CUKUROVA UNIVERSITY

INSTITUTE OF NATURAL AND APPLIED SCIENCES

MSc THESIS

Evaluation of drought tolerance of *Triticum araraticum* and *Triticum timopheevii*: A neglected GGAA genome

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Field Crops Department

January, 2025

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This master's Thesis was evaluated by the following Jury Members on 27/12/2024 and was approved by unanimity / majority of votes.

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This Thesis was written in the Department of Field crops, Institute of Natural and Applied Sciences.
Thesis Number:

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This work was supported by TÜBİTAK.
Project ID: 221N405

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Advisor: Prof. Dr. Hakan ÖZKAN

Department of Field crops

ABSTRACT

Wheat is an essential cereal crop, and its production is limited by several biotic and abiotic stress factors, specifically drought. Climate change and depletion of groundwater due to erratic rainfalls have increased the severity and intensity of drought stress. Genetic erosion in domesticated wheat and increased drought stress highlight the need to evaluate the potential of wheat wild relatives. Thus, two different approaches, i.e., a PEG-induced drought stress experiment at the seedling stage and a two-year field experiment under rainfed conditions, were conducted in the molecular genetics lab and research and application area of the Field Crops Department of Çukurova University, respectively, to decipher the potential of an overlooked GGA^tA^t genome of *Triticum araraticum*. A panel of 90 *Triticum araraticum* genotypes was used in both experiments 15 *Triticum dicoccoides* genotypes, and five commercial cultivars of durum wheat were used in the drought stress experiment for comparison. The findings of the seedling stage experiment revealed that drought stress significantly affected all the studied traits, with the maximum effect on mean seminal root length (42.26%), followed by shoot length and total root length (40.34 and 40.32, respectively) and the minimum effect on total root number (9.50%).
On the other hand, the results of the field experiment revealed significant variations among genotypes for all the traits under investigation, while the genotypic response for most of the traits was constant in response to the change in environment. The results revealed valuable genetic diversity among the genotypes that can be used in wheat breeding programs. Moreover, based on the results of the seedling stage experiment, some promising *T. araraticum* genotypes (TR60, TR14, TR41, TR1, TR45, TR62, TR103, TR96, TR38, TR97, TR55, TR30, TR7) were identified and it was observed that *T. araraticum* showed comparable performance with *T. dicoccoides.* Therefore, it is concluded that *T. araraticum* holds significant potential for drought stress tolerance in wheat and should be utilized in wheat breeding programs to develop drought-tolerant wheat cultivars.

Keywords: Drought stress, Wheat, *Triticum araraticum*, Shoot length, Total root length.

ÇUKUROVA ÜNİVERSİTESİ
FEN BİLİMLERİ ENSTİTÜSÜ

YÜKSEK LİSANS TEZİ

Triticum araraticum ve *Triticum timopheevii*'nin kuraklık toleransının değerlendilmesi: Göz ardı edilen GGAA genomu

