (RWC) in the Leaves

Salinity					**Drought**			
Genotypes	***(control) 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means***	***(control) 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	88.37	75.5	56.57	73.48	87.47	75.33	53.43	72.08

Wafea«**BW**»	85.87	69.33	50.57	68.59	85.13	69.67	49.43	68.08
Latefiya«**CL**»	87.53	70.33	63.73	73.87	86.63	70.17	60.43	72.41
Binekal«**DB**»	83.53	63.67	45.07	64.09	80.13	59.83	48.27	62.74
Urok«**EU**»	81.37	68.83	51.57	67.26	83.97	68.67	45.1	65.91
Sham«**FS**»	72.03	51.83	49.57	57.81	71.13	51.67	40.77	54.52
Fateh«**GF**»	82.7	71.33	64.57	72.87	82.8	63.5	41.77	62.69
Buhoth10«**HB**»	85.63	72.5	50.57	69.57	77.3	61.33	44.77	61.13
Buhoth158«**IB**»	85.87	69.83	59.07	71.59	76.97	59	46	60.66
Babol113«**JB**»	75.7	64.17	46.23	62.03	84.97	54.17	43.43	60.86
Alraq«**KA**»	83.03	59.5	41.07	61.2	81.3	56.83	43.43	60.52
Bwru«**LB**»	85.7	64.33	46.57	65.53	80.8	62.17	52.27	65.08
Baghdad«**MB**»	78.2	61.33	47.9	62.48	82.8	60.5	41.77	61.69
Faris«**NF**»	89.2	80.83	75.23	81.76	84.47	73.67	61.93	73.36
Tamuz«**OT**»	82.2	61	36.9	60.03	81.3	60.83	33.6	58.58
Buhoth«**PB**»	74.77	59	43.9	59.22	82.3	48.83	37.93	56.36
Abaá95«**QA**»	84.7	69	48.23	67.31	81.3	72.33	47.6	67.08
Abaá99«**RA**»	87.03	63.33	47.07	65.81	80.47	68.67	48.27	65.8
AbóGhuriyb «**SA**»	95.7	85.5	76.9	86.03	88.47	80.67	71.93	80.36
Buhoth22«**TB**»	85.37	76.83	74.23	78.81	89.13	76.33	64.6	76.69
Dujela«**UD**»	89.87	86.5	78.9	85.09	94.8	85.33	73.6	84.58
Nemichinovka «**VN**»	85.87	69.67	52.57	69.37	90.8	63.33	44.07	66.07
AbóRaghef «**WA**»	81.03	71	62.4	71.48	84.97	69.67	55.77	70.13
Means	83.97	68.92	55.19	69.36	83.45	65.76	50.01	66.41
LSD.05	T=0.837	V=3.295	TXV	5.706	T=1.008	V=3.685	TXV	6.383

1.1.67 Results of Enzymatic Physiological Parameters

1.1.67.1 Evaluation of Genotypes for Superoxide Dismutase (SOD) Content (*units.mg^{-1}fw*) in flag leaves

The statistical analysis results in the ANOVA (Appendix 4-4) and Table 35 indicated that superoxide dismutase (SOD) enzyme activity concentration was increased by increasing stress levels, with drought being the most effective at 30% field capacity (1.18 units mg^{-1} FW) compared to the control level of 0.66 units mg^{-1} FW. The UD and TB genotypes also outperformed all other genotypes, recording 1.07 and 1.05 units. mg^{-1}FW, respectively.

Salinity stress significantly enhanced the activity of the enzyme superoxide dismutase. The maximum enzyme activity was 1.12 units mg^{-1} FW at the highest salinity level (15 dS m^{-1}) compared to 0.59 units mg^{-1} FW at control. Among the genotypes studied, the UD treatment at 15 dS m^{-1} showed the highest enzymatic activity (1.19 units mg^{-1} FW). SA, UD, and NF genotypes showed the highest SOD activities across salinity levels when considering genotypic means and these were (0.96, 0.95, and 0.95) units mg^{-1} FW, respectively. These accumulation patterns are useful biochemical markers for distinguishing tolerant and sensitive genotypes. SOD is an important component of the first line of defence of the antioxidant system. It catalyses the dismutation of superoxide anions (O 2 −) to H 2 O 2 and O 2 to reduce oxidative damage to cellular components. The enhanced SOD activity under saline conditions confirms the efficiency of SOD in protecting biological membranes and in alleviating the toxicity of hydrogen peroxide during exposure to stress. Genotypic variation in the SOD activity also indicates differential stress response and is likely to be associated with the underlying differences in gene expression level in tolerant varieties with the highest enzyme concentration per unit fresh weight. The results are consistent with previous studies [106,113] which also demonstrated the significant role of SOD in the alleviation of oxidative stress and its utility as a physiological marker for stress tolerance in plants.

Table 35. Evaluation of Genotypes in SOD Units mg^{-1} FW for Flag Leaf

Salinity	Drought

Genotypes	***Control 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means***	***Control 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	0.65	1	1.11	0.92	0.7	1.06	1.18	0.98
Wafea«**BW**»	0.58	0.85	1.15	0.86	0.64	0.94	1.22	0.93
Latefiya«**C**L»	0.68	0.97	1.14	0.93	0.71	1.09	1.23	1.01
Binekal«**DB**»	0.58	0.84	1.1	0.84	0.64	0.92	1.15	0.9
Urok«**EU**»	0.6	0.84	1.13	0.85	0.64	0.92	1.18	0.91
Sham«**FS**»	0.47	0.77	1.01	0.75	0.59	0.91	1.07	0.86
Fateh«**GF**»	0.57	0.91	1.16	0.88	0.63	0.9	1.15	0.89
Buhoth10«**HB**»	0.6	0.87	1.12	0.86	0.65	0.91	1.15	0.9
Buhoth158«**IB**»	0.58	0.88	1.14	0.87	0.63	0.9	1.12	0.88
Babol113«**JB**»	0.54	0.82	1.1	0.82	0.61	0.9	1.16	0.89
Alraq«**KA**»	0.51	0.81	1.11	0.81	0.62	0.91	1.19	0.91
Bwru«**LB**»	0.56	0.87	1.11	0.85	0.67	0.95	1.21	0.94
Baghdad«**MB**»	0.57	0.81	1.11	0.83	0.65	0.91	1.14	0.9
Faris«**NF**»	0.68	1.01	1.17	0.95	0.75	1.02	1.26	1.01
Tamuz«**OT**»	0.51	0.83	1.08	0.81	0.61	0.91	1.1	0.87
Buhoth«**PB**»	0.52	0.85	1.02	0.8	0.6	0.91	1.09	0.87
Abaá95«**QA**»	0.55	0.87	1.15	0.86	0.65	0.99	1.13	0.92
Abaá99«**RA**»	0.59	0.87	1.11	0.85	0.64	0.92	1.18	0.91
AbóGhuriyb «**SA**»	0.71	1.01	1.17	0.96	0.75	1.07	1.23	1.02
Buhoth22«**TB**»	0.69	0.98	1.16	0.94	0.72	1.17	1.25	1.05
Dujela«**UD**»	0.7	0.97	1.18	0.95	0.77	1.15	1.28	1.07
Nemichinovka «**VN**»	0.57	0.86	1.15	0.86	0.65	0.93	1.18	0.92
AbóRaghef «**WA**»	0.51	0.86	1.15	0.84	0.66	0.95	1.2	0.94
Means	0.59	0.88	1.12	0.86	0.66	0.97	1.18	0.93
LSD.05	T=0.024	V=0.030	TXV	0.051	T=0.007	V=0.030	TXV	0.051

1.1.67.2 Evaluation of Genotypes for Peroxidase (POD) Content (*units.mg^{-1}.fw*) in Flag Leaf

In ANOVA Appendix 4-4 and Table 36, the results of the statistical analysis showed the effects of salinity and drought stresses on the activity rate of the POD

enzyme. Wheat genotypes grown under irrigation water salinity at a level of 15 dS m^{-1} recorded the highest POD enzyme activity rate of 92.21 units mg^{-1} FW, compared to the control level at a salinity of 5 dS m^{-1}, which reached 55.83 units mg^{-1} FW. The SA variety showed the highest average POD activity of 122.36 units mg^{-1} FW among genotypes capable of increasing antioxidant enzyme rates such as peroxidase. With respect to the effect of drought stress on the activity of the peroxide enzyme, there was a significant difference at the significance level of 0.05 between the three levels; at 30% field capacity, the POD activity reached 98.122 units mg^{-1} FW, compared with the control level (90% field capacity) at 65.249 units mg^{-1} FW.

This study on wheat indicated that both salinity and drought significantly increase peroxidase activity as part of the antioxidant defence system, with the severity of the response depending on the wheat variety's tolerance to stress. Under salinity, POD activity increases in salt-tolerant wheat varieties but decreases in salt-sensitive varieties [206]. Similarly, drought stress stimulates peroxidase activity [103,106]. The magnitude of the peroxidase response varies across varieties, with salt-tolerant genotypes showing a greater increase in enzyme activity under stress conditions [207].

Table 36. Evaluation of Genotypes for POD Content (*units.mg^{-1}.fw*) in Flag Leaf

	Salinity				**Drought**			
Genotypes	***(control) 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means***	***(control) 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	61.13	88	120.27	89.8	87.47	100.67	97.27	95.13

Wafea«**BW**»	48.47	80	81.93	70.13	71.13	82	119.3	90.8
Latefiya«**C**L»	73.8	91	128.93	97.91	73.13	111	120.3	101.5
Binekal«**DB**»	51.13	70	77.27	66.13	52.13	87.33	87.6	75.69
Urok«**EU**»	44.13	79.33	84.27	69.24	56.47	98	91.93	82.13
Sham«**FS**»	35.13	50.67	54.6	46.8	33.13	48.67	53.93	45.24
Fateh«**GF**»	55.13	87	96.27	79.47	59.13	78	77.93	71.69
Buhoth10«**HB**»	57.13	81.33	86.27	74.91	62.8	80	80.27	74.36
Buhoth158«**IB**»	53.13	91.27	90.67	78.36	43.13	77.67	82.27	67.69
Babol113«**JB**»	44.47	73.67	73.6	63.91	55.8	82.67	79.93	72.8
Alraq«**KA**»	45.13	63.67	71.6	60.13	62.13	79	86.6	75.91
Bwru«**LB**»	53.47	71.67	77.27	67.47	69.13	82.67	125.6	92.47
Baghdad«**MB**»	54.13	71	72.6	65.91	54.13	86.67	85.6	75.47
Faris«**NF**»	76.47	93.67	131.6	100.6	84.47	95.67	132.9	104.4
Tamuz«**OT**»	39.8	58.33	65.6	54.58	47.8	63.67	66.27	59.24
Buhoth«**PB**»	32.47	54	60.6	49.02	40.47	62	54.6	52.36
Abaá95«**QA**»	59.47	72.67	76.6	69.58	65.13	99.33	94.27	86.24
Abaá99«**RA**»	54.8	72	77.6	68.13	52.47	88.33	87.6	76.13
AbóGhuriyb «**SA**»	101.8	117	148.27	122.4	84.47	101.67	143.6	109.9
Buhoth22«**TB**»	63.13	103	131.93	99.36	93.8	111	151.6	118.8
Dujela«**UD**»	85.8	103	150.27	113.0	109.8	125	154.3	129.7
Nemichinovka «**VN**»	46.13	78.67	86.27	70.36	61.13	105	91.93	86.02
AbóRaghef «**WA**»	47.8	74.67	76.6	66.36	81.47	99.67	91.27	90.8
Means	55.83	79.37	92.21	75.8	65.25	88.94	98.12	84.1
LSD.05	T=3.15	V=5.38	TXV	9.31	T=3.8	V=7.12	TXV	12.33

1.1.67.3 Evaluation of Genotypes for Catalase (CAT) Content (*units.mg^{-1}fw*) in Flag Leaf

ANOVA results Appendix 4-4 and Table 37, showed significant increases in catalase (CAT) enzyme activity under both salinity and drought stress regimes. CAT activity increased significantly ($p < 0.05$) in salinity stress from 39.17 units mg^{-1} FW in control to 62.85 units mg^{-1} FW in highest salinity (15 dS m^{-1}). The highest CAT activity among the genotypes evaluated was observed in UD (74.52 units mg^{-1} FW) under saline conditions.

Similarly, drought stress induced a pronounced elevation in CAT activity, increasing from 42.486 units mg^{-1} FW under well-watered conditions (90% field capacity) to 67.483 units mg^{-1} FW at the most severe drought level (30% field

capacity), also significant at $p < 0.05$. The genotypic means were compared by the least significant difference (LSD) test at 0.05 significance level. It was observed that UD variety showed the highest CAT activity (79.8 units mg^{-1} FW), followed by genotypes TB, SA, NF, and CL with mean values of (70.93, 70.3, 65.7, and 65.55) units mg^{-1} FW, respectively. The obtained results support the importance of CAT in the reduction of oxidative stress by decomposition of hydrogen peroxide (H2O2) to water and molecular oxygen, thus protecting cellular membranes against oxidative damage and maintaining cellular integrity in stressful environmental conditions . The high genotypic variation indicates that wheat genotypes vary in their capacity to induce efficient antioxidant responses. UD is very effective in increasing the CAT activity in both type of stresses. The high genotypic variation indicates that the wheat genotypes vary in their ability to elicit efficient antioxidant responses. UD is quite effective to increase the CAT activity in both types of stresses. CAT enzyme concentration increases alongside proline activity under these stresses, providing an indication of variation in stress tolerance and gene expression in tolerant varieties, which exhibited the highest enzyme concentrations per fresh weight, as reported by [106,113].

Table 37. Evaluation of Genotypes for Catalase (CAT) Content (units. mg^{-1} FW) in Flag Leaf

	Salinity				**Drought**			
Genotypes	***(control) 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means***	***(control) 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	50.4	69.84	63.3	61.18	52.25	78.66	63.52	64.81
Wafea«**BW**»	38.82	48.9	65.04	50.92	41.8	51.17	75.49	56.16
Latefiya«**C**L»	55.02	75.54	67.8	66.12	51.62	80.56	64.47	65.55
Binekal«**DB**»	37.02	57.9	62.34	52.42	44.97	52.44	60.61	52.67
Urok«**EU**»	35.22	46.2	60.54	47.32	42.12	52.76	69.79	54.89
Sham«**FS**»	25.02	39.9	56.04	40.32	33.88	40.72	56.49	43.7
Fateh«**GF**»	40.62	57	63.24	53.62	32.3	52.12	66.94	50.46
Buhoth10«**HB**»	41.52	48.6	56.34	48.82	38.32	49.91	65.04	51.09
Buhoth158«**IB**»	32.82	55.8	67.14	51.92	31.98	50.86	67.26	50.03
Babol113«**JB**»	30.72	45.6	64.44	46.92	33.57	49.27	69.16	50.67
Alraq«**KA**»	29.52	48.3	62.34	46.72	38	54.66	65.68	52.78

Bwru«**LB**»	37.08	47.4	59.34	47.94	44.02	61.31	67.89	57.74
Baghdad«**MB**»	38.52	47.4	70.44	52.12	40.28	51.17	63.78	51.74
Faris«**NF**»	48.42	80.64	67.5	65.52	54.34	74.86	67.96	65.72
Tamuz«**OT**»	36.72	49.2	69.24	51.72	35.15	45.47	65.68	48.77
Buhoth«**PB**»	34.92	50.7	61.14	48.92	27.55	43.26	60.29	43.7
Abaá95«**QA**»	32.22	42	61.14	45.12	35.78	60.04	72.01	55.94
Abaá99«**RA**»	29.22	47.1	62.64	46.32	42.12	57.51	64.41	54.68
AbóGhuriyb «**SA**»	48.42	73.44	59.1	60.32	52.25	86.26	72.39	70.3
Buhoth22«**TB**»	47.82	75.24	60	61.02	59.22	80.88	72.71	70.93
Dujela«**UD**»	61.02	88.44	74.1	74.52	65.55	94.49	79.36	79.8
Nemichinovka «**VN**»	38.82	53.4	59.94	50.72	39.9	53.07	74.23	55.73
AbóRaghef «**WA**»	31.02	37.5	52.44	40.32	40.22	62.26	66.94	56.47
Means	39.17	55.91	62.85	52.65	42.49	60.16	67.48	56.71
LSD.05	T=1.611	V=3.054	TXV	5.289	T=1.611	V=3.054	TXV	5.289

1.1.67.4 Evaluation of Genotypes in Hydrogen Peroxide (H_2O_2) Content in Flag Leaf (µmol g^{-1} FW)

The ANOVA results Appendix 4-4 and Table 38 showed that the concentration of hydrogen peroxide (H_2O_2) increased progressively with increasing severity of salinity and drought stresses. H_2O_2 concentration increased significantly under salinity treatments from 1.7 µmol g^{-1} FW under control (5 dS m^{-1}) to 3.5 µmol g^{-1} FW at the highest salinity (15 dS m^{-1}). This increase indicates the accumulation of damaging reactive oxygen species (ROS) in plant tissues and is a reliable biochemical marker for the distinction of stress-tolerant and stress-sensitive genotypes. Statistical analysis, comparing the genotype means by least significant difference (LSD) test at 0.05 significance level, showed that the FS variety had the highest H_2O_2 concentration (3.09 µmol g^{-1} FW), and this confirmed its high sensitivity to salinity stress. Under drought stress, H_2O_2 concentration increased from 2.45 µmol g^{-1} FW under well-watered conditions to 4.02 µmol g^{-1} FW at the most severe drought level (30% field capacity). Genotypic comparison by LSD test ($p < 0.05$) showed that genotypes FS, PB and OT

had the highest H_2O_2 concentrations with mean values of 3.95, 3.80 and 3.75 µmol g^{-1} FW, respectively.

The concentration of hydrogen peroxide is a key physiological indicator of stress tolerance, reflecting the balance between ROS production and the efficiency of the antioxidative defence mechanisms. Although the antioxidant enzymes were highly active in the varieties studied, the levels of H_2O_2 were relatively high, and the extent of accumulation was dependent on the stress type, stress severity and genotypic constitution. These results are in accordance with previous studies [106,113,208] that also reported H_2O_2 accumulation as a reliable marker of oxidative stress and genotypic differences in ROS homeostasis as important determinants of stress resilience in wheat.

Table 38. Evaluation of Genotypes for H_2O_2 Content (µmol g^{-1} FW) in Flag Leaf

	Salinity				**Drought**			
Genotypes	***(control) 5 ds/m***	***10 ds/m***	***15 ds/m***	***Means***	***(control) 90% FC***	***60%***	***30%***	***Means***
Baraka«**AB**»	1.8	1.32	2.52	1.88	2.66	2.08	3.48	2.74
Wafea«**BW**»	1.51	2.2	3.14	2.29	2.26	3.06	4.1	3.14
Latefiya«**C**L»	1.27	1.77	2.52	1.85	1.88	2.62	3.48	2.66
Binekal«**DB**»	1.87	2.4	3.36	2.54	2.59	3.15	4.23	3.32
Urok«**EU**»	1.6	2.29	3.2	2.36	2.29	3.1	4.16	3.18
Sham«**FS**»	2.29	3.84	3.15	3.09	3.05	4.79	4.01	3.95
Fateh«**GF**»	1.35	2.24	3.1	2.23	2.78	3.45	4.53	3.58
Buhoth10«**HB**»	1.52	2.19	3.14	2.28	2.62	3.28	4.32	3.41
Buhoth158«**IB**»	1.39	2.12	3.28	2.26	2.87	3.49	4.53	3.63
Babol113«**JB**»	2.02	2.59	3.57	2.73	2.73	3.41	4.49	3.55
Alraq«**KA**»	2.63	2.12	3.57	2.77	2.5	3.15	4.23	3.29
Bwru«**LB**»	1.83	2.29	3.27	2.46	2.1	2.97	4.06	3.05
Baghdad«**MB**»	1.97	2.56	3.54	2.69	2.6	3.26	4.23	3.36
Faris«**NF**»	1.58	1.16	2.33	1.69	2.62	2.03	3.29	2.65
Tamuz«**OT**»	2.22	3.39	3.07	2.89	2.98	3.72	4.54	3.75
Buhoth«**PB**»	2.27	2.87	3.7	2.95	3.03	3.72	4.66	3.8
Abaá95«**QA**»	1.53	2.24	3.18	2.32	2.27	3.07	4.1	3.15
Abaá99«**RA**»	1.74	2.3	3.24	2.43	2.36	3.14	4.16	3.22
AbóGhuriyb «**SA**»	1.13	1.53	2.15	1.6	1.92	2.44	3.29	2.55
Buhoth22«**TB**»	1.13	1.8	2.33	1.75	1.89	2.41	3.23	2.51
Dujela«**UD**»	1.14	1.56	2.27	1.65	1.88	2.39	3.11	2.46
Nemichinovka «**VN**»	1.5	2.21	3.14	2.28	2.27	3.1	4.13	3.17

AbóRaghef «**WA**»	1.84	2.42	3.27	2.51	2.15	3.05	4.1	3.1
Means	1.7	2.23	3.05	2.33	2.45	3.08	4.02	3.18
LSD.05	T=0.159	V=0.279	TXV	0.483	T=0.143	V=0.263	TXV	0.456

1.1.68 Correlation between Morphological and Physiological Traits Affected by Abiotic Factors

In Table 39, Pearson correlation analysis for morphological and physiological traits under abiotic stress revealed positive correlations among nearly all traits, though the correlation strengths varied from one trait to another. Under drought stress, the yield trait showed the highest positive correlation (0.917) with organic mass for plant (Bio.pl) and significant correlations at a significance level of 0.05 with relative water content (RWC), organic mass for square metre (Bio.sq), flag leaf chlorophyll content (Chlo), No. of tillers for plant (№.T.P), number of spikes per plant (N.Sq.P), grain weight per spike (G.W.Sq), 1000-grain weight (W.1000), plant height, and flag leaf area (Fl.A). However, it had the lowest correlation with Fl.A. The Chlo trait exhibited the highest positive correlation (0.910) with RWC and significant correlations with RWC, Bio.pl, yield, Bio.sq, W.1000, №.T.P, P.H, N.Sq.P, G.W.Sq, and Fl.A. The G.W.Sq showed the highest positive correlation (0.602) with Fl.A and significant correlations with Fl.A, W.1000, P.H, N.Sq.P, RWC, Chlo, Bio.pl, №.T.P, yield, and Bio.sq. Under salinity stress Table 39, the yield trait had the highest positive correlation (0.923) with Bio.pl and significant correlations with the following traits: Bio.pl, RWC, Chlo, Bio.m2, №.T.P, №.Sp.P, W.1000, P.H, G.W.Sq, and Fl.A. The N.T.P trait had the highest positive correlation (0.836) with spike number (№.Sp.P) and significant correlations with №.Sp.P, Bio.m2, yield, Chlo, Bio.pl, RWC, G.W.Sq, P.H, and W.1000 but lower correlation with Fl.A. The correlation between yield and plant biomass under both salinity and drought stresses was highly positive, consistent with findings from other researchers.[209,210]. Therefore, understanding and

improving organic mass for plants, along with its correlation to grain yield traits, is crucial for enhancing overall productivity in wheat and barley cultivation.

Table 39. Pearson Correlation of Morphological and Physiological Traits Under Drought (under the diagonal) and salinity (on top of the diagonal) stress.

Pearson's correlation between traits under salinity stress

Pearson's correlation between traits under drought stress	Traits	Yield	Bio.pl	Bio.sq	N.T.P	N.Sq.P	G.W.Sq	W.1000	Fl.A	P.H	Chlo	RWC
	yield	1*	**0.92***	0.78*	0.55*	0.52*	0.43*	0.44*	0.36*	0.43*	0.80*	0.89*
	Bio.pl	**0.92***	1*	0.74*	0.49*	0.44*	0.36*	0.39*	0.32*	0.40*	0.80*	0.88*
	Bio.sq	0.81*	0.84*	1*	0.60*	0.62*	0.37*	0.45*	0.23*	0.54*	0.73*	0.78*
	N.T.P	0.68*	0.62*	0.62*	1*	0.84*	0.35*	0.26*	0.15ns	0.28*	0.53*	0.48*
	N.Sq.P	0.61*	0.55*	0.66*	0.77*	1*	0.49*	0.37*	0.31*	0.46*	0.48*	0.44*
	G.W.Sq	0.45*	0.46*	0.44*	0.45*	0.49*	1*	0.63*	0.61*	0.59*	0.43*	0.39*
	W.1000	0.42*	0.49*	0.49*	0.41*	0.42*	0.58*	1*	0.63*	0.60*	0.45*	0.45*
	Fl.A	0.25*	0.27*	0.29*	0.25*	0.32*	0.60*	0.68*	1*	0.67*	0.38*	0.33*
	P.H	0.39*	0.47*	0.58*	0.38*	0.49*	0.57*	0.64*	0.70*	1*	0.53*	0.46*
	Chlo	0.79*	0.88*	0.78*	0.55*	0.48*	0.47*	0.56*	0.41*	0.54*	1*	0.83*
	RWC	0.87*	0.89*	0.81*	0.60*	0.52*	0.49*	0.49*	0.37*	0.51*	0.91*	1*

*=significant at 5 % and ns = non-significant

Effect of Abiotic Stress on Biochemical Indicators of Genotypes

1.1.69 Evaluation of Sodium (Na^+) and Potassium (K^+) Content in Genotypes Under Salinity Stress

The ANOVA results Appendix 4-5 and Table 40, statistical analysis of sodium absorption in wheat leaves revealed the highest sodium content at level of 15 ds m^{-1} (22%) while at the control treatment (14%). K^+ concentration in wheat leaves at the control (5 ds m^{-1}) level was 33% but decreased to 28% (10 ds m^{-1}) and 20% (15 ds m^{-1}) respectively, as high Na^+ concentrations in saline soil and irrigation water inhibit K^+ influx into cells, reducing cellular K^+ levels [211]. Consequently, the Na^+/K^+ ratio increased significantly across all NaCl treatments, with a significant treatment effect at 0.05, with the control level being 46% (control), 71% (10 ds m^{-1}), and 1.35% (15 ds m^{-1}). However, genotypes (SA, UD, TB, NF, CL, AB) exhibited lower Na^+ accumulation and reduced Na^+/K^+ ratios relative to other cultivars, indicating superior capacity for maintaining ionic balance. This enhanced Na^+ and K^+ homeostasis likely contributes to minimising salt stress-induced damage to cellular structures and metabolic processes, thereby conferring greater salinity tolerance. These findings underscore the importance of ion selectivity and compartmentalisation as key determinants of genotypic adaptation to saline conditions [212].

Table 40. Evaluation of Genotypes for Na^+ and K^+ content in Leaves under Salinity Stress

%Na^+ (dS m^{-1})					**%K^+ (dS m^{-1})**				**Na^+/K^+ (dS m^{-1})**			
Genotype	***Control***	***10***	***15***	***Means***	***Control***	***10***	***15***	***Mean***	***Control***	***10***	***15***	***Means***
Baraka«**AB**»	13	19	19	17	40	30	28	33	36	64	73	57
Wafea«**BW**»	15	18	22	18	37	29	16	27	41	64	136	81

Latefiya«**C**L»	13	18	18	16	35	35	29	33	38	51	64	51
Binekal«**DB**»	15	19	23	19	30	21	12	21	51	88	201	114
Urok«**EU**»	15	18	23	19	34	25	19	26	50	72	124	82
Sham«**FS**»	17	21	28	22	22	18	15	18	78	114	195	129
Fateh«**GF**»	14	17	24	18	36	36	21	31	38	47	115	67
Buhoth10«**HB**»	14	16	24	18	41	33	15	29	42	51	165	86
Buhoth158«**IB**»	15	17	22	18	38	30	23	30	39	57	100	65
Babol113«**JB**»	14	19	24	19	28	24	10	21	52	77	242	124
Alraq«**KA**»	15	20	26	20	27	22	13	21	56	92	203	117
Bwru«**LB**»	15	17	24	19	32	23	16	24	47	76	152	92
Baghdad«**MB**»	15	17	24	19	30	19	14	21	55	91	182	109
Faris«**NF**»	12	18	17	16	37	37	35	37	33	48	49	43
Tamuz«**OT**»	17	21	26	21	25	20	15	20	66	103	174	114
Buhoth«**PB**»	15	23	27	22	24	20	16	20	62	114	170	115
Abaá95«**QA**»	14	18	23	19	33	29	16	26	43	63	148	85
Abaá99«**RA**»	14	18	23	19	36	24	13	24	41	76	181	99
AbóGhuriyb «**SA**»	11	15	15	14	42	43	39	41	26	35	38	33
Buhoth22«**TB**»	13	18	18	16	37	34	29	34	34	53	62	50
Dujela«**UD**»	13	17	17	16	40	38	33	37	33	46	51	43
Nemichinovka «**VN**»	14	17	23	18	38	30	17	28	39	59	145	81
AbóRaghef«**WA**»	15	18	23	19	26	21	17	21	58	86	137	94
Means	14	18	22	18	33	28	20	27	46	71	135	84
LSD 0.05	T=0.01, V=0.02, TXV =0.037				T=0.008, V=0.043, TXV =0.074				T=0.1, V=0.164, TXV=0.285			

1.1.70 Evaluation of Genotypes for Nitrogen (N) Content in Wheat Plants Under Drought Stress

In the ANOVA tables from Appendix 4-5 and Table 41, nitrogen content in plant leaves at the control level of 2.56% was higher than at 60% and 30% field capacity, which had means of 2.15% and 1.96%, respectively, LSD test ($p < 0.05$). These conclusions complement prior findings on the challenge of feeding plants with

adequate nitrogen from the soil under drought stress, since the presence and availability of nitrogen in the soil depends on both water and temperature [116]. Among the genotypes, the UD, CL, TB, and SA varieties demonstrated significant superiority at ($p < 0.05$), with averages of 2.59%, 2.58%, 2.58%, and 2.55%, respectively. These were followed by NF and AB varieties, with averages of 2.49% and 2.40%, respectively. The FS and PB varieties exhibited the lowest nitrogen content in leaves, with averages of 1.87% and 1.9%. Genotypes that maintain the highest possible levels of macro- and micronutrients under water-deficient conditions are of particular interest to plant breeders [103,115].

Table 41. Evaluation of Nitrogen concentration (N%) of Genotypes under Drought Stress.

Genotype	***(Control) 90% FC***	***60% FC***	***30%FC***	***Means***
Baraka«**AB**»	2.71	2.34	2.13	**2.4**
Wafea«**BW**»	2.63	2.2	2.01	2.28
Latefiya«**C**L»	2.96	2.51	2.27	**2.58**
Binekal«**DB**»	2.46	2.08	1.92	2.15
Urok«**EU**»	2.58	2.15	1.86	2.2
Sham«**FS**»	2.17	1.82	1.63	1.87
Fateh«**GF**»	2.29	1.91	1.78	1.99
Buhoth10«**HB**»	2.4	1.97	1.82	2.06
Buhoth158«**IB**»	2.22	1.88	1.77	1.95
Babol113«**JB**»	2.35	1.95	1.84	2.04
Alraq«**KA**»	2.49	2.1	1.91	2.17
Bwru«**LB**»	2.79	2.23	2.08	2.37
Baghdad«**MB**»	2.39	2	1.82	2.07
Faris«**NF**»	2.85	2.45	2.17	**2.49**
Tamuz«**OT**»	2.19	1.85	1.69	1.91
Buhoth«**PB**»	2.2	1.83	1.67	1.9
Abaá95«**QA**»	2.58	2.21	1.95	2.25
Abaá99«**RA**»	2.54	2.09	1.88	2.17
AbóGhuriyb«**SA**»	2.91	2.51	2.24	**2.55**
Buhoth22«**TB**»	2.96	2.51	2.27	**2.58**
Dujela«**UD**»	2.95	2.54	2.28	**2.59**

Nemichinovka«**VN**»	2.58	2.13	1.98	2.23
AbóRaghef«**WA**»	2.72	2.26	2.06	2.35
Means	2.56	2.15	1.96	2.22
LSD 0.05	T= 0.022	V= 0.047	TXV	0.082

Dendrogram and Dissimilarity Matrix Analysis of Genotypes

1.1.71 Classification of Genotypes Based on Tolerance to Salt Stress

In the matrix in Appendix 4-9, Euclidean distances among the various genotypes were evaluated using mean values of morphological, physiological, and biochemical indicators, employing Ward's method in SPSS for the analysis. The genetic dissimilarity matrix revealed that the maximum Euclidean distance, measuring 8.57, was recorded between genotypes SA and PB, indicating significant genetic divergence. Conversely, the minimum Euclidean distance of 1.125 was observed between genotypes MB and DB, suggesting a closer genetic relationship between these two. This quantitative assessment provides critical insights into the genetic relationships among the examined genotypes.

According to the results of morpho-physiological characteristics, yield components and sensitivity indices of genotypes to salt stress, the 23 genotypes were classified into four groups based on their salinity tolerance: highly salinity-tolerant genotypes (A), moderately salinity-tolerant genotypes (B), moderately salinity-sensitive genotypes (C) and highly salinity-sensitive genotypes (D) In Figure 37. Results of morphological and physiological traits indicated that genotypes SA, UD and NF were tolerant to salinity and were included in the cluster A. Cluster B (genotypes AB, GF, CL and TB) exhibited moderate tolerance based on some morphological and physiological traits related to biomass and chlorophyll content but grain yield was less than that of cluster (A). Cluster (C) comprised genotypes EU, QA, RA, LB, BW, HB, IB, and VN, and cluster (D) comprised genotypes DB, MB, WA, JB, KA, OT, PB, and FS, which exhibited high sensitivity to salinity concentrations through grain

productivity and yield-related traits that deteriorated with the increase in salt concentration. Researchers [54,198] have reported some of these genotypes in previous studies, citing the principles of genetic variation and similarity in morphological and physiological traits, thereby lending further support to the present findings.

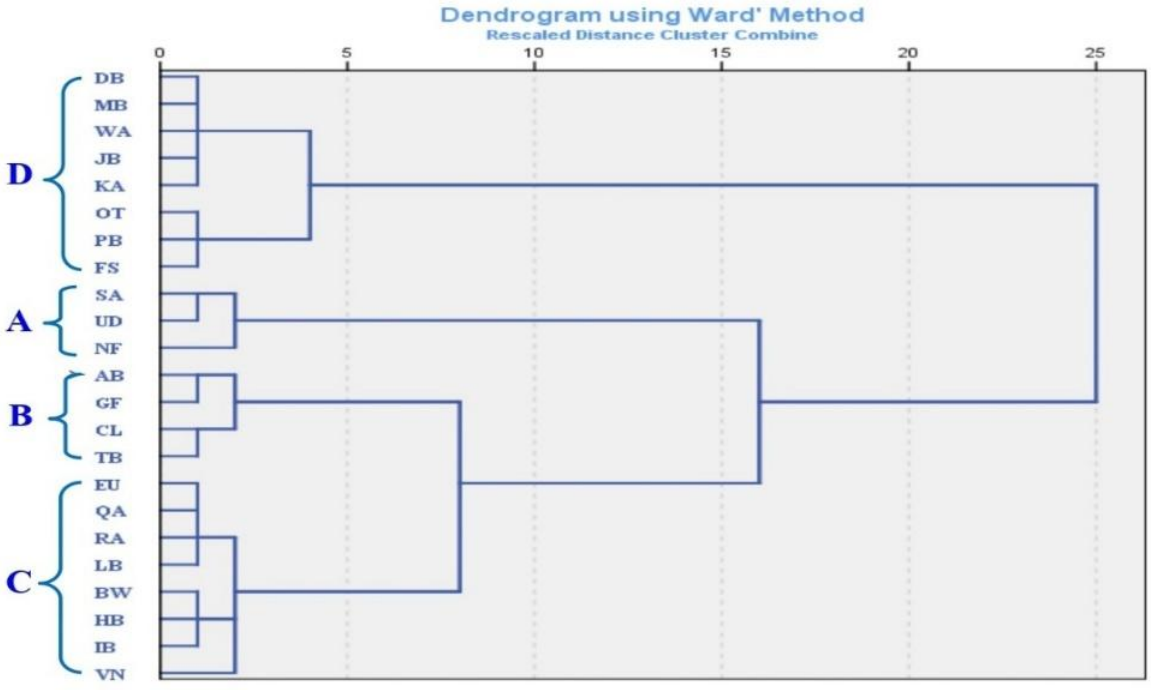


Figure 37. A tree diagram for classifying genotypes based on tolerance of salt stress.

1.1.72 Classification of Genotypes Based on Tolerance to Drought Stress

For the purpose of determining the genetic divergence among the 23 genotypes of wheat by morphological and physiological indicators under drought stress, a

dissimilarity matrix was prepared based on Euclidean distance coefficients Appendix 0-9 .

The pairwise distance analysis showed considerable genetic variability, with the maximum Euclidean distance (10.37) observed between genotypes UD and MB indicating a high degree of phenotypic divergence. The least distance (1.087) was observed between genotypes VN and WA which indicated the close phenotypic similarity. The yield components and stress susceptibility indices under drought condition. Hierarchical classification of 23 genotypes into four distinct clusters was performed using the integrated assessment of morphological and physiological traits, yield components, and stress susceptibility indices Figure 38: Cluster (A) – Highly Drought Tolerant Genotypes: This cluster included genotypes UD, SA and TB which exhibited consistently better performance for all the morphological and physiological parameters studied and favourable tolerance indices indicating higher tolerance to water deficit. Cluster (B) – Moderately Drought Tolerant Genotypes: The genotypes (CL, NF, AB) formed this cluster. This cluster showed moderate tolerance in terms of acceptable expression of some morphological traits. However, grain productivity was much lower compared to that of Cluster (A), implying a partial trade-off between stress adaptation and yield potential. Cluster (C) – Genotypes with Moderate Drought Sensitivity The largest cluster consisted of genotypes (EU, RA, KA, DB, VN, BW, QA, WA, LB). Intermediate adaptability as indicated by yield-based sensitivity evaluations supported moderate sensitivity of the studied genotypes to water stress at 60% field capacity. Cluster (D) – Highly Drought-Sensitive Genotypes: The genotypes (FS, OT, PB, HB, MB, JB, GF, IB) belonging to this cluster were found to be highly sensitive to drought as evidenced by the significant reduction in P.H , biomass accumulation and grain yield under stress conditions thus validating their poor performance and limited adaptive potential. This classification system offers a reliable basis for genotype selection for drought prone areas and paves avenues for targeted breeding strategies for improving drought tolerance and yield stability in wheat.