Zain ALI

Danışman: Prof. Dr. Hakan ÖZKAN

Tarla Bitkileri Anabilim Dalı

ÖZ

Buğday önemli bir tahıl ürünüdür ve üretimi çeşitli biyotik ve abiyotik stres faktörleri, özellikle kuraklıktan etkilenmektedir. İklim değişikliği ve düzensiz yağışlar nedeniyle yeraltı sularının tükenmesi, kuraklık stresinin şiddetini ve yoğunluğunu artırmaktadır. Evcilleştirilmiş buğdaydaki genetik daralma ve kuraklık stresinin artması, buğdayın yabani akrabalarındaki genetik çeşitliliğin değerlendirilmesi ihtiyacını ön plana çıkarmaktadır. Buğdayın yabani gen kaynaklarından birisi olan *Triticum araraticum'un* potansiyelini araştırmak için hem Çukurova Üniversitesi Tarla Bitkileri Bölümü Moleküler Genetik Laboratuvarında fide aşamasında kuraklık stresi araştırması hem de Araştırma ve Uygulama alanında doğal koşullar altında iki yıllık tarla denemesi yürütülmüştür. Her iki denemede de 90 adet *T. araraticum* genotipinden oluşan bir panel kullanılırken, kuraklık stresi çalışmasında kontrol olarak 15 adet *Triticum dicoccoides* genotipi ve 5 adet ticari makarnalık buğday çeşidi de kullanılmıştır. Sonuçlar kuraklık stresinin incelenen tüm özellikleri önemli ölçüde etkilediğini, maksimum etkinin ortalama seminal kök uzunluğu üzerinde (%42.26), ardından sürgün uzunluğu ve toplam kök uzunluğu üzerinde (sırasıyla 40.34 ve 40.32) ve minimum etkisi toplam kök sayısı üzerinde (%9,50) olduğunu göstermiştir.Öte yandan, tarla deneme sonuçları, incelenen tüm agro-morfolojik özellikler için genotipler arasında önemli genetik varyasyonun olduğunu göstermiştir. Ayrıca kuraklık deneme sonuçlarına göre bazı ümit verici *T. araraticum* genotipleri (TR60, TR14, TR41, TR1, TR45, TR62, TR103, TR96, TR38, TR97, TR55, TR30, TR7) tanımlanmıştır. Elde edilen tüm sonuçlar birlikte değerlendirildiğinde, *T. araraticum*'un buğdayda kuraklık stresine dayanıklılık açısından önemli bir potansiyele sahip olduğu ve kuraklığa dayanıklı buğday çeşitlerinin geliştirilmesi için buğday ıslah programlarında kullanılması gerektiği sonucuna varılmıştır.

Anahtar Kelimeler: Kuraklık stresi, Buğday, Triticum araraticum, Sürgün uzunluğu, kök uzunluğu.

GENİŞLETİLMİŞ ÖZET

Buğday (*Triticum aestivum* L.), dünyanın en önemli tahıl ürünlerinden biri olarak bilinir ve insan vücudunun ihtiyaç duyduğu toplam kalorinin %19'unu ve toplam küresel proteinin yaklaşık %20'sini sağlar. Ancak buğday üretimi, başta kuraklık stresi olmak üzere çeşitli biyotik ve abiyotik stresler nedeniyle engellenmektedir. Kuraklık stresi bitki verimini azaltan, büyüme ve gelişmeyi etkileyen en kritik çevresel faktörlerden biridir. Bu zararlı stres, tüm bitki dokularında meydana gelen agronomik, morfolojik, fizyolojik, biyokimyasal ve metabolik değişiklikler yoluyla birçok özelliği aynı anda değiştirebilir ve sonuçta bitkinin verimini azaltabilir. Bu nedenle, mevcut stres koşullarında bile daha yüksek verim sağlayabilecek küresel iklim değişikliğine uygun buğday çeşitlerinin geliştirilmesi, çağımızın en acil zorlukları arasında yer alıyor. Bu bağlamda, buğdayın yabani akrabaları, iklime dayanıklı çeşitler geliştirmek için kullanılabilecek büyük bir genetik çeşitlilik sunmaktadır.

Buğdayın yabani akrabaları arasında araştırma faaliyetleri, hem makarnalık buğdayının hem de ekmeklik buğdayın atası olması nedeniyle esas olarak *T. dicoccoides'*de yapılmıştır. Ancak *T. araraticum* ve *T. timopheevii* de buğdayın geliştirilmesine katkıda bulunmuştur ancak bu yabani akrabaların potansiyelini değerlendiren çok az çalışma yapılmıştır. Bu nedenle, bu araştırma göz ardı edilen GGAA genomunun kuraklığa tolerans açısından potansiyelini değerlendirmek ve doğal koşullarında koşullar altında *T. araraaticum* genotipleri arasındaki genetik çeşitliliği ortaya çıkarmak için planlanmıştır. Kısaca, fide aşamasında PEG kaynaklı kuraklık stresi deneyi ve doğal yağış koşulları altında iki yıllık bir tarla denemesi gerçekleştirilmiştir. Fide döneminde yaratılan kuraklık denemesi faktöriyel deneme desenine göre kurulurken, tarla denemesi tesadüf blokları deneme deseni göre kullanılmıştır. Her iki denemede de 90 adet *Triticum araraticum* genotipinden oluşan bir panel kullanılmıştır. Fide dönemindeki kuraklık denemesine kontrol olarak 15 adet *Triticum dicoccoides* genotipi ve 5 adet ticari makarnalık buğday çeşidi eklenmiştir.