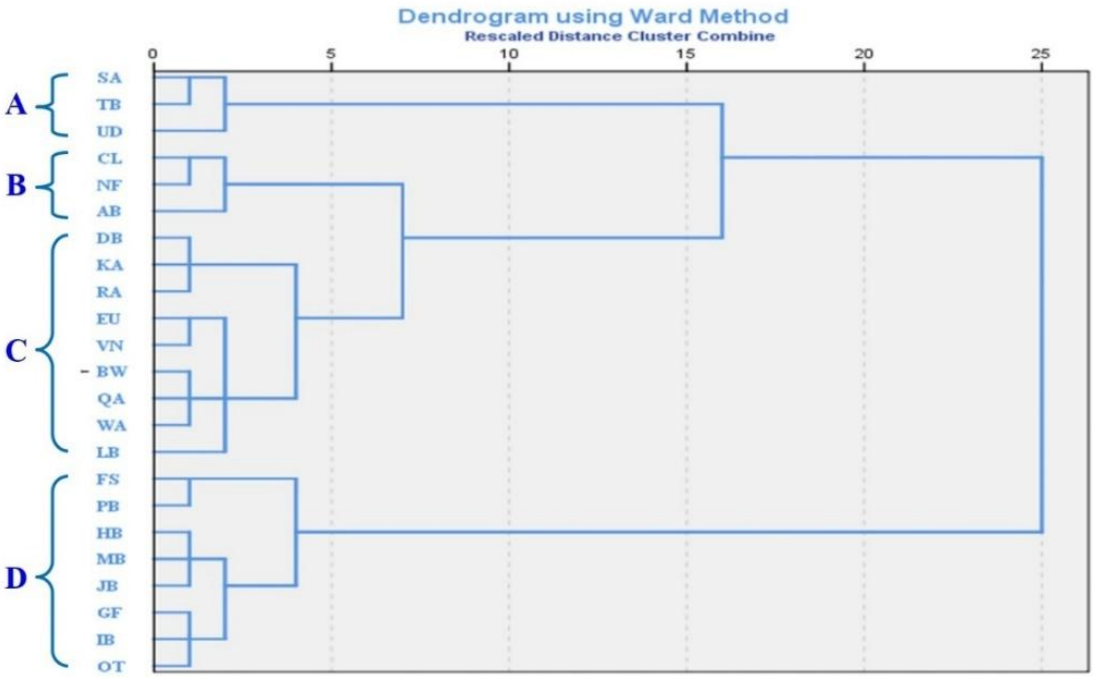


Figure 38. A tree diagram for classifying genotypes based on tolerance of water stress.

Results of Molecular Diagnosis

1.1.73 Results of ISSR-PCR Markers

1.1.73.1 Evaluation of Novel ISSR-PCR Markers

The 23 wheat genotypes were subjected to PCR-based molecular analysis using twenty inter-simple sequence repeat (ISSR) primers (Appendix 4-10 and Table 42). A total of 821 amplification fragments were obtained with an average multiplex ratio (MR) of (41.05) bands to each primer. No amplification products were observed for primers ISSR-(8, 20) using gel electrophoresis as a standard. This suggests that the primers ISSR- (8, 20) do not discriminate among the genotypes studied.

An average of 37.6 bands per primer was polymorphic out of the total amplified fragments, a total of polymorphic bands (Pb) ranging from 18 ISSR- (6, 7) primers to 71 ISSR- (18, 3) primers. Polymorphism (P%) ranged from 37 to 100% and 68% as an average for the primer. The dataset showed a total of 69 monomorphic bands (Mb), which were distributed among the primers ISSR-(1, 15, 19). In addition, 55 unique bands (Ub) were detected, and ISSR-15 primer was obtained the high number (7) unique bands. The MI a combined measure of polymorphic information content and multiplex ratio, was highest for primer ISSR-1 (11.34), with an overall mean of 5.0 for all the primers. The highest resolving power (RP), which indicates the discriminatory power of each primer, was found for primers ISSR(3,18) with a value of 9.45. The mean polymorphic information content (PIC) for all primers as an indicator of allele diversity was 0.2, and the maximum value (0.29) was obtained for primer ISSR-11. The amplified fragments were in the molecular weight (MW) range of (184.45-2042.3) bp with the high MW (3388 bp) in primer ISSR-1. The results of PCR-ISSR profiling indicated that most of the primers were efficient in discriminating the genotypes, confirming the usefulness of ISSR markers as a powerful tool for estimating genetic diversity and identifying genotypes in wheat breeding programmes.

Table 42. Features of ISSR markers in the study

Primers ISSR-№	Mb	Ub	Non-Ub	Pb	Tb	P%	EMR	PIC	RP	MI	MW Base pair (bp)
ISSR-1	1	2	5	7	8	87.5%	612.5	0.15	1.39	92.0	25-3388
ISSR-2		3	4	7	7	100%	700	0.23	1.91	158.8	424-1315

ISSR-3		5	8	13	13	100%	1300	0.20	3.30	253.9	302-2877
ISSR-4		2	5	7	7	100%	700	0.23	2.09	158.8	145-2457
ISSR-5		4	7	11	11	100%	1100	0.23	3.74	257.8	77-3004
ISSR-6		1	5	6	6	100%	600	0.22	1.65	132.3	153-1603
ISSR-7		2	2	4	4	100%	400	0.27	1.57	106.6	75-1814
ISSR-9		3	4	7	7	100%	700	0.21	2.96	148.7	700-2729
ISSR-10		2	7	9	9	100%	900	0.25	2.78	222.3	605-2872
ISSR-11		5	9	14	14	100%	1400	**0.29**	1.74	**410.2**	268-1622
ISSR-12		2	2	4	4	100%	400	0.19	0.87	74.1	78-313
ISSR-13		3	8	11	11	100%	1100	0.21	2.96	235.2	2-1740
ISSR-14		4	11	15	15	100%	1500	0.21	4.17	319.8	187-3091
ISSR-15	1	7	6	13	14	92.9%	1207.1	0.15	2.52	181.9	52-2105
ISSR-16		2	4	6	6	100%	600	0.24	1.91	142.9	88-2473
ISSR-17		2	13	15	15	100%	1500	0.21	2.43	315.3	13-2898
ISSR-18		4	9	13	13	100%	1300	0.25	**4.70**	330.4	74-1996
ISSR-19	1	2	8	10	11	90.9%	909.1	0.18	2.43	166.9	189-2549
SUM	3	55	117	172	175	1771.3	16929	3.9	45.1	3708	3689-40846
Means	0.15	2.75	5.85	8.6	8.75	88.6	846.4	0.2	2.3	185.4	184.5-2042

Total of bands (Tb), Polymorphic bands (Pb), Polymorphism (P%), Monomorphic bands (Mb), number of Unique bands (Ub), Non-Unique bands (Non-Ub), Marker Index (MI), Resolving Power (RP), Polymorphic Information Content (PIC), and Molecular Weight (MW).

1.1.73.2 ISSR-PCR Analysis of Genotypes based on the Number of Bands

For the genotypes in Figure 39 and Appendix 4-10, the resulting largest average number of bands was observed for genotype KA, which was 45 bands. The WA genotype had the lowest (23 bands), with an average of 1.21. Genotypes (UD, TB, and NF) produced 41, 43, and 32 bands, respectively, with averages of 2.05, 2.15, and 1.60 bands per primer.

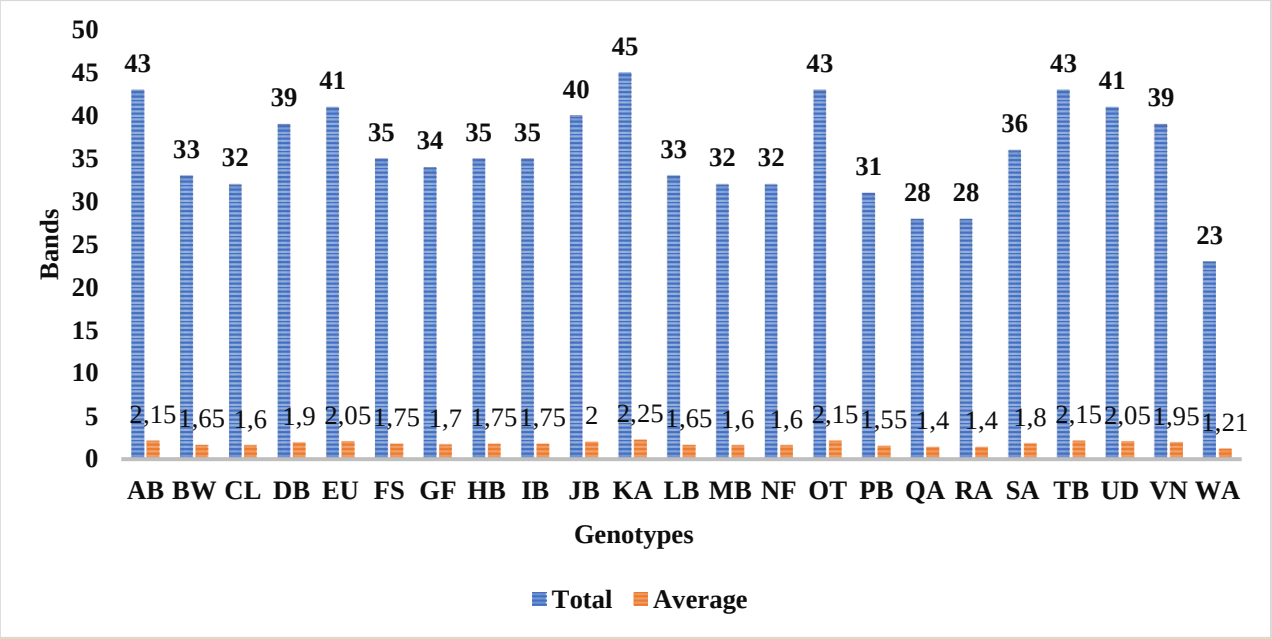


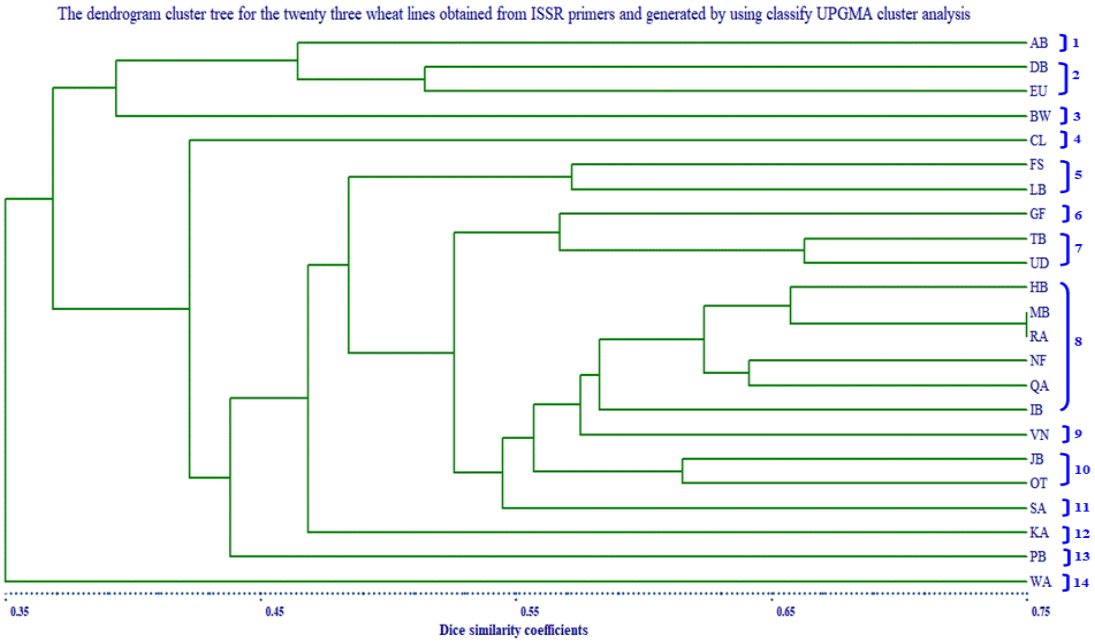
Figure 39. Genotypes, Number of Bands, and Average Number of Bands for each Variety

1.1.73.3 Genetic similarity and fingerprinting of varieties using ISSR-PCR

Similarity (GS) and fingerprinting of 23 wheat varieties calculated from the ISSR marker matrix data Appendix 4-11 revealed a high genetic divergence. The lowest GS value (0.21) was observed between the WA and CL genotypes with high genetic distance. However, the highest similarity (0.75) was observed between the MB and RA genotypes, meaning that these two genotypes were genetically closely related. The average genetic similarity of all genotypes was 0.48, which implies that the analysed genotypes were genetically dissimilar by an average of 0.52. The dendrogram based on the similarity matrix Figure 40 was divided into two main clusters. Cluster 1 contained only the WA genotype, which is from Turkey, and the distance between this cluster and all other clusters was 0.79, indicating its different genetic background. The second major cluster was further subdivided into several subclusters. The BW genotype from France was detected in Cluster 3, with a genetic distance of about 0.63 from Clusters 1 and 2. Cluster 1 (genotype AB) and Cluster 2 (genotypes DB and EU) were the genetically closest clusters. A majority of the genotypes in Cluster 8 were found to have similar parental genetic backgrounds, which was supported by pedigree

information in Table 5. The similarity value between clusters (8, 9) of the VN genotype and its origin from Russia was found to be 0.57. The RA and QA genotypes are closely related and come from common genetic sources of the International Maize and Wheat Improvement Centre (CIMMYT). RA is one of the parental lines that was used in the hybridisation programme for the development of variety HB. The highest genetic similarity (0.75) was observed between genotypes MB and RA, which also supports their close relationship. Cluster 10 included genotypes JB and OT, both mutants obtained by radiation mutation breeding, with a common genetic background, and originated from the parental line MEXIPAK, as described in Table 5. The cluster pattern of the present study indicates the utility of ISSR markers in identifying genetic relationships and tracing associations based on pedigree and thus provides vital information for the selection of parents and management of genetic resources in wheat breeding programmes.

Figure 40. A tree diagram for genetic similarity and fingerprinting of wheat



genotypes based on ISSR-PCR Markers.

1.1.74 Results of SSR-PCR Markers

1.1.74.1 Identification of resistant drought varieties employing SSR primers

The genetic variation among the wheat genotypes was analysed by PCR-based simple sequence repeat (SSR) marker analysis using gel electrophoresis as a standard. The amplification products for the primer (Malek-1) were observed in (CL, NF, SA, UD, TB) genotypes in Figure 41. Likewise, the primer (Malek-2) showed visible bands in (AB, CL, TB, UD, SA, NF) genotypes, also shown in Figure 41. The identification of these amplification products confirms successful binding of the primers to the genomic DNA of the respective candidate genotypes, indicating the presence of conserved target loci. Conversely, genotypes (PB, JB and LB) did not show any amplification products with either primer, thus corroborating previous morphological and physiological assessments indicating that these genotypes are stress sensitive. Moreover, primer pairs Xgwm130 and Xwmc245 failed to generate any binding products in all samples probably because of divergence of nucleotide sequence or absence of loci of wheat varieties tested, which demonstrated the genetic differences inherent to the germplasm tested.

The main aim of this work was to select new wheat varieties with improved tolerance to adverse environmental conditions. This will help in breeding programmes for developing wheat that can survive in the face of stress. Based on the integrated molecular and phenotypic characterisation, the genotypes (NF, UD, SA, TB, AB and CL) were selected for further sequencing and genetic mapping analyses. The genotypes exhibited consistent marker amplification, better stress tolerance and good agronomic performance and hence are good candidates for further genetic improvement and functional genomic studies.

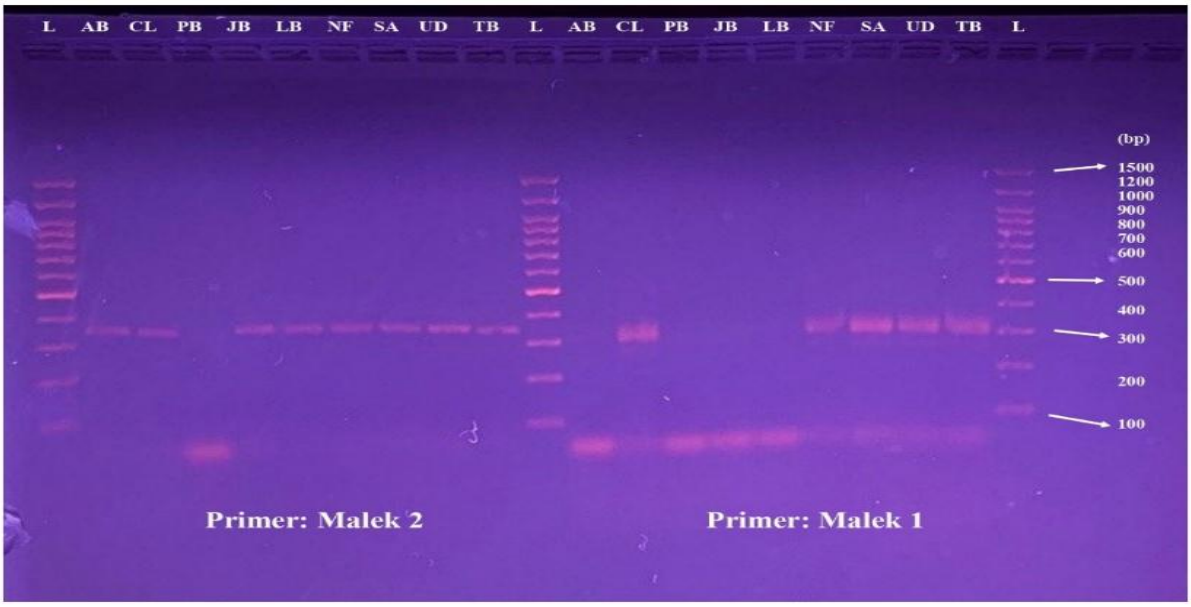


Figure 41. Results of SSR-PCR (Malek1, Malek2) primers.

1.1.74.2 Identification of resistant salinity varieties employing SSR primers

Further validation of the genetic distinctness of the selected stress-tolerant genotypes was performed using additional SSR markers via electrophoresis gel analysis. Primer Xgwm-493 was successful in the amplification of DNA fragments in the genotypes (AB, NF, CL, SA, UD, TB) as shown in Figure 42. Meanwhile, primer Xcfd-18 produced a detectable amplification product only in genotype CL in Figure 42. The presence of these radioactive bands confirms the annealing of the primer-template and the genetic integrity of the candidate genotypes, thus corroborating the physiological and morphological data obtained from field experiments. The genotype PB did not produce any amplification bands for any of the selected primers, which further confirms that PB is a genetically distinct and stress-sensitive genotype as observed during the previous phenotypic evaluation.

These molecular data give a strong genetic basis to the physiological and agronomical observations and confirm the robustness of the integrated screening method. The same amplification patterns were found in (NF, UD, SA, TB, AB, CL)

genotypes, which further supports their selection as promising candidates for downstream applications. Thus, these findings provide the basis for future work on sequencing to characterise candidate genes and quantitative trait loci (QTLs) for salinity and drought tolerance and to facilitate marker-assisted selection and breeding of stress-tolerant wheat cultivars.

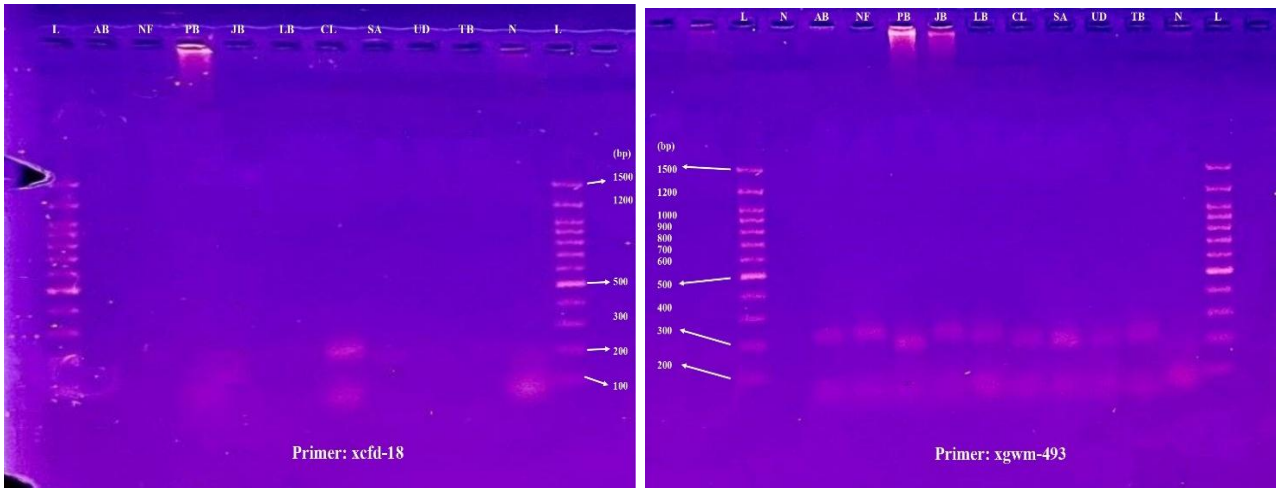


Figure 42. Results of SSR-PCR (xcfd-18, xgwm-493) primers

1.1.75 Sequencing and BLAST analysisof genetic loci resistant to abiotic stress

The study focused on three loci within the Triticum sequences analysed: the *DRF1* gene, the *NAC20L* gene, and *microsatellite* sequences. The samples were used to partially amplify these loci within the same organism. The sequencing reactions indicated the exact identity after performing the *NCBI BLASTn* for these PCR amplicons.

The *NCBI BLASTn* analysis for the DRF1 gene showed that the sequenced samples in Table 44 (E1, E2, R1, R2, and R3) exhibited up to 99% sequence similarity

with the targeted *DRF1* gene sequences of Triticum turgidum (GenBank accession KM504244.1)

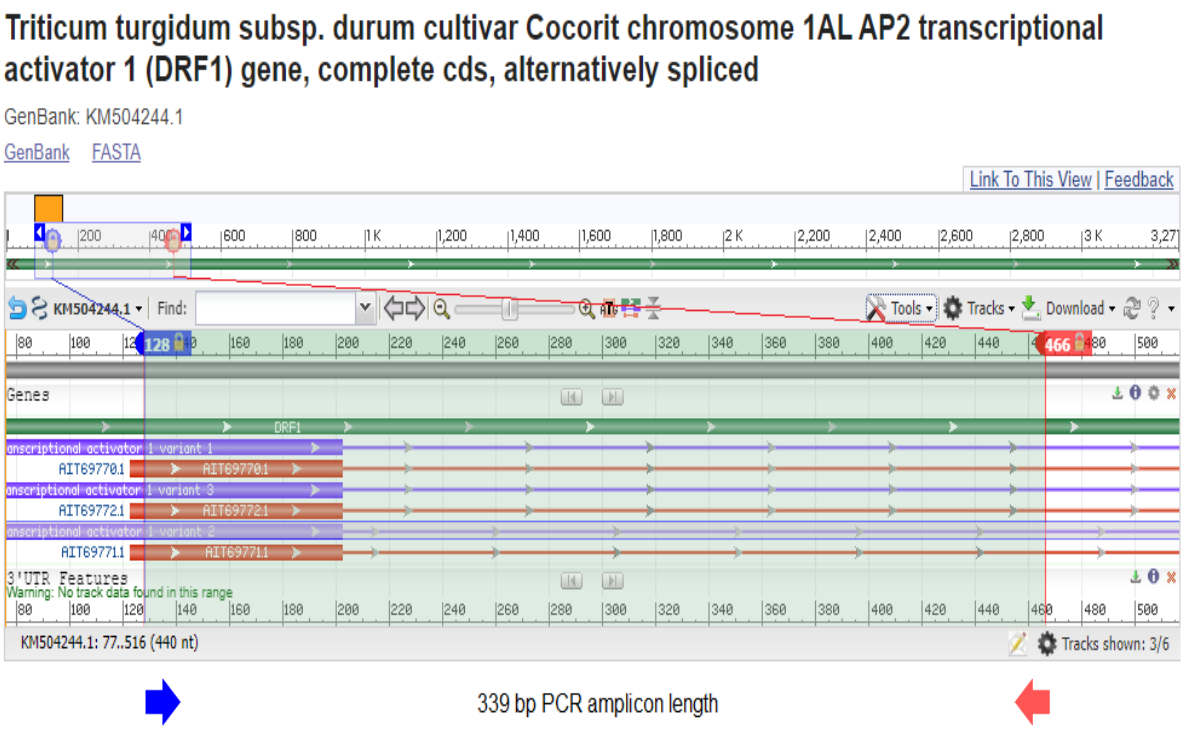
Figure 43. Similarly, the *NCBI BLASTn* analysis showed 100% sequence similarity between the sequenced samples (S1, S2, S3, S4, and S5) in Table 44 and the *NAC20L* gene sequence of *Triticum aestivum* (GenBank accession XM_044571539.1), which is also shown in

Figure 43. In addition, the *NCBI BLASTn* analysis confirmed the total sequence similarity between the sequenced samples (assigned Q1, Q2, Q3 and Q4) in Table 44 and the microsatellite sequences of the Triticum turgidum (GenBank accession AF275898.1) as illustrated in

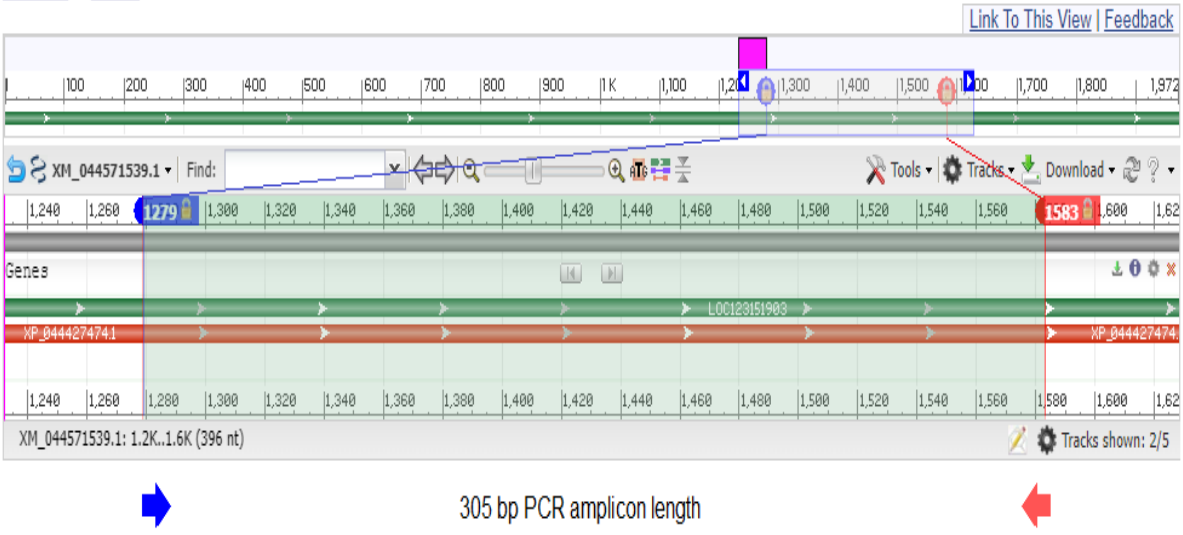
Figure 43. The precise positions and characteristics of the retrieved PCR fragments were determined for the targeted sequences. The total lengths of the targeted loci were mapped onto the NCBI database, and the locations of the amplified PCR fragments were further confirmed based on the most homologous reference sequences available.

The high similarity alignments are a convincing validation for the successful amplification and sequencing of the target loci and provide a strong molecular basis for the identification of stress associated genetic markers in the selected wheat genotypes.

A) *DRF1 gene*



B) *NAC20L gene*



C) *microsatellite sequences*

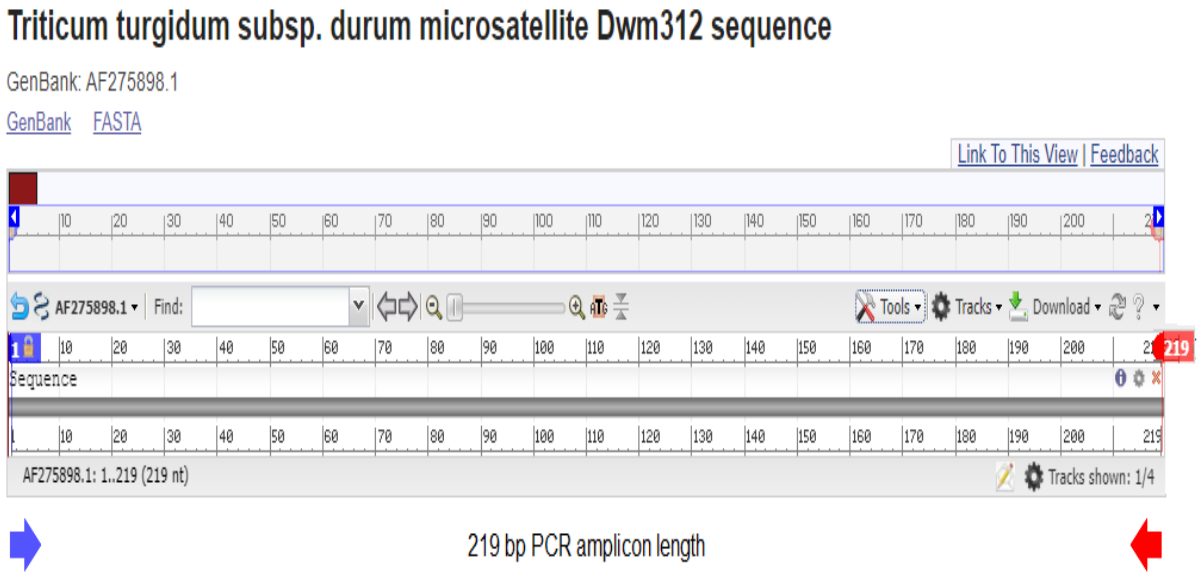


Figure 43. The DRF1 (in branch A), NAC20L (in branch B), and microsatellite sequences (in branch C) within Triticum sequences.

Following the alignment of the PCR amplicon sequences within the Triticum genomic sequences, the distinctive features of these fragments were characterized, and the total lengths of the amplified products were subsequently determined (Table 43).

Table 43. Features of the DRF1 gene sequences (Branch A), the NAC20L gene sequences (Branch B), and the microsatellite sequences (Branch C) within the wheat genomic sequences.

Genes	Sequences (5′ - 3′)	Length(base pair)
***A) DRF1* gene sequences**	*GGTAGATCGGAAGGACGCCGAGGCGGCGGCGGCGGCGGCGACGCC CTTCGAGATCCCGGCGCTCCAGCCTGGAAGGTGAGATCTTCTGTCCG GTGCCTGCTTCTTGTTAGGGTTTGCTCTGGGGGTTCGAAATCGGTTCG GGATACGGTCCCGGGAGTGTTTAATTCTCTGTTGGCTGGTCGATTTG GGTGCTTGGAGTTGGGAATTGTGGGGTTCGGTGGTAGAGTTGGCCGG TCTTGGTGCCTGTGTTGTAGGGATTTGGGGATTAGGGTTTCCGGTTAT	339 bp

	GGTTGTATTGGCAATTGGGAGTTACTTTCTAGTTCCAATTTGGTTATG AGCCCCCTG**	
B) *NAC20L gene* sequences	*ATTGCAAGGAGCACATCTGAAGAGGTTGTCTTTGAGCCATTGGAGC CTGTTTCCAATTTGCTGGATGAGGAGGCAGATGGTTTTGACCTTGAA GAACTAATGAGAATGATGGAAGACGACCCAATTGAAGTTGAGCCGG TCACTGGAGCCAGCACTGGCGTGGAGATGGGCCAACAGGAACCTCT GTACCTGGATACCTTGGACCAAGGCAGGCTGGAGGACATGCTGCAG TCCGATTGCCCTTACCCAATGTGGTGGAGATCAGAGGACGGGGCCAT GCACAACCCTGCCTCCCATGATGCTGA**	305 bp
C) *microsatellite sequences* sequences	*ATCGCATGATGCACGTAGAGTAGATGTGATGTAGGGCTCGTCGTTA CTTGGGTGGTGGAGTGAGTGTGAAGCCATTATGATTTTTGACCACTG CCCCGTGCCCCCGGGAAAACAAAGGCGGAGAGAGAGAGAGAGAGA GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG TGGCCGGCCTCCCCCACCATTAGGTAGGCATGCATGT**	219 bp
* Forward primer (placed in the forward direction) ** Reverse primer (placed in reverse complement direction)		

The amplified DRF1 gene sequences were aligned with the closest reference sequence (GenBank KM504244.1), and two nucleotide polymorphisms were detected, as shown in Table 44 and

Figure 44.

The first variant was found only in sample E1 and was a cytosine (C) to thymine (T) transition at position 19 (19C>T). In all samples (E1, E2, R1, R2, and R3) a second variant was detected: an adenine (A) to guanine (G) substitution at position 265 (265A>G) (Fig. 2a).

Sequence alignment of the NAC20L gene amplicons from samples S1, S2, S3, S4 and S5 with the reference sequence (GenBank XM_044571539.1), however, did

not reveal any nucleotide polymorphisms, suggesting that the sequence was conserved among the samples analysed Table 44 and

Figure 44.

Likewise, microsatellite sequence alignment of samples Q1, Q2, Q3 and Q4 to the reference sequence (GenBank AF275898.1) revealed no genetic variation, indicating complete sequence identity for all analysed samples Table 44 and

Figure 44.

The results suggest the presence of specific SNPs in the DRF1 gene that may be linked to genotypic variation, whereas the NAC20L gene and the microsatellite loci are highly conserved in the wheat genotypes examined. The identified SNPs in the DRF1 gene need further studies to understand their potential functional implications in stress response pathways.

A) *DRF1 gene*

```
                10        20        30        40        50        60        70        80        90       100
        ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
ref.    GGTAGATCGGAAGGACGCCGAGGCGGCGGCGGCGGCGACGCCCTTCGAGATCCCGGCGCTCCAGCCTGGAAGGTGAGATCTTCTGTCCGGTGCCTGC
E1      ..................T.....................................................................................
E2      ..................T.....................................................................................
R1      ..................T.....................................................................................
R2      ..................T.....................................................................................
R3      ..................T.....................................................................................

               110       120       130       140       150       160       170       180       190       200
        ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
ref.    TTCTTGTTAGGGTTTGCTCTGGGGGTTCGAAATCGGTTCGGGATACGGTCCCGGGAGTGTTTAATTCTCTGTTGGCTGGTCGATTTGGGTGCTTGGAGTT
E1      ..................................................................................................
E2      ..................................................................................................
R1      ..................................................................................................
R2      ..................................................................................................
R3      ..................................................................................................

               210       220       230       240       250       260       270       280       290       300
        ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
ref.    GGGAATTGTGGGGTTCGGTGGTAGAGTTGGCCGGTCTTGGTGCCTGTGTTGTAGGGATTTGGGGATTAGGGTTTCCGGTTATGGTTGTATTGGCAATTGG
E1      ..........................................................G.......................................
E2      ..................................................................................................
R1      ..................................................................................................
R2      ..................................................................................................
R3      ..................................................................................................

               310       320       330
        ....|....|....|....|....|....|....|....
ref.    GAGTTACTTTCTAGTTCCAATTTGGTTATGAGCCCCCTG
E1      ........................................
E2      ........................................
R1      ........................................
R2      ........................................
R3      ........................................
```

B) *NAC20L gene*

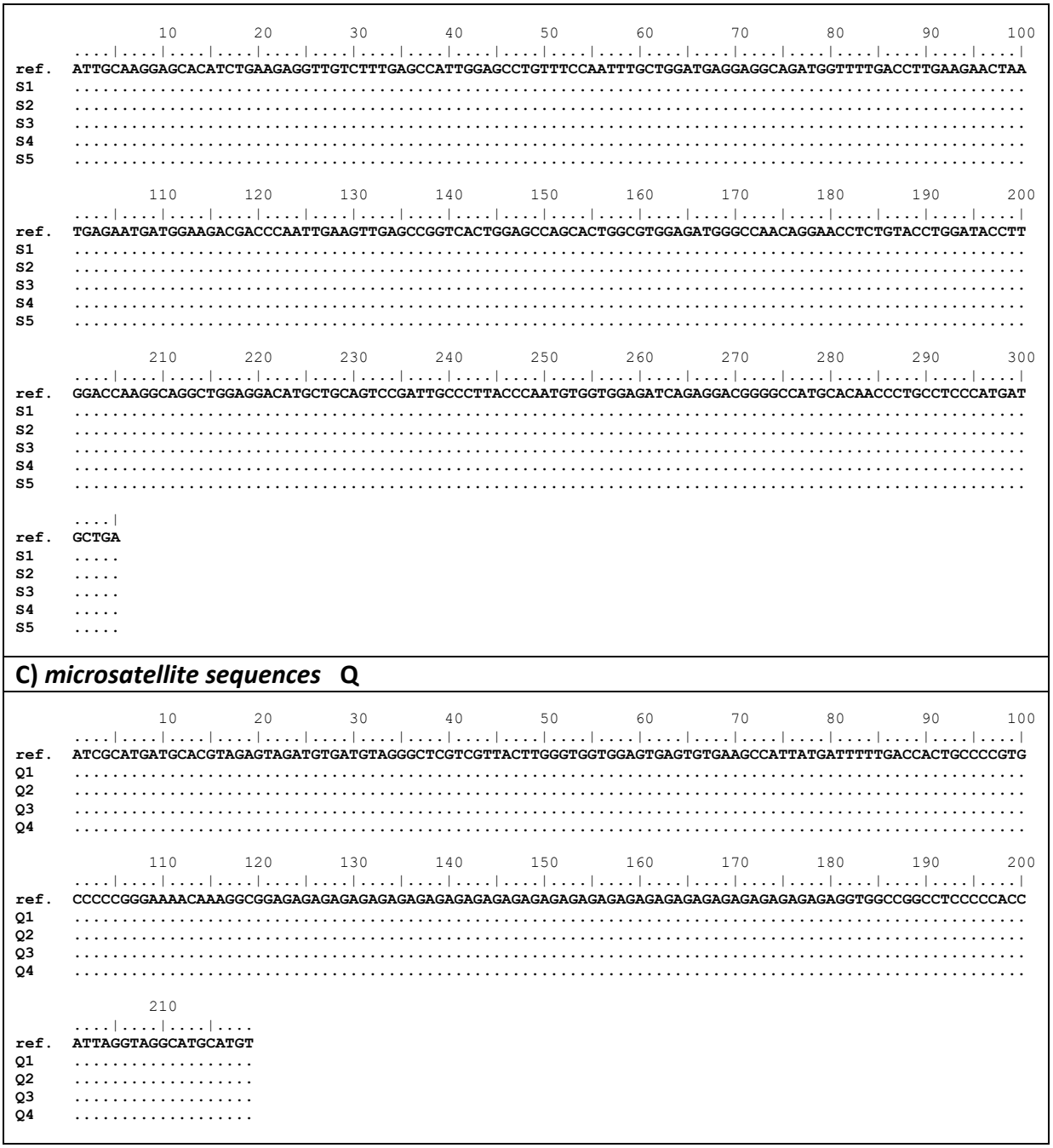


Figure 44. Nucleic acid sequences alignment of five samples (E1–E2, R1–R3) of DRF1gene(branch A), five samples (S1–S5) of the NAC20L gene (branch B), and four samples (Q1–Q4) of microsatellite sequences (branch C) with the most similar Triticum genomic sequences.