Kuraklık çalışmasının sonuçları, tüm fide özellikleri açısından genotipler arasında önemli varyasyonun olduğunu ve kuraklığın da incelenen tüm özellikler üzerinde önemli etki gösterdiğini ortaya çıkarmıştır. İncelenen genotip ile stres arasındaki etkileşimin tüm fide özellikleri için önemsiz olması genotiplerin kuraklık stresine benzer tepkiler verdiğini belirlenmiştir. Kuraklık stresi, sürgün uzunluğu (%40,34), birincil kök uzunluğu (%32,49), seminal kök uzunluğu (%38,49), ortalama seminal kök uzunluğu (42,26) ve toplam kök uzunluğu (40,32) gibi özelliklerin çoğunda önemli düşüşe neden olmuştur. Düşüş oranı hem *T. araraticum* hem de *T. dicoccoides* genotipleri için neredeyse benzer bulunurken makarnalık buğday genotiplerinde oldukça düşük bulunmuştur. Sürgün uzunluğu ve toplam kök uzunluğu gibi bazı fide özellikleri açısından, bazı *T. araraticum* genotipleri, *T.dicoccoides* genotiplerinden bile daha iyi performans göstermiş, diğer özellikler için de karşılaştırılabilir düzeyde olduğu saptanmıştır.

Öte yandan, tarla denemesinin sonuçları, incelenen tüm özellikler için genotipler arasında önemli varyasyon olduğunu, aynı zamanda çevrenin, incelenen tüm özellikler için genotiplerin performansı üzerinde önemli bir etkiye sahip olduğunu göstermiştir. Bununla birlikte, genotip ve çevre arasındaki etkileşim, çoğu özellik için önemli bulunmuş, genotipo x çevre interaksiyonu görülmüştür. Hasat öncesi parametrelerden, ortalama başaklanma süresi iki yetiştirme sezonunda da benzer olduğu, ortalama bitki boyunun ise ikinci yetiştirme sezonunda daha düşük olduğu saptanmıştır. Ayrıca, başak uzunluğu ve başakta başakçık sayısının da her iki yetiştirme sezonunda tutarlı olduğu tespit edilmiştir. Hasat sonrası parametrelerden ortalama başakta başakçık sayısı ve bitki verimi verimi ikinci yetiştirme sezonunda oldukça düşük bulunmuştur. Bunlara ek olarak, fizyolojik parametreler arasında, bayrak yaprağı üzerinde ölçülen ortalama stoma iletkenliği, üçüncü bazal yapraktan kaydedilenden önemli ölçüde düşük bulunmuştur. Bayrak yaprağı üzerinde ölçülen fotosistem II'nin ortalama kuantum verimi, üçüncü bazal yapraktan gözlemlenene göre fotosentetik verimde bir azalmaya işaret eden bir düşüş göstermiştir.

Çalışma sonunda incelenen tüm özellikler için genotipler arasında yüksek genetik varyasyonun bulunduğu, bu varyasyonun küresel iklim değişikliğine dayanıklı ekmeklik ve makarnalık buğday çeşitleri geliştirmek için buğday ıslah programlarında kullanılabileceğini göstermiştir. Başaklanma süresi ve tane verimi gibi özelliklere dayanarak, erkenci buğday çeşitleri geliştirmek için kullanılabilecek bazı umut verici genotipler (TR98, TR87, TR85, TR49, TR16, TR51, TR83, TR55, TR45, TR81, TR76, TR96, TR49) belirlenmıştir. Ancak diğer yabani akrabalar gibi *T. araraticum*'da da tane verimi oldukça düşüktür. Bu nedenle, yukarıda adı geçen genotiplerin de novo evcilleştirilmesi sırasında tane verimi ve başak kırılganlığı gibi özelliklerin hedeflenerek doğrudan yetiştiricilikte veya buğday ıslah programlarında kullanılabileceği değerlendirilmiştir.

ACKNOWLEDGEMENTS

I would like to express my deepest gratitude to my advisor, Prof. Dr. Hakan ÖZKAN, for his exceptional guidance and unwavering support throughout my Master studies and research. His patience, encouragement, and profound expertise have been invaluable throughout this journey. His thoughtful mentorship has greatly contributed to both my academic and personal development, and I consider myself incredibly fortunate to have had him as a mentor during this pivotal phase of my academic career.

I would also like to extend my heartfelt thanks to Prof. Dr. Rüştü HATİPOĞLU for his insightful feedback, encouragement, and steadfast support throughout my studies. His expertise and guidance have played a crucial role in shaping my research and fostering my academic growth.

My sincere appreciation goes to Dr. Esra ÇAKIR for the unwavering support and guidance throught out my research work. I am also deeply grateful to my family, friends and my colleagues especially İbrahim Barış ÇANKAYA and Melike BİÇİCİ, for their constant support, encouragement, and understanding throughout this journey. Their belief in me has been a source of strength and motivation in overcoming challenges and reaching this significant milestone.

Additionally, I am thankful to Türkiye-Islamic bank development scholarship program and TÜBİTAK for providing the financial assisstance. I am truly appreciative of both organizations for their support in making this research possible.

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SYMBOLS AND ABBREVIATIONS

CL : Coleoptile length

DTH : Days to heading

GP : Germination percentage

gsw : Stomatal conductance

MSRL : Mean seminal root length

PH : Plant height

PhiPSII : Quantum yield of photosystem

PRL : Primary root length

SL : Shoot length

SL : Spike length

SPS : Number of spikelets per spike

SRL : Seminal root length

SVI : Seedling vigour index

SY : Spikelet yield per plant

TRL : Total root length

1. INTRODUCTION

Wheat (*Triticum aestivum L.)* is one of the world's most essential grain crops and belongs to the Poaceae family. It provides 19% of the total calories required by the human body and accounts for approximately 20% of total global protein (Biel et al. 2020; Huertas-García et al. 2023). Moreover, as an essential component of the global human diet, wheat provides the human body with dietary fibers, vitamin B, calcium, fats, zinc, and iron (Mobley et al. 2013). The genus *Triticum* on the basis of chromosome numbers includes diploid einkorn wheat (2n=2x=14), tetraploid emmer wheat (2n=4x=28), tetraploid timopheevii wheat (2n=4x=28) and hexaploid bread wheat (2n=6x=42). Hexaploid bread wheat (*Triticum aestivum* L. 2n=6x=42, BBAADD) covers about 90% of wheat production, and tetraploid durum wheat (*Triticum durum* Desf. 2n=4x=28, BBAA) is the 10th most vital staple crop (International Grains Council, 2020). In 2023, wheat was cultivated on an area of 220.4 Mha globally, with the second highest cereal crop production (799 Mt), next to maize (1.24 billion tons) (FAO, 2024). The projected yield trends in agricultural production will likely not satisfy the food demands of the increasing human population (Zandalinas et al. 2018). Because of the continuous increase in the global population, the demand for wheat is growing rapidly, and the wheat production is required to be increased to 70% by 2050 (Semenov et al. 2014). Although the global need for wheat is becoming high, crop production and food security are under severe threat from the predicted rounds of extreme climatic events, including drought and heat stress (Hussain et al. 2015; Semenov et al. 2014). The world has perceived intense heatwaves and drought stress due to continuous change in climate in recent decades, especially in major wheat-growing countries of the world such as Turkey, Australia, Western Europe, Russia, United States, India, and Pakistan (Özdoğan, 2011; El Habti et al. 2020).