The sequencing chromatograms of each variant identified, their complete annotations and the chromatograms of the polymorphisms observed were

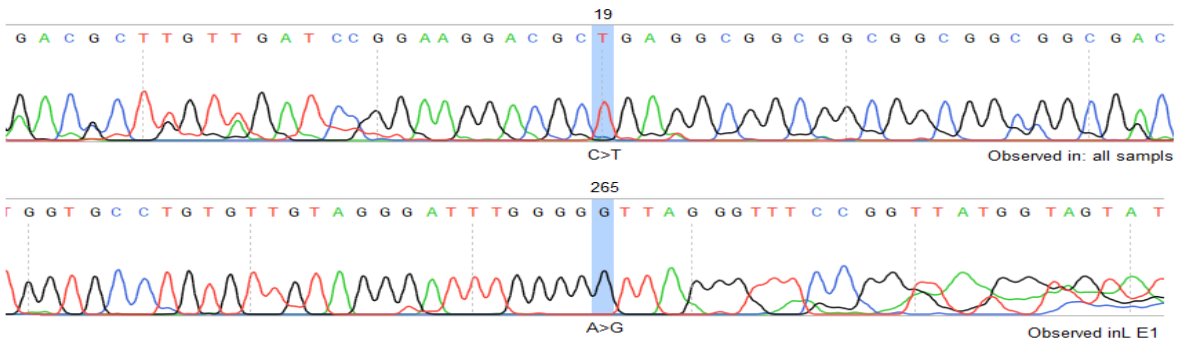
systematically recorded. The two single nucleotide polymorphisms (SNPs) identified are presented in

Figure 45 19C>T and 265A>G within DRF1 gene.

In contrast, no genetic variation was detected in the amplicons of the *NAC20L* gene and from the microsatellite sequences, as confirmed by the chromatographic data presented in

Figure 45. These observations provide additional support for the conserved nature of the *NAC20L* locus and the microsatellite regions among the genotypes analysed, but also highlight the presence of sequence divergence specifically within the *DRF1* gene.

A) *DRF1 gene*



B) *NAC20L gene*

----------NO VARIATION DETECTED----------

C) *microsatellite sequences*

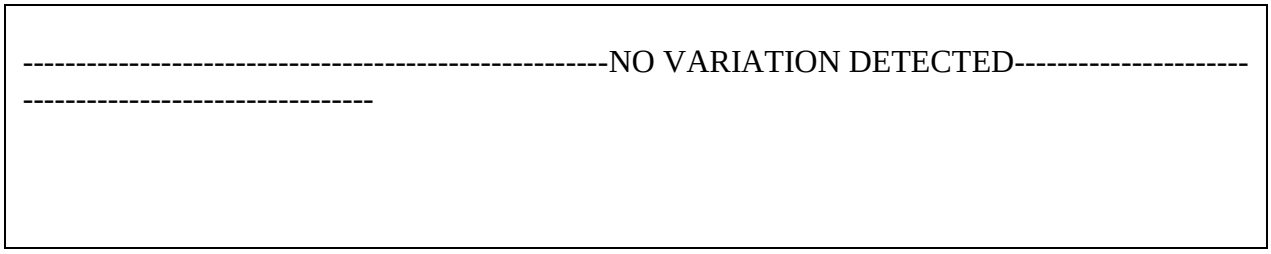


Figure 45. The pattern of the detected variant within the DNA chromatogram of the targeted loci of the DRF1 gene (branch A), NAC20L gene (branch B), and microsatellite sequences (branch C) within Triticum genomic sequences.

The identified variants are highlighted based on their positions within the PCR amplicons. The symbol “>” denotes a substitution mutation. The observed nucleic acid substitutions were further examined to assess their potential impact on the corresponding amino acid sequences of the translated products. All nucleotide sequences derived from the DRF1 gene amplicons (samples E1-E2, R1-R3 in Table 44) and the *NAC20L* gene amplicons (S1, S2, S3, S4, and S5; Table 44) were translated into their deduced amino acid sequences using the ExPASy Translate server. In contrast, samples (Q1, Q2, Q3, and Q4 Table 44; microsatellite sequences) were not subjected to translation, owing to their non-coding, repetitive nature. The amplified fragments of the DRF1 gene encompassed 25 amino acid residues within the AP2 transcriptional activator 1 variant 1 protein. Direct translation of the coding sequence containing the identified variant 19C>T revealed a synonymous (silent) mutation, designated as p.Ala19=, which does not alter the amino acid residue at position 19

Figure 46. The second variant, 265A>G, was localised within the intronic regions of the gene, thereby precluding any direct effect on the protein's primary structure. Regarding the NAC20L gene, the amplified products partially covered the NAC domain-containing protein 20-like protein, which comprises 479 amino acid

residues in its full-length form; the sequenced region encompassed 101 amino acid residues of the total protein

Figure 46. No nucleotide substitutions were detected in this locus, consistent with the earlier alignment results. As anticipated, no translation was performed for the microsatellite sequences, given their non-coding and repetitive characteristics

Figure 46.

These in silico studies validate the silent nature of the identified SNP in the DRF1 gene with no probable influence on the protein function, while the intronic variation could have regulatory implications deserving further investigation. The absence of non-synonymous mutations in NAC20L further confirms its conserved status across the analysed genotypes.

A) *DRF1 gene*

```
          10        20
     ....|....|....|....|....|
ref.  VDRKDAEAAAAAATPFEIPALQPGR
E1    .........................
E2    .........................
R1    .........................
R2    .........................
R3    .........................
```

>AIT69770.1 AP2 transcriptional activator 1 variant 1 [Triticum turgidum subsp. durum]
MTVDRKDAEAAAAAATPFEIPALQPGRTCGAEESTRSHVLVKPIGSSNLPCNEYAFLARQNPKGDALPVASI
LRKKRPRRSRDGPNSVSETIRRWKEVNQQLEHDPQGAKRARKPPAKGSKKGCMQGKGGPENTQCGFRGV
RQRTWGKWVAEIREPNRVSRLWLGTFPTAEDAARAYDEAARAMYGALARTNFPAHPAQAPAVALPAAIE
GVVRGASASCESTTTSANHSDVASNLPRQAQALEIYSQPDVLESTESVVLESVEHYSHKDTVPDAGSSIARS
TSEEDVFEPLEPISSLPDGEADGFDIEELLRLMEADPIEVEPVTGGSWNCGTNTGVEMGLQEPLYLDGLDQG
MLEGMLQADYPYPMWISEDRAMRNPAFHDAEMSEFFEGL

B) *NAC20L* gene

```
          10        20        30        40        50        60        70        80        90       100
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
ref.
IARSTSEEVVFEPLEPVSNLLDEEADGFDLEELMRMMEDDPIEVEPVTGASTGVEMGQQEPLYLDTLD
QGRLEDMLQSDCPYPMWWRSEDGAMHNPASHD
S1    ..............................................................................................
S2    ..............................................................................................
S3    ..............................................................................................
S4    ..............................................................................................
S5    ..............................................................................................


     .
ref.  A
S1    .
S2    .
S3    .
```

S4 . **S5 .** >XP_044427474.1 NAC domain-containing protein 20-like [T. aestivum] MEGLDVFQHYRLNPTDVDAVTYYLPRLIAGQPHGAEKFIHHVDIYSCEPKDLAAKIAPVPQAASSGDRFFFT TRKSKNGSKTQSVRTAGGGTWTVNATTAVKHAGVEVGERKNLSFRKKGKSTGWVMEEYRCLLPKATVA DGVKVFCKIHLAQHPPDAARQESAAYMLQEPQREPVTVSTHAQKRPATAATADPHPSRPNKRMRGAVPVP APATPSFLMYDEAARAMYGPLARTNFPVQDAVAVPAAIEGASASCEFTTTSYHSDVASSSHDMQRQAQAP AISSQSDVLESVKQYSQQQMIVPEAGSSIARSTSEEVVFEPLEPVSNLLDEEADGFDLEELMRMMEDDPIEVE PVTGASTGVEMGQQEPLYLDTLDQGRLEDMLQSDCPYPMWWRSEDGAMHNPASHDADKEKRYNAASDL DAPSLQGHDHLFKPRPCFFDPFEAALKAEEALEKEKRDNLHAGPLGGHNNFFSSASVH
C) microsatellite sequences
---------- non-encoding sequences----------

Figure 46. Amino acids within the DRF1 (branch A), NAC20L (branch B), and microsatellite sequences (branch C) within Triticum genomic sequences.

The grey highlights indicate the amplified regions. The yellow colour represents the silent amino acid variation in the protein sequence. All genetic sequences investigated in this study Table 44 were deposited in the National Centre for Biotechnology Information (NCBI) database, and unique accession numbers were successfully obtained for each of the analysed sequences in Appendix 4-12 and Appendix 4-14.

Five GenBank accession numbers for the DRF1 amplicons (PP873665, PP873666, PP873667, PP873668, and PP873669) were deposited in NCBI to represent the (E1, E2, R1, R2, and R3) samples, respectively. Five GenBank accession numbers for the NAC20L amplicons (PP873670, PP873671, PP873672, PP873673, and PP873674) were deposited in NCBI to represent the (S1, S2, S3, S4, and S5) samples, respectively, in Appendix 0-13. Four GenBank accession numbers for the microsatellite amplicons (PP873642, PP873643, PP873644, and PP873645) were deposited in NCBI to represent the Q1, Q2, Q3, and Q4 samples, respectively, in Appendix 0-15.

Table 44. Genetic sequences of loci resistant to abiotic stress.

№.Sq	GenBank. Loc.№	№.GenBank	Gene. Loci	Primers	Strain &Sample	Genotypes	
1.Sq	PP873665	BankIt2835921	*DRF1*	„Malek1"	„Malek-E1"	AB	Baraka

2.Sq	PP873666		*(Triticum turgidum)*	(drought)	„Malek-E2"	CL	Latifiya
3.Sq	PP873667				„Malek-R1"	NF	Faris
4.Sq	PP873668				„Malek-R2"	SA	Abo Ghurayb
5.Sq	PP873669				„Malek-R3"	TB	Buhuth 22
6.Sq	PP873670		*NAC20L (Triticum aestivum)*	„Malek2" (drought)	„Malek-S1"	CL	Latifiya
7.Sq	PP873671				„Malek-S2"	NF	Faris
8.Sq	PP873672				„Malek-S3"	SA	Abo Ghurayb
9.Sq	PP873673				„Malek-S4"	TB	Buhuth 22
10.Sq	PP873674				„Malek-S5"	UD	Dujela
11.Sq	PP873642	BankIt2835923	*Microsatellite (Triticum turgidum)*	„xgwm-493" (salinity)	„Malek-Q1"	NF	Faris
12.Sq	PP873643				„Malek-Q2"	UD	Dujela
13.Sq	PP873644				„Malek-Q3"	SA	Abo Ghurayb
14.Sq	PP873645				„Malek-Q4"	TB	Buhuth 22

CONCLUSION

1- Based on the results of a three-year field study (2022–2024) conducted under representative agroecological conditions of southern Iraq, a comprehensive assessment of the yield potential of 23 winter wheat genotypes was performed under the combined effect of soil drought and salinity stress. Based on the calculation of stress tolerance indices (SSI, STI) and cluster analysis, an agrotechnical differentiation of the studied material was carried out, allowing the ranking of genotypes according to their degree of adaptability to limiting environmental factors. A group of lines (Dujela, Abo Ghurayb, Buhuth 22, Faris, Baraka, Latifiya) was identified, which maintain stable formation of vegetative biomass and structural components of yield under critical values of the water-salt regime. The obtained results provide a methodological basis for optimising the regional varietal composition, adjusting crop management parameters, and integrating stress-tolerant genotypes into adaptive farming systems of arid zones, thereby ensuring stabilisation of total grain yields while maintaining resource efficiency of production.

2- The identified physiological, agronomic, and biochemical indicators confirm that the stabilisation of the production process of winter wheat under abiotic stress conditions is determined by the ability of genotypes to maintain the functional stability of the photosynthetic apparatus and water relations. In the selected adaptive genotypes, the relative water content in leaf tissues remained within the range of 50.0–55.2% even when critical values of soil drought and salinity were reached, which prevented the deterioration of transpiration activity. The simultaneous stabilisation of the chlorophyll pool (40.5–47.7 SPAD units) created a metabolic basis for osmoregulation through the targeted accumulation of proline and the synchronous activation of enzymatic antioxidant defences (SOD, POD, CAT), minimising oxidative degradation of cellular structures. A key element of the adaptive response was the regulation of ion homeostasis: tolerant genotypes restricted sodium translocation to the shoots,

maintaining the Na^+/K^+ ratio at 0.33–0.57 and preserving the intensity of nitrogen metabolism under stress conditions. The combination of these physiological indicators makes it possible to reliably differentiate the varietal composition for specific soil-climatic boundaries, adjust water and nutrient management regimes, and develop technological cultivation maps for winter wheat in arid zones with the risk of combined salinity-drought stress, which in the long term ensures yield stabilisation and enhances the resource efficiency of crop production.

3- An approach for accelerated agroecological passportisation (genetic passporting) of winter wheat varietal material, based on the combined use of ISSR and SSR markers, has been developed and validated. The application of a panel of 18 ISSR primers provided an objective assessment of genetic diversity and verification of the origin of the initial forms. The diagnostic markers *Malek 1, Malek 2 and xgwm-493* demonstrated high information content for the rapid screening of genotypes regarding tolerance to a complex of limiting abiotic factors. The first time identified and deposited in the *NCBI GenBank* repository, 14 nucleotide sequences associated with the functional loci *DRF1* and *NAC20L*, as well as with groups of microsatellite sequences, have expanded the instrumental basis for molecular monitoring of the seed stock. The implementation of molecular marker-mediated diagnostic elements into the regulations of regional variety testing makes it possible to differentially select tolerant varieties for soil and climatic conditions, adjust the elements of cultivation technology (sowing rates, sowing dates, and mineral nutrition regimes), and reduce the period of production tests, which ensures an increase in the predictability of gross grain harvests and optimisation of resource provision for crop production in arid zones.

4- It has been experimentally established that the preservation of grain technological properties under abiotic stress conditions is achieved primarily through the use of genotypes integrated into adaptive farming systems. When the electrical conductivity of the soil solution increased to 15 dS/m, activation of compensatory mechanisms of nitrogen metabolism was observed, manifested as an increase in the mass fraction of crude protein by 14.6% and crude gluten by 26.6% relative to the

control treatment. In stress-susceptible forms, this metabolic shift was accompanied by a critical reduction in thousand-grain weight and total yield, which negated the agronomic feasibility of growing such genotypes under limiting conditions. A comprehensive comparison of field experiment data, physiological diagnostics, and molecular profiling made it possible to substantiate a technological approach: the structure of regional crop rotations and the production variety testing programme should include genotypes in which the presence of stable DNA markers is reliably correlated with the stability of yield structural components. Such differentiation of the varietal composition ensures predictable product quality, optimisation of sowing rates and nutrient management regimes, and enhances the resource efficiency of winter wheat cultivation in arid and saline agricultural lands.

5- Based on the obtained data, practical guidelines have been formulated for improving the regional farming systems of Southern Iraq. The varieties Dujela, Faris, and Buhuth 22 have been selected as priority components of the adaptive varietal composition of winter wheat, ensuring stable realisation of yield potential under the combined impact of soil drought and salinity stress. The proposed scheme for evaluating varietal material, combining the calculation of ecological plasticity parameters, rapid diagnostics of the physiological status of crops, and molecular genetic screening, allows for the differentiated selection of genotypes according to specific soil-climatic conditions. The integration of this approach into production variety testing practice increases the reliability of yield prediction and forms a scientific-methodological basis for differentiated regulation of crop management practices (optimal sowing dates, optimal plant stand density, and water supply regime). The implementation of these solutions contributes to the stabilisation of total grain yields and enhances the resource sustainability of crop production in arid zones with the risk of soil salinisation.

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APPENDICIES

Appendix 0-1. ANOVA for growth traits and grain yield under three salinity levels and 23 genotypes represented by means of squares for the growing seasons (2022-2024).

Analysis of variance table for genotypes and morphological traits for the year (2021-2022).

S.O.V	*D.F.*	*Biomass (g/pl)*	*Biomass (g/m2)*	*N.Tillers. Plant*	*N.spikes .plant*	*Grain weight*	*W.1000 gra*	*Flag leaf*	*P.H*	*Yield (t/ha)*
MSr	2	37	179.967	3.1806	1.9618	1.5919	144.25	11.35	213.9	1080
MS.F.A	2	38372.5	1.013	54.6673	47.0145	15.2790	6950.28	3153.82	16773.7	1548812
MS. Er.(a)	4	13.1	252.159	0.4540	0.4884	0.1990	38.31	2.16	7.8	207
MS.F.B	22	2859.6	1211623	46.8373	58.4331	5.3168	1047.83	1549.76	3736.4	206128
MS.Ax B	44	224.3	181426	1.2418	1.2543	0.8025	161.21	77.34	460.7	4947
MS.E.(b)	132	7.6	187.332	0.3538	0.3249	0.2071	25.72	6.69	29.9	237

Analysis of variance table for genotypes and morphological traits for the year (2022-2023).

S.O.V	*D.F.*	*Biomass (g/pl)*	*Biomass (g/m2)*	*N.Tillers. Plant*	*N.spikes. plant*	*Grain weight*	*W.1000 gra*	*Flag leaf*	*P.H*	*Yield (t/ha)*
MSr	2	14(5.0	698.1	12.7	8.1	6.4	557.4	42.1	829.1	3144.9
MS.F.A	2	38591.7	10228780.9	58.2	50.2	15.6	7000.7	2755.9	17114.8	1516588
MS. Er.(a)	4	49.5	978.5	1.7	1.7	0.7	150.4	9.1	28.8	754.5
MS.F.B	22	2778.0	1174659.4	45.5	56.8	5.1	1019.1	1433.7	3630.6	192755.1
MS.Ax B	44	217.3	175023.5	1.2	1.2	0.8	157.5	69.5	448.5	4403.6
MS.E.(b)	132	29.3	725.2	1.4	1.3	0.8	100.0	25.0	116.2	760.4

Analysis of variance table for genotypes and morphological traits for the year (2023-2024).