Wheat production is hampered by several abiotic stress factors worldwide. Drought is one of the most significant abiotic stress factors that leads to a sharp decline in wheat production and is expected to increase more with the changing climate (Kang et al. 2009). It is one of the most critical environmental factors that reduces crop yields and affect growth and development. This detrimental stress can simultaneously alter many traits through agronomic, morphological, physiological, biochemical, and metabolic changes, which occur in all plant tissues and ultimately reduce plant yield (Cochard et al. 2002). Plants can experience drought stress at any growth stage (germination, seedling, vegetative, flowering, and reproductive) depending on the local environment, and it disturbs almost every aspect of plant growth through alterations in gene expression and metabolic pathways (Sallam et al. 2019). Early growth stages, such as the seedling stage, are crucial and very sensitive stages to water deficit because they affect all the following stages, including grain yield (Samarah, 2005). Consequently, exploring tolerance to drought at these stages is very important to enhance the selection efficiency for breeding drought-tolerant varieties (Hameed et al. 2010). With the consequences of climate change, the severity of drought is projected to increase at any growth

stage, especially the seedling stage, which is important for plant stature and development. Drought stress is causing a great loss to the farmer community by reducing the plant yield up to 50% (Akpinar et al. 2013).

Climate change significantly affects temperature and rainfall patterns, causing a great uplift in the rate and severity of drought (Budak et al. 2013). It has been anticipated that continuous climate change may adversely affect wheat production by 29% (Muthamilarasan et al. 2014). Therefore, the development of climate smart crops, which can provide us with higher yields even under prevailing stress conditions, is among the most urgent challenges of our time (Brunazzi et al. 2018). However, the complex quantitative nature of drought tolerance requires a great understanding of the genetic architecture of drought tolerance, that is still underway. Breeding high-yielding drought-tolerant cultivars of major crops, such as wheat (*Triticum* spp.), is considered a sustainable approach to mitigate this challenge. The increase in wheat grain yield, which was significantly uplifted by the 'Green Revolution' has reduced over the last three decades (Fischer and Edmeades, 2010; Challinor et al. 2014; Curtis and Halford, 2014). Therefore, development of drought tolerant wheat cultivars for ensuring food security has become a serious challenge for plant breeders.

Wild relatives of bread wheat are the vital source of genes related to biotic and abiotic stress resistance and have a long history in wheat breeding, predominantly for salinity, drought, heat, and cold tolerance (Zaharieva et al. 2001; Yesayan et al. 2009; Arabbeigi et al. 2014; Kiani et al. 2015; Masoomi-Aladizgeh et al. 2015). The stagnant wheat yield worldwide requires new sources of resistance or tolerance to combat biotic and abiotic stresses. In this context, the wheat wild relatives are among the key sources for bread wheat and durum wheat improvement (Dante et al. 2013; Placido et al. 2013; Zhang et al. 2017). However, wheat has no hexaploid progenitor. Only two wild tetraploid wheats (2n = 4x = 28) were discovered, namely (1) wild emmer wheat *T. dicoccoides* (Körn. ex-Asch. et Graebn.) Körn. ex Schweinf. (Schweinfurth 1908) [syn. *T. turgidum subsp. dicoccoides* (Körn. ex-Asch. & Graebn.) Thell.] and (2) Armenian, or Araratian wheat *T. araraticum* Jakubz. (Jakubziner 1947) [syn. *T. timopheevii* (Zhuk.) Zhuk. *ssp. armeniacum* (Jakubz.) van Slageren)]. Morphologically, both species are nearly identical but differ in their genome constitution (Zohary et al. 2012). The wheat section Timopheevii mainly consists of wild tetraploid *T. araraticum*, domesticated tetraploid *T. timopheevii* (Zhuk.) Zhuk. and hexaploid *T. zhukovskyi* (Dorofeev et al. 1979; Goncharov, 2012). The timopheevii group of species *T. timopheevii* Zhuk. and *T. araraticum* Jackubz. belongs to the secondary pool of modern bread wheat and have partial homology to the genome of this bread wheat (Timonova et al. 2013).

To date, research and pre-breeding activities have focused on *T. dicoccoides* because of its role as the ancestor of both economically most important wheats, *T. durum* Desf. and *T. aestivum* L. (Avni et al. 2017; El Haddad et al. 2021). However, *T. araraticum* and *T. timopheevii* have also contributed to bread wheat improvement. Important genes were transferred, such as genes controlling resistance against stem rust, leaf rust, powdery mildew, or wheat leaf blotch (Allard and Shands,

1954; Brown-Guedira et al. 1996, 2003; Dyck, 1992; McIntosh and Gyarfas, 1971). Therefore, this study aimed to explore the potential of neglected wild wheat species, *T. araraticum,* for drought tolerance at seedling stage and to assess the phenotypic diversity under rainfed conditions to utilize it in future wheat breeding programs.

2. LITERATURE REVIEW

Triticum araraticum Jakubz, a wild tetraploid (2n=4x=28) wheat with the genome formula GGA^tA^t, is one of the least studied or neglected species of the genus *Triticum* (Badaeva et al. 1998) and *Triticum timopheevii* (Zhuk.) Zhuk (2x=4n=28, GGA^tA^t) is the domesticated form of *T. araraticum*. Cytogenetic and molecular analyses revealed that *T. araraticum*, like another tetraploid wild wheat *T. dicoccoides*, originated autonomously from *T. dicoccoides* as a consequence of hybridization between *Aegilops speltoides* Tausch (2n=2x=14, SS) and *Triticum urartu* Thumanjan ex Gandilyan (2n=2x=14, AA) (Dvorak et al. 1993; Rodríguez et al. 2000a,b). Although these two tetraploid wheat lineages share potentially the same ancestry, they have significant differences in the genome structure and time of origin (Adonina et al. 2015). *Ae. speltoides* shared nuclear and cytoplasmic loci with *T. araraticum* and *T. dicoccoides* which differed between the two wild tetraploid wheat species. Therefore, *Ae. speltoides* is considered as the maternal donor of both *T. araraticum* and *T. dicoccoides* (Kilian et al. 2007a; Golovnina et al. 2007). However, hybridization between *T. araraticum* and *T. dicoccoides* produced sterile hybrids because of meiotic disorders and gene interactions (Makushina 1938; Svetozarova 1939; Tanaka and Ishii 1973; Wagenaar 1961). Although, a few authors (Noda and Ge, 1989; Sachs, 1953; Tanaka and Ichikawa, 1972; Kawahara and Tanaka 1977) described comparatively good chromosome pairing in the F_1 hybrids produced by crossing *T. araraticum* and *T. dicoccoides*. It is reported that B and G genomes have greater degree of sequence divergence compared to the A and A^t genomes (Rodríguez et al. 2000; Huang et al. 2002; Salina et al. 2006). The single nucleotide polymorphisms (SNPs) obtained from genotyping-by sequencing (GBS) revealed that the *T. timopheevii* genome is clustered more closely to the AABB lineage (Hyun et al. 2020).