S.O.V	*D.F.*	*Biomass (g/pl)*	*Biomass (g/m2)*	*N.Tillers. Plant*	*N.spikes. plant*	*Grain weight*	*W.1000 gra*	*Flag leaf*	*P.H*	*Yield (t/ha)*
MSr	2	136.0	659.5	11.8	7.6	5.8	523.7	44.1	777.5	4030.0

MS.F.A	2	39109.1	10437704.7	65.9	55.5	16.3	7120.8	3926.9	17869.0	1616033
MS. Er.(a)	4	46.0	920.3	1.5	1.5	0.7	141.7	7.6	25.3	729.3
MS.F.B	22	2612.3	1099925.2	42.8	53.5	4.8	959.8	1489.0	3418.0	195403.3
MS.Ax B	44	203.5	162115.4	1.1	1.1	0.7	149.8	77.1	424.1	4931.6
MS.E.(b)	132	27.6	677.7	1.3	1.2	0.8	94.5	26.0	109.7	784.0

Appendix 0-2. ANOVA for growth traits and grain yield under three drought levels and 23 genotypes represented by means of squares for the growing seasons (2022-2024).

Analysis of variance table for genotypes and morphological traits for the year (2021-2022).

S.O.V	*D.F.*	*Biomass (g/pl)*	*Biomass (g/m2)*	*N.Tillers .Plant*	*N.spikes .plant*	*W.1000 gra*	*Flag leaf*	*P.H*	*Yield (t/ha)*
MSr	2	38.1	185.201	3.0067	10.3329	204.66	11.52	942.6	650
MS.F.A	2	47755.6	1.213	87.1116	72.4053	9890.91	3851.90	23043.1	1391574
MS. Er.(a)	4	9.9	260.197	0.2608	0.7233	16.45	1.88	33.4	237
MS.F.B	22	2824.7	1251851	43.0255	57.4501	1077.73	1532.62	3854.1	201888
MS.AxB	44	218.2	188501	1.9324	0.8968	212.05	79.41	485.2	2853
MS.E.(b)	132	8.8	193.602	0.2833	1.1235	27.05	6.65	122.5	213

Analysis of variance table for genotypes and morphological traits for the year (2022-2023).

S.O.V	*D.F.*	*Biomass (g/pl)*	*Biomass (g/m2)*	*N.Tillers .Plant*	*N.spikes .plant*	*W.1000 gra*	*Flag leaf*	*P.H*	*Yield (t/ha)*
MSr	2	156.53	698.06	11.09	11.74	754.71	41.18	861.83	2382.20
MS.F.A	2	47501.79	12057310.90	96.83	77.04	9747.46	4063.65	23334.27	1409253
MS. Er.(a)	4	35.65	978.53	0.91	1.13	56.84	7.01	25.60	855
MS.F.B	22	2575.99	1174659.45	39.51	52.35	989.32	1403.55	3591.24	184256.94
MS.AxB	44	196.47	175023.5	1.74	1.10	192.78	73.08	463.70	2370.77
MS.E.(b)	132	32.05	725.20	1.04	1.07	99.20	24.84	116.12	781.55

Analysis of variance table for genotypes and morphological traits for the year (2023-2024).

S.O.V	*D.F.*	*Biomass (g/pl)*	*Biomass (g/m2)*	*N.Tillers .Plant*	*N.spikes .plant*	*W.1000 gra*	*Flag leaf*	*P.H*	*Yield (t/ha)*
MSr	2	161.52	698.06	11.05	7.95	770.78	43.83	910.01	2524.31

MS.F.A	2	47706.78	12468230.90	90.33	77.28	9852.56	3928.67	23719.51	1398336.29
MS. Er.(a)	4	38.30	978.53	0.95	0.39	61.51	7.50	34.41	916.70
MS.F.B	22	2741.47	1174659.45	41.74	61.25	1038.52	1488.47	3677.38	195798.29
MS.AxB	44	210.44	175023.53	1.86	0.81	204.80	77.12	455.70	2682.42
MS.E.(b)		34.29	725.20	1.11	1.33	105.92	25.98	115.87	826.33

Appendix 0-3. ANOVA table for stress sensitivity and tolerance indices (Average to three years)

ANOVA table for stress sensitivity and tolerance indices of genotypes under drought stress

S.O.V	DF	SSI	STI	Yi	YSI	Yield (t/ha)
MSr	2	0.0046	0.00029	0.000828	0.00029	0.02
MS.F.A	2	25.7809	3.34453	1.45E-06	3.95653	139.97
MS. Er.(a)	4	0.0034	0.00018	0.000279	0.00019	0.008
MS.F.B	22	0.4684	1.52527	0.97566	0.0544	19.388
MS.AxB	44	0.1568	0.00535	0.0668	0.02017	0.264
MS.E.(b)	132	0.0016	0.00058	0.000313	0.00014	0.007

ANOVA table for stress sensitivity and tolerance indices of genotypes under salinity stress

S.O.V	DF	SSI	STI	Yi	YSI	Yield (t/ha)
MSr	2	0.0054	0.00038	0.00134	0.00044	0.033
MS.F.A	2	25.5402	3.11132	4.83E-07	3.70717	156.007
MS. Er.(a)	4	0.0025	0.00014	0.000335	0.00013	0.007
MS.F.B	22	0.5112	1.26166	0.84004	0.057	19.795
MS.AxB	44	0.17	0.00656	0.07003	0.02129	0.459
MS.E.(b)	132	0.0018	0.00046	0.000291	0.00014	0.007

Appendix 0-4. ANOVA table for physiological indicators

ANOVA table for physiological indicators under the influence of genotype and drought stress

S.O.V	DF	proline	RWC	Chlo	H2O2	SOD	POD	CAT
MSr	2	0.004	64.5	19.25	0.3	0.003	408.5	5.5
MS.F.A	2	10.981	19316.8	8101.39	43.2	4.701	19851.4	3156.6
MS. Er.(a)	4	0.003	4.5	2.98	0.1	0.000	64.6	11.6
MS.F.B	22	0.088	509.7	83.24	1.7	0.032	3686.4	200.1
MS.AxB	44	0.013	72.1	10.26	0.2	0.003	343.7	41.210
MS.E.(b)	132	0.002	15.6	3.31	0.1	0.001	58.2	10.720

ANOVA table for physiological indicators under the influence of genotype and salinity stress

S.O.V	DF	proline	RWC	Chlo	H2O2	SOD	POD	CAT

MSr	2	0.001	78.0	13.9	0.5	0.0002	149.7	5.5
MS.F.A	2	9.180	14296.2	2625.0	31.6	4.978	23492.9	3156.6
MS. Er.(a)	4	0.003	3.1	6.9	0.1	0.003	44.5	11.6
MS.F.B	22	0.084	565.5	87.7	1.7	0.028	3426.0	200.1
MS.AxB	44	0.017	83.9	32.5	0.3	0.003	254.8	41.2
MS.E.(b)	132	0.002	12.5	3.8	0.1	0.001	33.2	10.7

Appendix 0-5. ANOVA table for biochemical indicators under the influence of genotype and drought stress

S.O.V	***DF***	***N***	***Na^+***	***K^+***	***Na^+/K^+***
MSr	2	0.001	0.003	0.004	0.09
MS.F.A	2	6.541	0.109	0.322	14.61
MS. Er.(a)	4	0.002	0.000	0.000	0.05
MS.F.B	22	0.481	0.003	0.037	0.74
MS.AxB	44	0.006	0.001	0.004	0.22
MS.E.(b)	132	0.003	0.001	0.002	0.03

Appendix 0-6. ANOVA table for grain component content

ANOVA table for grain component content under the influence of genotype and drought stress

S.O.V	DF	Moisture	Protein	Gluten	Starch
MSr	2	1.6	0.10	1.61	22.0
MS.F.A	2	206.5	145.84	206.53	8803.7
MS. Er.(a)	4	0.2	0.03	0.231	12.2
MS.F.B	22	44.4	0.94	44.42	211.2
MS.AxB	44	1.8	0.98	1.845	40.0
MS.E.(b)	132	0.6	0.03	0.604	6.1

ANOVA table for grain component content under the influence of genotype and salinity stress

S.O.V	DF	Moisture	Protein	Gluten	Starch
MSr	2	1.6	0.13	1.59	15.5
MS.F.A	2	177.3	153.00	177.29	8785.3
MS. Er.(a)	4	0.2	0.03	0.18	9.7
MS.F.B	22	28.6	1.52	28.6	209.7

MS.AxB	44	2.1	0.68	2.09	42.3
MS.E.(b)	132	0.5	0.04	0.54	5.3

Appendix 0-7. The purity values of the genetic material DNA extracted from the plant leaves of the studied genotypes.

	genotypes	**Purity of DNA**		**genotypes**	**Purity of DNA**		**genotypes**	**Purity of DNA**		**genotypes**	**Purity of DNA**
1	AB	1.89	8	HB	1.87	**15**	OT	1.87	**22**	VN	1.90
2	BW	1.84	9	IB	1.92	**16**	PB	1.81	**23**	WA	1.85
3	CL	1.86	10	JB	1.76	**17**	QA	1.84			
4	DB	1.84	11	KA	1.95	**18**	RA	1.80			
5	EU	1.91	12	LB	1.90	**19**	SA	1.84			
6	FS	1.89	13	MB	1.90	**20**	TB	1.90			
7	GF	1.93	14	NF	1.92	**21**	UD	1.90			

Appendix 0-8.Materials and steps of DNA extraction.

Step	**Materials Used**	**Quantities**
Tissue Disintegration	Liquid nitrogen, mortar, pestle, 15 mL tube	~1 g tissue, 15 mL tube
Cellular Lysis	FAPG1 buffer, RNase A, FAPG2 buffer, ice, spin column, 50 mL tube	4 mL FAPG1, 50 µL RNase A, 1 mL FAPG2, 5 min ice, 50 mL tube
DNA Binding	FAPG3 buffer, FAPG-Maxi spin column, 50 mL tube	7.5 mL FAPG3, 5 min centrifugation
Washing	W1 wash buffer, ethanol-amended wash solution	4 mL W1, 6 mL ethanol wash, 3 min centrifugation
DNA Elution	Elution buffer, sterile 50 mL tube	1 mL elution buffer, 5 min incubation, 3 min centrifugation
Purity Check	Nanodrop spectrophotometer, TE buffer	260/280 nm absorbance, 25 ng/µL final concentration

Appendix 0-9. The matrix of the Euclidean distances between the 23 genotypes, according to morphological and physiological traits, salinity (above the diameter) and drought (below the diameter) stress.

Euclidean distance of genotypes according to morphological and physiological traits under drought stress(below the diameter)	Euclidean distance of genotypes according to morphological and physiological traits under the influence of salinity stress (above the diameter)																							
	AB	BW	CL	DB	EU	FS	GF	HB	IB	JB	KA	LB	MB	NF	OT	PB	QA	RA	SA	TB	UD	VN	WA
AB		3.594	4.192	4.696	5.532	7.59	4.506	4.745	5.985	5.301	4.877	7.008	4.721	3.339	6.19	6.522	5.745	4.91	5.173	3.847	6.692	8.223	4.92
BW	3.462		3.666	2.267	2.234	4.72	2.153	2.034	2.844	2.945	2.44	3.888	1.923	5.031	3.565	3.792	2.844	2.387	5.884	3.836	5.69	5.295	2.195
CL	1.768	3.227		4.391	4.957	6.903	2.968	4.816	5.266	4.58	5.035	5.501	4.411	3.609	5.605	5.849	4.515	3.847	3.292	1.812	4.101	6.376	3.83
DB	3.161	4.399	3.722		2.637	3.518	2.456	3.195	3.747	1.258	1.519	3.643	1.125	6.2	2.172	2.486	3.459	2.137	6.901	4.797	6.576	5.299	1.819
EU	4.761	5.345	4.443	2.586		3.098	2.454	1.965	2.3	3.138	3.125	2.538	2.263	6.995	2.567	2.862	2.209	2.253	7.122	4.98	5.938	3.773	2.211
FS	5.123	4.527	5.213	3.276	3.765		4.534	4.69	4.803	3.575	4.1	2.873	3.44	9.354	1.859	2.404	4.268	3.723	9.118	7.02	7.681	4.153	3.66
GF	3.124	4.775	3.98	2.22	4.097	3.53		2.672	3.144	2.898	3.449	3.713	2.677	5.279	3.355	3.743	2.712	2.013	5.307	3.318	4.896	4.623	2.08
HB	3.708	4.557	3.673	2.605	3.551	3.467	2.812		1.722	3.761	3.295	4.313	2.907	6.164	3.805	3.82	2.325	2.757	7.08	4.943	6.529	5.195	2.996
IB	3.793	3.113	3.472	3.064	3.706	2.211	3.152	2.664		4.017	3.641	4.111	3.403	6.845	4.148	3.924	2.147	3.236	7.662	5.691	6.759	4.772	3.302
JB	3.079	3.581	3.545	2.916	4.521	2.957	2.535	2.672	2.075		1.844	3.888	1.543	6.699	1.964	1.931	3.313	1.953	7.327	5.245	6.98	5.495	2.047
KA	5.172	5.483	5.169	2.909	2.904	4.494	5.007	4.049	4.47	4.717		4.187	1.29	6.387	2.947	2.764	3.687	2.817	7.677	5.549	7.382	6.022	2.464
LB	2.232	3.126	2.372	2.276	3.458	3.438	2.739	2.725	2.29	1.964	3.978		3.2 22	8.054	3.179	3.487	3.642	3.425	7.44	5.476	5.421	2.624	2.846
MB	5.048	3.904	5.573	6.412	7.978	5.818	5.718	6.204	5.079	4.278	8.078	5.129		6.297	2.199	2.252	2.945	1.83	6.992	4.742	6.401	5.112	1.477
NF	3.329	4.584	2.231	3.953	3.78	5.724	4.586	4.264	4.257	4.964	5.038	3.454	7.5		7.999	8.198	6.894	6.33	3.867	3.703	6.095	9.071	6.115
OT	4.944	4.942	4.876	2.816	2.962	2.039	3.184	3.067	2.31	3.293	3.969	3.188	6.9	4.839		1.217	3.249	2.207	8.056	5.895	7.165	4.584	2.509
PB	5.176	5.351	5.686	2.822	4.112	2.895	3.069	3.754	3.438	3.73	4.309	3.982	6.998	5.813	2.293		3.009	2.224	8.574	6.285	7.604	4.951	2.586
QA	2.984	2.974	2.976	2.399	3.312	3.435	2.842	3.227	2.249	3.045	4.207	1.981	5.726	3.219	2.789	3.241		1.834	7.142	4.978	6.187	4.311	2.604
RA	3.485	1.561	3.574	4.19	5.222	4.396	4.643	4.697	3.513	3.746	5.41	3.337	3.771	4.858	5.16	5.491	3.387		6.554	4.24	5.892	4.686	1.505
SA	4.232	3.486	3.83	6.2	6.776	7.427	6.646	6.686	5.943	6.176	7.129	5.005	5.877	4.696	7.433	7.933	4.925	3.633		2.639	3.544	7.981	6.336
TB	5.776	5.132	5.375	6.569	6.728	8.231	7.896	7.502	7.092	7.424	6.185	6.094	8.027	5.541	8.083	8.508	6.038	5.025	3.394		3.152	6.372	4.041

	UD	5.954	7.328	5.536	6.229	6.043	8.802	7.454	6.661	7.708	8.02	6.074	6.497	10.372	4.384	7.819	8.241	6.33	7.445	6.346	5.571		5.839	5.44
	VN	2.595	2.672	2.719	2.124	3.401	3.502	3.164	3.059	2.351	2.525	3.367	1.374	5.369	3.482	3.151	3.635	1.549	2.976	4.728	5.403	6.135		4.555
	WA	1.894	2.605	2.007	2.313	3.473	3.828	3.029	3.021	2.584	2.676	3.969	1.282	5.215	2.957	3.586	4.174	1.646	2.749	4.247	5.352	5.784	1.087	

Appendix 0-10. Shows the sum and average of the bands resulting from the interaction of 20 primers with the genotyped DNA using PCR-ISSR technology.

Primers ISSR-n	Genotypes																								
	AB	BW	CL	DB	EU	FS	GF	HB	IB	JB	KA	LB	MB	NF	OT	PB	QA	RA	SA	TB	UD	VN	WA	*Total*	*Average*
ISSR-1	3	5	4	5	4	4	5	4	4	5	4	3	4	5	5	2	4	4	4	4	5	3	4	94	4.09
ISSR-2	3	1	0	1	1	0	0	0	0	1	1	0	0	1	2	0	0	0	2	4	3	3	3	26	1.13
ISSR-3	2	4	3	3	2	3	4	3	3	3	3	3	4	2	3	4	2	4	5	3	4	3	1	71	3.09
ISSR-4	1	1	1	0	1	3	0	1	0	2	0	4	1	1	1	3	0	0	1	0	2	1	0	24	1.04
ISSR-5	2	3	2	2	4	3	3	4	3	3	3	1	4	4	5	0	3	4	4	2	3	5	3	70	3.04
ISSR-6	1	1	1	0	1	3	0	1	0	2	0	3	0	0	1	0	0	0	1	0	2	1	0	18	0.78
ISSR-7	2	0	1	0	0	0	0	1	1	1	1	1	1	0	0	2	2	1	1	1	1	1	0	18	0.78
ISSR-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00
ISSR-9	0	2	1	0	3	2	0	0	0	1	0	0	2	0	0	1	1	2	1	3	0	1	0	20	0.87
ISSR-10	2	1	2	3	3	1	2	1	1	1	5	2	2	1	1	0	0	1	0	2	0	1	0	32	1.39
ISSR-11	3	0	2	3	2	3	1	2	3	5	2	3	3	2	2	2	2	1	1	2	2	3	2	51	2.22
ISSR-12	2	2	1	0	0	1	1	1	2	1	0	1	1	1	1	1	1	1	2	1	1	1	1	24	1.04
ISSR-13	1	1	1	1	1	1	1	3	3	1	6	2	2	2	4	3	2	2	1	2	4	2	3	49	2.13
ISSR-14	2	4	0	4	3	4	3	3	1	4	3	1	1	1	4	0	0	0	1	6	3	0	0	48	2.09
ISSR-15	5	1	3	3	5	2	3	1	4	3	4	2	1	1	4	2	2	1	1	1	1	1	1	52	2.26
ISSR-16	2	0	1	0	2	1	1	1	2	1	1	1	0	1	2	2	1	2	1	2	2	2	1	29	1.26
ISSR-17	4	3	3	5	3	1	4	3	1	1	2	0	0	3	2	2	3	0	3	4	4	4	0	55	2.39
ISSR-18	1	2	4	4	2	2	5	3	5	2	4	4	3	4	3	4	2	2	4	3	3	4	1	71	3.09
ISSR-19	7	2	2	5	4	1	1	3	2	3	6	2	3	3	3	3	3	3	3	3	1	3	3	69	3.00
ISSR-20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00
MIN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00
MAX	7	5	4	5	5	4	5	4	5	5	6	4	4	5	5	4	4	4	5	6	5	5	4	110	4.78
Total	43	33	32	39	41	35	34	35	35	40	45	33	32	32	43	31	28	28	36	43	41	39	23	821	35.70

Average	2.2	1.7	1.6	2	2.1	1.8	1.7	1.8	1.8	2	2.3	1.7	1.6	1.6	2.2	1.6	1.4	1.4	1.8	2.2	2.1	2	1.2	41.1	1.78

Appendix 0-11. Similarity matrix (Dice) for 23 genotypes of winter wheat by molecular markers