2.1. Origin and geographical distribution of *Triticum araraticum*

Wild *T. araraticum* was collected for the first time by M.G. Tumanyan and A.G. Araratyan during 1925–28 from the southeast of Erevan, Armenia (Tumanyan 1930; Nazarova 2007), soon after the discovery of domesticated *T. timopheevii* by P.M. Zhukovsky (Zhukovsky 1928). Northern Iraq is the center of diversity and origin of *T. araraticum* (Gornicki et al. 2014; Badaeva et al. 2021). Geographical distribution of *T. araraticum* covers southeastern Turkey, northern Iraq, western Iran, and some regions of Transcaucasia: the Nakhichevan Autonomous Republic, Armenia, and northeastern Azerbaijan (Badaeva et al. 1994b; Zohary and Hopf 2012). Different populations of *T. araraticum* differ in morphological and physiological traits (Dorofejev et al. 1979), spectra of the storage proteins (Konarev 1980), isozyme composition (Nishikawa et al. 1988), DNA content (Nishikawa et al. 1979), and karyotype structure (Tanaka and Ichikawa 1972; Kawahara and Tanaka 1977, 1981, 1983; Badaeva et al. 1988, 1990a). Single herbarium specimens resembling *T. araraticum* have been sporadically recorded among *T. dicoccoides* accessions collected from the

Fertile Crescent (Jakubziner 1932; Sachs 1953). More lately, *T. araraticum* was found in northwestern Syria (Valkoun et al. 1998). Especially in southeastern Anatolia, Turkey, the distribution area of *T. araraticum* overlaps with the distribution range of *T. dicoccoides.* From western to eastern Fertile Crescent, it is assumed that *T. araraticum* gradually substitutes *T. dicoccoides* (Johnson 1975), and *T. dicoccoides* is absent in Transcaucasia (Özkan et al. 2011). In most habitats, *T. araraticum* grows in patches and in mixed stands with other wild cereals (Troitzky 1932; Tumanyan 1930; Badaeva et al. 2021).

Recently, two genetic lineages i.e. ARA-0 and ARA-1 and one i.e. TIM, have been reported within *T. araraticum* and *T. timopheevii* respectively. The subgroup ARA-0 of *T. araraticum* have wide geographical distribution, while ARA-1 was found only in southeastern Turkey (Gaziantep, Kahramanmaraş, Adiyaman, Kilis) and in northwest Syria. Among these two genetic lineages, ARA-0 possesses more genetic diversity. Based on the results of *BARE-1* family of retrotransposons, Badaeva et al. (2021) revealed that ARA-0 is phylogenetically closely related to TIM than ARA-1. However, considering only the Jeli markers, ARA-1 was more closely related to TIM. Moreover, *T. dicoccoides* was genetically related most closely to the ARA-1 lineage.

2.2. Root system architecture and drought tolerance

Drought is one of the detrimental and complex abiotic stresses that significantly affect wheat growth and production in arid and semi-arid regions of the world (Ahmed et al. 2022). Continuous change in climate has further extended the periods of drought and heat stress, consequently threatening crop production worldwide (Vukovi´c et al. 2022). Drought stress can occur at any growth stage of the plant, i.e. seedling, flowering and grain filling stage. However, seedling stage is the most crucial stage of the plant that is affected by genetic and environmental factors (Sharma et al. 2022). Seedling emergence is influenced by water deficit conditions (Bayoumi et al. 2008), and rate as well as the degree of seedling establishment are crucial determinants of plant yield and maturity time (Rauf et al. 2007). The inconsistent occurrence of abiotic stress factors, especially drought, can be addressed through the employment of crop plants with improved root system architecture because it is proved to be an essential component of plant adaptation to different environmental factors including water deficit (Khan et al. 2016).

The root system architecture (RSA) is comprised of several structural aspects which embraces the length and number of primary and secondary or lateral roots along with the length and density of root hairs. These features show plasticity under water deficit environments and could be crucial for developing crop plants with effective root systems for adaptation to water deficit stress. RSA is reported to be a crucial agronomic trait and is potentially related to the plant growth and yield, nutrient uptake, abiotic stress tolerance, development of plasticity in response to environmental stresses and provision of mechanical support to plants (Fromm, 2019; Smith and de Smet, 2012). Therefore, it is critical to understand how root architecture traits are important to

cultivate crops plants with enhanced tolerance to abiotic stresses particularly drought. Plants can alter their root architecture in response to various soil conditions such as drought, salt and acidity stresses, by combining the biochemical, physiological and molecular programmes that drives the RSA (Jovanovic et al. 2007).