%	AB	BW	CL	DB	EU	FS	GF	HB	IB	JB	KA	LB	MB	NF	OT	PB	QA	RA	SA	TB	UD	VN
BW	37	100																				
CL	32	40	100																			
DB	47	40	41	100																		
EU	47	42	40	52	100																	
FS	30	40	41	35	40	100																
GF	26	44	51	44	49	47	100															
HB	35	29	47	46	38	55	51	100														
IB	31	26	51	39	33	44	54	62	100													
JB	29	27	41	46	48	54	45	57	53	100												
KA	33	30	41	45	49	38	49	46	39	45	100											
LB	30	26	41	36	30	58	39	56	51	47	36	100										
MB	37	33	46	40	42	51	53	67	65	51	48	55	100									
NF	32	36	46	45	45	54	59	64	50	57	55	49	58	100								
OT	35	39	37	54	56	50	59	58	54	62	53	43	55	61	100							
PB	26	24	30	29	26	39	38	46	43	43	32	51	54	42	44	100						
QA	31	29	43	39	44	55	47	62	56	54	47	46	65	65	53	57	100					
RA	28	36	43	40	48	46	54	66	60	58	51	44	75	62	68	45	67	100				
SA	41	41	45	47	46	56	51	56	43	50	49	42	53	62	56	41	59	57	100			
TB	40	45	40	42	49	48	62	51	44	50	58	41	53	58	58	42	53	56	59	100		
UD	26	35	38	39	40	56	53	55	47	56	50	39	51	57	62	40	60	52	50	67	100	
VN	27	25	42	37	34	55	41	64	57	53	44	45	58	56	54	49	56	57	57	49	55	100
WA	26	28	21	27	32	32	23	39	37	36	33	30	38	45	41	34	44	42	43	38	39	47

Appendix 0-12. NCBI Acceptance Letter for DRF1 and NAC20L Genes

NCBI ACCEPTANCE LETTER for DRF1 and NAC20L genes

Dear GenBank Submitter:

Thank you for your submission of sequence data to GenBank, a contribution which will benefit the scientific community.
We have provided GenBank accession numbers for your nucleotide sequences:

BankIt2835921 Seq1 PP873665
BankIt2835921 Seq2 PP873666
BankIt2835921 Seq3 PP873667
BankIt2835921 Seq4 PP873668
BankIt2835921 Seq5 PP873669
BankIt2835921 Seq6 PP873670
BankIt2835921 Seq7 PP873671
BankIt2835921 Seq8 PP873672
BankIt2835921 Seq9 PP873673
BankIt2835921 Seq10 PP873674

The GenBank accession numbers should appear in any publication that reports or discusses these data, as it gives the community a unique label with which they may retrieve your data from our on-line servers. You may prepare and submit your manuscript before your accessions are released in GenBank.
Submissions are not automatically deposited into GenBank after being accessioned. Each sequence record is individually examined and processed by the GenBank annotation staff to ensure that it is free of errors or problems.
You have not requested a specific release date for your sequence data. Therefore, your record(s) will be released to the public database once they are processed. If this is not what you intended, please contact us as soon as possible with the correct release date.
Since the flatfile record is a display format only and is not an editable format of the data, do not make changes directly to a flatfile. For complete information about different methods to update a sequence record, see: https://www.ncbi.nlm.nih.gov/Genbank/update.html
Any inquiries about your submission should be sent to gb-admin@ncbi.nlm.nih.gov
For more information about the submission process or the available submission tools, please contact GenBank User Support at info@ncbi.nlm.nih.gov.

Please reply using the current Subject line.
Sincerely,
Michael Fetchko
The GenBank Direct Submission Staff
Bethesda, Maryland USA
****
gb-admin@ncbi.nlm.nih.gov (for updates/replies to GenBank entries)
info@ncbi.nlm.nih.gov (for general questions regarding GenBank)
****

Appendix 0-13. Preliminary Sequences of The Submitted Amplicons for Drf1 and Nac20l Genes

```
Preliminary Sequences of The Submitted Amplicons for Drf1 and Nac20l Genes
LOCUS       Seq1                339 bp    DNA     linear   PLN 02-JUN-2024
DEFINITION  Triticum turgidum strain Malek-E1.
ACCESSION   Seq1
VERSION
KEYWORDS    .
SOURCE      Triticum turgidum
  ORGANISM  Triticum turgidum
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            clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 339)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
            Al-Muthanna University, University complex, AL Muthanna,
            Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:10

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            Sequencing Technology :: Sanger dideoxy sequencing
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      121 gggggttcga aatcggttcg ggatacggtc ccgggagtgt ttaattctct gttggctggt
      181 cgatttgggt gcttggagtt gggaattgtg gggttcggtg gtagagttgg ccggtcttgg
      241 tgcctgtgtt gtagggattt gggggttagg gtttccggtt atggttgtat tggcaattgg
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//
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DEFINITION  Triticum turgidum strain Malek-E2.
ACCESSION   Seq2
VERSION
KEYWORDS    .
SOURCE      Triticum turgidum
  ORGANISM  Triticum turgidum
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          Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
          clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 339)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
          Al-Muthanna University, University complex, AL Muthanna,
          Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:10

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          Sequencing Technology :: Sanger dideoxy sequencing
          ##Assembly-Data-END##
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                     /translation="VDRKDAEAAAAAATPFEIPALQPGR"
BASE COUNT       44 a     63 c    127 g    105 t
ORIGIN
        1 ggtagatcgg aaggacgctg aggcggcggc ggcggcggcg acgcccttcg agatcccggc
       61 gctccagcct ggaaggtgag atcttctgtc cggtgcctgc ttcttgttag ggtttgctct
      121 gggggttcga aatcggttcg ggatacggtc ccgggagtgt ttaattctct gttggctggt
      181 cgatttgggt gcttggagtt gggaattgtg gggttcggtg gtagagttgg ccggtcttgg
      241 tgcctgtgtt gtagggattt ggggattagg gtttccggtt atggttgtat tggcaattgg
      301 gagttacttt ctagttccaa tttggttatg agccccctg
//
LOCUS       Seq3                 339 bp    DNA     linear   PLN 02-JUN-2024
DEFINITION  Triticum turgidum strain Malek-R1.
ACCESSION   Seq3
VERSION
KEYWORDS    .
SOURCE      Triticum turgidum
  ORGANISM  Triticum turgidum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
          clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 339)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
          Al-Muthanna University, University complex, AL Muthanna,
          Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:10

          ##Assembly-Data-START##
          Sequencing Technology :: Sanger dideoxy sequencing
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        ##Assembly-Data-END##
FEATURES             Location/Qualifiers
   source          1..339
                   /organism="Triticum turgidum"
                   /mol_type="genomic DNA"
                   /strain="Malek-R1"
                   /isolation_source="Fresh green plant parts"
                   /db_xref="taxon:4571"
                   /country="Iraq"
                   /collected_by="Malek H. Walli"
   gene            <1..>79
                   /gene="DRF1"
   CDS             <1..>79
                   /gene="DRF1"
                   /codon_start=2
                   /product="AP2 transcriptional activator 1 variant 1"
                   /translation="VDRKDAEAAAAAATPFEIPALQPGR"
BASE COUNT      44 a     63 c    127 g    105 t
ORIGIN
        1 ggtagatcgg aaggacgctg aggcggcggc ggcggcggcg acgcccttcg agatcccggc
       61 gctccagcct ggaaggtgag atcttctgtc cggtgcctgc ttcttgttag ggtttgctct
      121 gggggttcga aatcggttcg ggatacggtc ccgggagtgt ttaattctct gttggctggt
      181 cgatttgggt gcttggagtt gggaattgtg gggttcggtg gtagagttgg ccggtcttgg
      241 tgcctgtgtt gtagggattt ggggattagg gtttccggtt atggttgtat tggcaattgg
      301 gagttacttt ctagttccaa tttggttatg agccccctg
//
LOCUS       Seq4                339 bp    DNA     linear   PLN 02-JUN-2024
DEFINITION  Triticum turgidum strain Malek-R2.
ACCESSION   Seq4
VERSION
KEYWORDS    .
SOURCE      Triticum turgidum
  ORGANISM  Triticum turgidum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
            clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 339)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
            Al-Muthanna University, University complex, AL Muthanna,
            Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:10

            ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
   source          1..339
                   /organism="Triticum turgidum"
                   /mol_type="genomic DNA"
                   /strain="Malek-R2"
                   /isolation_source="Fresh green plant parts"
                   /db_xref="taxon:4571"
                   /country="Iraq"
                   /collected_by="Malek H. Walli"
   gene            <1..>79
                   /gene="DRF1"
   CDS             <1..>79
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                /gene="DRF1"
                /codon_start=2
                /product="AP2 transcriptional activator 1 variant 1"
                /translation="VDRKDAEAAAAAATPFEIPALQPGR"
BASE COUNT      44 a    63 c    127 g    105 t
ORIGIN
      1 ggtagatcgg aaggacgctg aggcggcggc ggcggcggcg acgcccttcg agatcccggc
     61 gctccagcct ggaaggtgag atcttctgtc cggtgcctgc ttcttgttag ggtttgctct
    121 gggggttcga aatcggttcg ggatacggtc ccgggagtgt ttaattctct gttggctggt
    181 cgatttgggt gcttggagtt gggaattgtg gggttcggtg gtagagttgg ccggtcttgg
    241 tgcctgtgtt gtagggattt ggggattagg gtttccggtt atggttgtat tggcaattgg
    301 gagttacttt ctagttccaa tttggttatg agccccctg
//
LOCUS       Seq5                339 bp    DNA     linear   PLN 02-JUN-2024
DEFINITION  Triticum turgidum strain Malek-R3.
ACCESSION   Seq5
VERSION
KEYWORDS    .
SOURCE      Triticum turgidum
  ORGANISM  Triticum turgidum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
            clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 339)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
            Al-Muthanna University, University complex, AL Muthanna,
            Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:10

            ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..339
                     /organism="Triticum turgidum"
                     /mol_type="genomic DNA"
                     /strain="Malek-R3"
                     /isolation_source="Fresh green plant parts"
                     /db_xref="taxon:4571"
                     /country="Iraq"
                     /collected_by="Malek H. Walli"
     gene            <1..>79
                     /gene="DRF1"
     CDS             <1..>79
                     /gene="DRF1"
                     /codon_start=2
                     /product="AP2 transcriptional activator 1 variant 1"
                     /translation="VDRKDAEAAAAAATPFEIPALQPGR"
BASE COUNT      44 a    63 c    127 g    105 t
ORIGIN
      1 ggtagatcgg aaggacgctg aggcggcggc ggcggcggcg acgcccttcg agatcccggc
     61 gctccagcct ggaaggtgag atcttctgtc cggtgcctgc ttcttgttag ggtttgctct
    121 gggggttcga aatcggttcg ggatacggtc ccgggagtgt ttaattctct gttggctggt
    181 cgatttgggt gcttggagtt gggaattgtg gggttcggtg gtagagttgg ccggtcttgg
    241 tgcctgtgtt gtagggattt ggggattagg gtttccggtt atggttgtat tggcaattgg
    301 gagttacttt ctagttccaa tttggttatg agccccctg
//
LOCUS       Seq6                305 bp    DNA     linear   PLN 02-JUN-2024
```

```
DEFINITION  Triticum aestivum strain Malek-S1.
ACCESSION   Seq6
VERSION
KEYWORDS    .
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
            clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 305)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
            Al-Muthanna University, University complex, AL Muthanna,
            Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:10

            ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..305
                     /organism="Triticum aestivum"
                     /mol_type="genomic DNA"
                     /strain="Malek-S1"
                     /isolation_source="Fresh green plant parts"
                     /db_xref="taxon:4565"
                     /country="Iraq"
                     /collected_by="Malek H. Walli"
     CDS             <1..>305
                     /codon_start=1
                     /product="NAC domain-containing protein 20-like [Triticum
                     aestivum]"
                     /translation="IARSTSEEVVFEPLEPVSNLLDEEADGFDLEELMRMMEDDPIEV
                     EPVTGASTGVEMGQQEPLYLDTLDQGRLEDMLQSDCPYPMWWRSEDGAMHNPASHDA"
BASE COUNT       77 a     69 c     93 g     66 t
ORIGIN
        1 attgcaagga gcacatctga agaggttgtc tttgagccat tggagcctgt ttccaatttg
       61 ctggatgagg aggcagatgg ttttgacctt gaagaactaa tgagaatgat ggaagacgac
      121 ccaattgaag ttgagccggt cactggagcc agcactggcg tggagatggg ccaacaggaa
      181 cctctgtacc tggatacctt ggaccaaggc aggctggagg acatgctgca gtccgattgc
      241 ccttacccaa tgtggtggag atcagaggac ggggccatgc acaaccctgc ctcccatgat
      301 gctga
//
LOCUS       Seq7                305 bp    DNA     linear   PLN 02-JUN-2024
DEFINITION  Triticum aestivum strain Malek-S2.
ACCESSION   Seq7
VERSION
KEYWORDS    .
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
            clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 305)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
            Al-Muthanna University, University complex, AL Muthanna,
```

```
          Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:10

          ##Assembly-Data-START##
          Sequencing Technology :: Sanger dideoxy sequencing
          ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..305
                     /organism="Triticum aestivum"
                     /mol_type="genomic DNA"
                     /strain="Malek-S2"
                     /isolation_source="Fresh green plant parts"
                     /db_xref="taxon:4565"
                     /country="Iraq"
                     /collected_by="Malek H. Walli"
     CDS             <1..>305
                     /codon_start=1
                     /product="NAC domain-containing protein 20-like [Triticum
                     aestivum]"
                     /translation="IARSTSEEVVFEPLEPVSNLLDEEADGFDLEELMRMMEDDPIEV
                     EPVTGASTGVEMGQQEPLYLDTLDQGRLEDMLQSDCPYPMWWRSEDGAMHNPASHDA"
BASE COUNT       77 a     69 c     93 g     66 t
ORIGIN
        1 attgcaagga gcacatctga agaggttgtc tttgagccat tggagcctgt ttccaatttg
       61 ctggatgagg aggcagatgg ttttgacctt gaagaactaa tgagaatgat ggaagacgac
      121 ccaattgaag ttgagccggt cactggagcc agcactggcg tggagatggg ccaacaggaa
      181 cctctgtacc tggatacctt ggaccaaggc aggctggagg acatgctgca gtccgattgc
      241 ccttacccaa tgtggtggag atcagaggac ggggccatgc acaaccctgc ctcccatgat
      301 gctga
//
LOCUS       Seq8                305 bp    DNA     linear   PLN 02-JUN-2024
DEFINITION  Triticum aestivum strain Malek-S3.
ACCESSION   Seq8
VERSION
KEYWORDS    .
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
          clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 305)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
          Al-Muthanna University, University complex, AL Muthanna,
          Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:10

          ##Assembly-Data-START##
          Sequencing Technology :: Sanger dideoxy sequencing
          ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..305
                     /organism="Triticum aestivum"
                     /mol_type="genomic DNA"
                     /strain="Malek-S3"
                     /isolation_source="Fresh green plant parts"
                     /db_xref="taxon:4565"
                     /country="Iraq"
                     /collected_by="Malek H. Walli"
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CDS             <1..>305
                /codon_start=1
                /product="NAC domain-containing protein 20-like [Triticum
                aestivum]"
                /translation="IARSTSEEVVFEPLEPVSNLLDEEADGFDLEELMRMMEDDPIEV
                EPVTGASTGVEMGQQEPLYLDTLDQGRLEDMLQSDCPYPMWWRSEDGAMHNPASHDA"
BASE COUNT      77 a     69 c     93 g     66 t
ORIGIN
      1 attgcaagga gcacatctga agaggttgtc tttgagccat tggagcctgt ttccaatttg
     61 ctggatgagg aggcagatgg ttttgacctt gaagaactaa tgagaatgat ggaagacgac
    121 ccaattgaag ttgagccggt cactggagcc agcactggcg tggagatggg ccaacaggaa
    181 cctctgtacc tggatacctt ggaccaaggc aggctggagg acatgctgca gtccgattgc
    241 ccttacccaa tgtggtggag atcagaggac ggggccatgc acaaccctgc ctcccatgat
    301 gctga
//
LOCUS       Seq9                305 bp    DNA     linear   PLN 02-JUN-2024
DEFINITION  Triticum aestivum strain Malek-S4.
ACCESSION   Seq9
VERSION
KEYWORDS    .
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
            clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 305)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
            Al-Muthanna University, University complex, AL Muthanna,
            Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:10

            ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..305
                     /organism="Triticum aestivum"
                     /mol_type="genomic DNA"
                     /strain="Malek-S4"
                     /isolation_source="Fresh green plant parts"
                     /db_xref="taxon:4565"
                     /country="Iraq"
                     /collected_by="Malek H. Walli"
     CDS             <1..>305
                     /codon_start=1
                     /product="NAC domain-containing protein 20-like [Triticum
                     aestivum]"
                     /translation="IARSTSEEVVFEPLEPVSNLLDEEADGFDLEELMRMMEDDPIEV
                     EPVTGASTGVEMGQQEPLYLDTLDQGRLEDMLQSDCPYPMWWRSEDGAMHNPASHDA"
BASE COUNT      77 a     69 c     93 g     66 t
ORIGIN
      1 attgcaagga gcacatctga agaggttgtc tttgagccat tggagcctgt ttccaatttg
     61 ctggatgagg aggcagatgg ttttgacctt gaagaactaa tgagaatgat ggaagacgac
    121 ccaattgaag ttgagccggt cactggagcc agcactggcg tggagatggg ccaacaggaa
    181 cctctgtacc tggatacctt ggaccaaggc aggctggagg acatgctgca gtccgattgc
    241 ccttacccaa tgtggtggag atcagaggac ggggccatgc acaaccctgc ctcccatgat
    301 gctga
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LOCUS       Seq10                  305 bp    DNA     linear   PLN 02-JUN-2024
DEFINITION  Triticum aestivum strain Malek-S5.
ACCESSION   Seq10
VERSION
KEYWORDS    .
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
            clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 305)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
            Al-Muthanna University, University complex, AL Muthanna,
            Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:10

            ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..305
                     /organism="Triticum aestivum"
                     /mol_type="genomic DNA"
                     /strain="Malek-S5"
                     /isolation_source="Fresh green plant parts"
                     /db_xref="taxon:4565"
                     /country="Iraq"
                     /collected_by="Malek H. Walli"
     CDS             <1..>305
                     /codon_start=1
                     /product="NAC domain-containing protein 20-like [Triticum
                     aestivum]"
                     /translation="IARSTSEEVVFEPLEPVSNLLDEEADGFDLEELMRMMEDDPIEV
                     EPVTGASTGVEMGQQEPLYLDTLDQGRLEDMLQSDCPYPMWWRSEDGAMHNPASHDA"
BASE COUNT       77 a     69 c     93 g     66 t
ORIGIN
        1 attgcaagga gcacatctga agaggttgtc tttgagccat tggagcctgt ttccaatttg
       61 ctggatgagg aggcagatgg ttttgacctt gaagaactaa tgagaatgat ggaagacgac
      121 ccaattgaag ttgagccggt cactggagcc agcactggcg tggagatggg ccaacaggaa
      181 cctctgtacc tggatacctt ggaccaaggc aggctggagg acatgctgca gtccgattgc
      241 ccttacccaa tgtggtggag atcagaggac ggggccatgc acaaccctgc ctcccatgat
      301 gctga
//
```

Appendix 0-14. NCBI Acceptance Letter for Microsatellite Sequences

NCBI Acceptance Letter for Microsatellite Sequences

Dear GenBank Submitter:

Thank you for your submission of sequence data to GenBank, a contribution which will benefit the scientific community.

We have provided GenBank accession numbers for your nucleotide sequences:
BankIt2835923 Seq1 PP873642
BankIt2835923 Seq2 PP873643
BankIt2835923 Seq3 PP873644
BankIt2835923 Seq4 PP873645

The GenBank accession numbers should appear in any publication that reports or discusses these data, as it gives the community a unique label with which they may retrieve your data from our on-line servers. You may prepare and submit your manuscript before your accessions are released in GenBank.
Submissions are not automatically deposited into GenBank after being accessioned. Each sequence record is individually examined and processed by the GenBank annotation staff to ensure that it is free of errors or problems.
You have not requested a specific release date for your sequence data. Therefore, your record(s) will be released to the public database once they are processed. If this is not what you intended, please contact us as soon as possible with the correct release date.
Since the flatfile record is a display format only and is not an editable format of the data, do not make changes directly to a flatfile. For complete information about different methods to update a sequence record, see: https://www.ncbi.nlm.nih.gov/Genbank/update.html
Any inquiries about your submission should be sent to gb-admin@ncbi.nlm.nih.gov
For more information about the submission process or the available submission tools, please contact GenBank User Support at info@ncbi.nlm.nih.gov.
Please reply using the current Subject line.
Sincerely,
Michael Fetchko
The GenBank Direct Submission Staff
Bethesda, Maryland USA
****
gb-admin@ncbi.nlm.nih.gov (for updates/replies to GenBank entries)
info@ncbi.nlm.nih.gov (for general questions regarding GenBank)
****

Appendix 0-15.Preliminary Sequences of The Submitted Amplicons for Microsatellite Sequences.

Preliminary Sequences of The Submitted Amplicons for Microsatellite Sequences

```
LOCUS       Seq1                 219 bp    DNA     linear   PLN 02-JUN-2024
DEFINITION  Triticum turgidum strain Malek-Q1.
ACCESSION   Seq1
VERSION
KEYWORDS    .
SOURCE      Triticum turgidum
  ORGANISM  Triticum turgidum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
            clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 219)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
            Al-Muthanna University, University complex, AL Muthanna,
            Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:4

            ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..219
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                     /mol_type="genomic DNA"
                     /strain="Malek-Q1"
                     /isolation_source="Fresh green plant parts"
                     /db_xref="taxon:4571"
                     /country="Iraq"
                     /collected_by="Malek H. Walli"
     repeat_region   1..219
                     /satellite="microsatellite:Xgwm"
BASE COUNT       63 a     37 c     81 g     38 t
ORIGIN
        1 atcgcatgat gcacgtagag tagatgtgat gtagggctcg tcgttacttg ggtggtggag
       61 tgagtgtgaa gccattatga tttttgacca ctgccccgtg cccccgggaa aacaaaggcg
      121 gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga
      181 ggtggccggc ctccccccacc attaggtagg catgcatgt
```

```
//
LOCUS       Seq2                219 bp    DNA     linear   PLN 02-JUN-2024
DEFINITION  Triticum turgidum strain Malek-Q2.
ACCESSION   Seq2
VERSION
KEYWORDS    .
SOURCE      Triticum turgidum
  ORGANISM  Triticum turgidum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
            clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 219)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
            Al-Muthanna University, University complex, AL Muthanna,
            Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:4

            ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..219
                     /organism="Triticum turgidum"
                     /mol_type="genomic DNA"
                     /strain="Malek-Q2"
                     /isolation_source="Fresh green plant parts"
                     /db_xref="taxon:4571"
                     /country="Iraq"
                     /collected_by="Malek H. Walli"
     repeat_region   1..219
                     /satellite="microsatellite:Xgwm"
BASE COUNT       63 a     37 c     81 g     38 t
ORIGIN
        1 atcgcatgat gcacgtagag tagatgtgat gtagggctcg tcgttacttg ggtggtggag
       61 tgagtgtgaa gccattatga tttttgacca ctgccccgtg cccccgggaa aacaaaggcg
      121 gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga
      181 ggtggccggc ctccccccacc attaggtagg catgcatgt
```

```
//
LOCUS       Seq3                   219 bp    DNA     linear   PLN 02-JUN-2024
DEFINITION  Triticum turgidum strain Malek-Q3.
ACCESSION   Seq3
VERSION
KEYWORDS    .
SOURCE      Triticum turgidum
  ORGANISM  Triticum turgidum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
            clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 219)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
            Al-Muthanna University, University complex, AL Muthanna,
            Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:4

            ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..219
                     /organism="Triticum turgidum"
                     /mol_type="genomic DNA"
                     /strain="Malek-Q3"
                     /isolation_source="Fresh green plant parts"
                     /db_xref="taxon:4571"
                     /country="Iraq"
                     /collected_by="Malek H. Walli"
     repeat_region   1..219
                     /satellite="microsatellite:Xgwm"
BASE COUNT       63 a     37 c     81 g     38 t
ORIGIN
        1 atcgcatgat gcacgtagag tagatgtgat gtagggctcg tcgttacttg ggtggtggag
       61 tgagtgtgaa gccattatga tttttgacca ctgccccgtg ccccccgggaa aacaaaggcg
      121 gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga
      181 ggtggccggc ctccccccacc attaggtagg catgcatgt
//
```

```
LOCUS       Seq4                219 bp    DNA     linear   PLN 02-JUN-2024
DEFINITION  Triticum turgidum strain Malek-Q4.
ACCESSION   Seq4
VERSION
KEYWORDS    .
SOURCE      Triticum turgidum
  ORGANISM  Triticum turgidum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP
            clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
REFERENCE   1  (bases 1 to 219)
  AUTHORS   Walli,M.H., Zargar,M. and Hussein,A.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2024) Basic Medical Sciences, College of Nursing,
            Al-Muthanna University, University complex, AL Muthanna,
            Al-Muthanna 34010, Iraq
COMMENT     Bankit Comment: TOTAL # OF SEQS:4

            ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..219
                     /organism="Triticum turgidum"
                     /mol_type="genomic DNA"
                     /strain="Malek-Q4"
                     /isolation_source="Fresh green plant parts"
                     /db_xref="taxon:4571"
                     /country="Iraq"
                     /collected_by="Malek H. Walli"
     repeat_region   1..219
                     /satellite="microsatellite:Xgwm"
BASE COUNT       63 a     37 c     81 g     38 t
ORIGIN
        1 atcgcatgat gcacgtagag tagatgtgat gtagggctcg tcgttacttg ggtggtggag
       61 tgagtgtgaa gccattatga tttttgacca ctgccccgtg ccccccgggaa aacaaaggcg
      121 gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga
      181 ggtggccggc ctccccccacc attaggtagg catgcatgt
//
```

Appendix 0-16. Devices and equipment used in the laboratory.

	Instrument/equipment	**Company**	**Country**
1	Autoclave	HIRAYAMA	Japan
2	Cold centrifuge	Nuve	Turky
3	Digital camera	Sony	Japan
4	Electrophoresis	Rovigo	Italy
5	Eppendorf	deagon	China
6	Microwave oven	Panasonic	Korea
7	Conventional PCR	Bio-Rad	Singapore

8	Gel electrophoresis	Consort	Belgium
9	Incubator	Heraeus	Germany
10	Micropipettes (different volume)	Ependrof	Germany
11	Sensitive balance	Mettler Toledo	Switzerland
12	Shaker	Lab Tech	Korea
13	Tips	Sterellin Ltd.	UK
14	Ultraviolet transilluminator	Elettofor	Italy (EU)
15	Vortex mixer	Heidolph	Germany
16	Water bath	Labtech	Korea
17	Water distiller	Polar Bear	Canada
18	Slide	Superstar	India
19	Catton Swab	BDH	England
20	Test tube	BDH	England
21	Incubator	Memmert	Germany
22	Plastic plates	BDH	/England
23	Refrigerator	Concord Lebanon	Lebanon
24	Gel tubes	Afco-Dispo	Jordan
25	EDTA tubes	Afco-Dispo	Jordan
26	Banzen burner	Banzen burner	Banzen burner
27	Flask	Binder	Germany
28	Gloves and face mask	Malaysia	Malaysia
29	mortar	China	China
30	Nanodrop	Thermo Fisher	US

Appendix 0-17. Chemical and biological materials are used in DNA extraction and amplification.

	Type of material	**Manufacturer**	**Origin**
1	Agarose gel.	Difco	USA
2	Bromophenol blue.	BDH	UK
3	Ethanol (96%).	BDH	UK
4	Ethidium bromide.	BDH	UK
5	Free nuclease water	Bioneer	Korea
6	TBX Buffer	BDH	UK
7	liquid nitrogen	IRQ	IRQ

Appendix 0-18. Standard values (Z-score) for means genotypes under salinity and drought conditions

	Bio g/plant		**Tillers /Plant**		**Spikes/plant**		**Grain weight / spike /gm**	
Genotypes	S	D	S	D	S	D	S	D
Baraka«**AB**»	-0.11	-0.21	0.65	0.68	0.66	0.22	**2.77**	**3**
Wafea«**BW**»	0.14	0.24	-0.43	-0.6	-0.22	-0.23	0.43	0.33
Latefiya«**C**L»	1.26	1.23	0.88	1.19	1.06	0.88	0.11	0.34
Binekal«**DB**»	-0.66	-0.51	0.42	0.1	0.28	0.28	-0.09	-0.27
Urok«**EU**»	-0.03	0	-0.9	-1.03	-0.73	-0.77	-0.16	-0.33
Sham«**FS**»	-1.5	-1.28	-0.32	-0.48	-0.12	-0.13	-1.05	-1.12
Fateh«**GF**»	0.48	-0.82	0.07	-0.07	0.22	0.22	-0.21	-0.39
Buhoth10«**HB**»	0.26	-0.71	-1.54	-1.54	-1.22	-1.25	0.59	0.52
Buhoth158«**IB**»	0.32	-0.93	-2.03	0.27	-1.7	-1.75	-0.8	-0.94
Babol113«**JB**»	-0.85	-0.74	0.13	0.04	0.28	0.29	-0.41	-0.52
Alraq«**KA**»	-1.11	-0.34	-0.29	-0.46	-0.1	-0.11	-0.12	-0.19
Bwru«**LB**»	-0.46	0.43	0.18	-0.3	-0.4	0.57	-1.39	-1.67
Baghdad«**MB**»	-0.82	-0.54	-0.16	-0.33	0.02	0	0.05	-0.07
Faris«**NF**»	**1.42**	**1.32**	**1.17**	**1.37**	**1.14**	**1.19**	**1.6**	**1.67**
Tamuz«**OT**»	-1.18	-1.26	-0.19	-0.36	0	-0.01	-0.35	-0.54
Buhoth«**PB**»	-1.35	-1.51	-0.72	-0.95	-0.48	-0.5	-0.36	-0.55
Abaá95«**QA**»	0.06	0.21	-1.64	-1.93	-1.3	-1.35	-0.29	-0.39
Abaá99«**RA**»	-0.37	-0.09	-0.46	-0.66	-0.24	-0.26	0.25	0.15
AbóGhuriyb «**SA**»	**2.21**	**1.33**	**2.09**	**1.47**	**2.18**	**1.22**	0.75	0.7
Buhoth22«**TB**»	**1.04**	**1.42**	**1.18**	**1.62**	**1.18**	**1.32**	**1.2**	**1.21**
Dujela«**UD**»	**1.66**	**2.4**	**1.37**	**1.85**	**1.36**	**2.13**	-0.12	0.25
Nemichinovka «**VN**»	0.16	0.09	0.58	0.45	-1.94	-2	-2.24	-1.13
AbóRaghef«**WA**»	-0.57	0.28	-0.08	-0.26	0.1	0.08	-0.11	-0.19

	1000 grains weight /gm		Flag leaf length (cm2)		P.H (cm)		yield g/m	
Var	S	D	S	D	S	D	S	D
Baraka«**AB**»	**1.42**	**1.54**	**2.35**	**2.36**	0.52	0.51	0.58	0.57
Wafea«**BW**»	0.98	0.96	0.72	0.72	-0.25	-0.27	0.04	0.13
Latefiya«**C**L»	-0.04	0.03	0.2	0.2	1.49	1.48	0.71	0.82
Binekal«**DB**»	0.51	0.49	0.49	0.49	0.34	0.33	-0.77	-0.43
Urok«**EU**»	-0.16	-0.2	-0.18	-0.19	-1.17	-1.18	-0.16	-0.02
Sham«**FS**»	-1.26	-1.31	-0.68	-0.69	-1.59	-1.6	-1.4	-1.41
Fateh«**GF**»	-0.41	-0.45	0.39	0.39	0.28	0.27	0.56	-0.92
Buhoth10«**HB**»	0.43	0.41	0.75	0.75	-0.39	-0.4	0.13	-0.76
Buhoth158«**IB**»	0.6	0.58	0.23	0.23	-0.11	-0.11	0.27	-0.94
Babol113«**JB**»	0.02	-0.01	0.23	0.23	1.14	1.14	-0.94	-0.76
Alraq«**KA**»	1.56	1.56	0.47	0.47	0.61	0.6	-0.96	-0.32
Bwru«**LB**»	-0.39	-0.42	-1.86	-1.87	-1.68	-1.69	-0.43	0.55
Baghdad«**MB**»	0.66	0.64	-0.05	-0.06	0.13	0.12	-0.77	-0.73
Faris«**NF**»	2.46	2.48	1.72	1.73	**1.83**	**1.82**	**1.83**	**1.04**
Tamuz«**OT**»	-1.12	-1.17	-0.03	-0.03	-0.23	-0.24	-1.15	-1.13
Buhoth«**PB**»	-0.79	-0.84	-0.52	-0.53	0.5	0.49	-1.34	-1.47
Abaá95«**QA**»	-0.89	-0.94	-0.25	-0.25	0.43	0.42	-0.02	0.06
Abaá99«**RA**»	-0.82	-0.71	-0.19	-0.2	0.7	0.68	-0.33	-0.16
AbóGhuriyb«**SA**»	-0.13	-0.06	0.57	0.57	0.23	0.22	**2.03**	**1.79**
Buhoth22«**TB**»	-0.14	-0.17	-0.16	-0.13	0.34	0.5	**0.95**	**1.8**
Dujela«**UD**»	-0.69	-0.73	-2.09	-2.05	-1.2	-1.2	**1.85**	**1.98**
Nemichinovka«**VN**»	-1.87	-1.68	-1.5	-1.51	-2.16	-2.14	0.07	0.04
AbóRaghef«**WA**»	0.05	0.03	-0.61	-0.62	0.25	0.24	-0.75	0.26
Note: Salinity (S), Drought (D)								

Appendix 0-19. List of works published on the topic of the thesis

№ п/п	Название научного труда	Выходные данные	Объем работы	Соавторы
		МЦБ		
1.	Genetic and environment diversity to improve wheat (Triticum spp.) productivity: A review	Research on Crops, 23 (2): страницы 295-306, (2022) DOI:10.31830/2348-7542.2022.041 **Scopus**	12 стр.	Malek Hubaish Walli, Zina Al-Jubouri, Mukhriddin Mu Madumarov, Myrnenko Margaryta, Ahmed Abdalbare Abdiee Aldibe
2.	Influence of growth regulators on the formation of main indicators of photosynthetic activity in amaranth (Amaranthus tricolor) varieties	Research on Crops, 23 (1): стр 187-192 (2022) DOI:10.31830/2348-7542.2022.025 **Scopus**	7 стр.	Kristina Shevchenko, Malek Hubaish Walli, Mukhriddin Mu Madumarov, Rami Ben Hmida and Abdullah As Naji
3.	Impact of Global Climate Change on Soil Properties and Water Resources: Review Article	IOP Conf. Series: Earth and Environmental Science, E-ISSN (1755-1315), 1487(1): стр 012203 (2025) DOI:10.1088/1755-1315/1487/1/012203 **Scopus**	9 стр.	Malek Hubaish Walli, Meisam Zargar, Arshad Naji Al-Hasnawi and Zina Al-Jubouri
		Перечень ВАК		
4.	Identification of drought-tolerant bread wheat genetic resources using molecular markers	RUDN Journal of Agronomy and Animal Industries, 21(1), стр 41-54 (2026) DOI:10.22363/2312-797X-2026-21-1-41-54 agrojournal.rudn.ru **К2**	14 стр	Malek Hubaish Walli, Fatima Duksi, Zina Al-jubouri, Meisam Zargar, Arshad Alhasnawi
5.	Evaluation of 23 Wheat Genotypes for Water Stress Based on Physiological Indices and Grain Yield	Научный журнал КубГАУ, 217(03) 2026. http://dx.doi.org/10.21515/1990-4665-217-001 http://ej.kubagro.ru **К2**	14 стр	Walli. M. H, Duksi. F.
		Другие журналы		
6.	Biochemical Mechanisms Regulating Salt Tolerance in Plants	Journal of University of Babylon for Pure and Applied Sciences (JUBPAS), 33 (2): страницы 122-140 (2025)		Arshad Naji Alhasnawi, Malek Hubaish Walli, Febri Doni

		https://doi.org/10.29196/jubpas.v33i.5936		
7.	Оценка генетических и фенотипических параметров, а также корреляции и анализ динамики показателей продуктивности генотипов пшеницыв условиях солевого стресса	Проблемы развития АПК региона. – 2025. № 2(62). – С. 36-43.	Стр 8	Валли М.Х., Заргар Мейсам, Алхаснави А.Н., Нагави М.Р., Кузьмина М.В.
8.	Selection of Salinity-Tolerant Wheat (*Triticum aestivum L.)* Lines to Improve Production Yields Under Climate Change	International Journal of Environmental Sciences, 11(25s): страницы 2112-2126 (2025)	15 стр	Malek H Wall, Fatima Duksi, Yassir Dakheel, Kremsh Alasadiy, Meisam Zargar, Zina Al-jubouri
9.	Грибные заболевания пшеницы в России: распространение, симптомы, методы борьбы и экономический ущерб (обзор литературы)	Известия Кабардино-Балкарского научного центра РАН. Т. 27 № 3 С. 121–132. 2025 DOI: https :// do i . org / 10.35330/1991-6639-2025-27-3-121-132	12 стр	Дукси Ф., Валли М. Х., Заргар М.
Конференции				
10.	Climate change impacts food safety and reduction of cereal crops in agricultural land	IV международная конференция «Безопасность и качество продуктов питания» 30 сентября -02 октября 2024 г. РУДН им. Патриса Лумумбы, Москва	Стр 9	Малик Альбо Хуссейн, Заргар Мейсам.
11.	Изучение эндофитных грибов семян яровой пшеницы с применением микроскопии методов	Всероссийская научно-практическая конференция молодых ученых с международным участием «Фундаментальные и прикладные исследования в ботанике, экологии, растениеводстве» Российская Федерация, Республика Крым, 26 - 30 мая 2025 года	Стр 6	Дукси Фатима, Малик Хибайш Валли
12.	Endophytic bacteria of wheat seeds: PCR and sequencing	Сборник статей XVII Международной научно-практической конференции молодых ученых «Инновационные процессы в АПК», 2025. Москва, РУДН. 441-444	Стр 4.	Дукси Ф., Валли М., Заргар М.