RSA is considerably altered under water deficit conditions and stimulates the formation of root hairs and lateral roots (Koevoets et al. 2016; Nibau et al. 2008). The proliferative and deeper root system is proved to be beneficial for several plants including wheat (Becker et al. 2016; Kulkarni et al. 2017), rice (Abd Allah et al. 2011), chickpea (Zaman-Allah et al. 2011), soybean (Dayoub et al. 2021; Fenta et al. 2014), barley (Chloupek et al. 2010), maize (Hund et al. 2009), and cotton (Ullah et al. 2017). Additionally, drought stress alters the plasticity response of plant root system and boosts the development of fibrous roots, modifies root biomass and reduces lateral root diameter (Becker et al. 2016; Fromm, 2019; Smith and de Smet, 2012). However, crops with narrow seminal root angle and deep root system, like wheat, rice and sorghum, help plants absorb water from deep soil profiles during lengthy drought conditions cause less spatial distribution of RSA (Botwright Acuña and Wade, 2012). On the other hand, plants with wider seminal root angle have more spatial distribution of RSA that aids to uptake water from the superficial soil profiles (Alahmad et al. 2019). Roots are the first plant organs to sense the water deficiency by osmosensors, following the experience of dry soil conditions (Nongpiur et al. 2020). Therefore, the understanding of RSA of the crop plants is a critical strategy to cope with the water deficit conditions.

Keeping in view the importance of RSA, Siddiqui et al. (2023), conducted a study to record the variations in plasticity of wheat root architecture in response to water deficit under field conditions by using rain-out shelter and identified the loci associated with the root traits. They used a panel of 200 diverse bread wheat cultivars and phenotyped several root system traits i.e. root average diameter, total root length, root volume, number of root crossings, number of root tips, root surface area, by following the "Shovelomics" protocol. The findings of this study reported significant variations in all the root system traits under both control and water limited conditions.

Likewise, Akman et al. (2023), conducted a study to understand the phenotypic variations in root system traits of seven modern wheat cultivars and twelve accessions of different wheat species including *T. monococcum*, *T. polonicum*, *T. mirabile, T. turanicum*, *T. aestivum* and *T. durum,* at early growth stages. The results revealed significant variations among the studied material for root biomass, seminal and nodal root numbers, rooting depth, root to shoot ratio, and shoot traits. The drought adaptive cultivar 'Taner' and some wild wheats i.e. *T. monococcum* and *T. turanicum* showed deeper roots which help plant to absorb water from deep soil profiles. The findings suggest that genotypes with deep root system can be utilized to breed drought tolerant varieties.

Recently, Sallam et al. (2024), unravel the diversity for RSA and identified the genetic loci associated with root and shoot architecture traits in a core collection of 146 highly diverse spring wheat genotypes representing twenty-eight different countries under drought stress at seedling stage.

The drought stress was applied to genotypes for 13 days by withholding water. Root traits including root length, emerging angle, maximum width, number of roots, emergence angle and tip angle were scored. Furthermore, leaf traits such as shoot length, leaf rolling, leaf wilting, days to wilting and leaf area were also measured. They found significant variations among genotypes for all the traits under study. GWAS analysis revealed 169 marker trait associations for both leaf and root traits under drought stress and identified 95 candidate genes out of which 53 were reported to be associated with tolerance to drought stress. The results hold significant promise to breed wheat drought tolerant cultivars by selecting the lines with drought tolerant genes.

Moreover, Robin et al. (2021), studied the impact of PEG-induced drought stress on the root architecture and other stem traits of 22 wheat genotypes. The genotypes were grown in the hydroponic system and 0% and 10% PEG was applied to control and plants under stress respectively, after 14 days of germination. PEG-induced water deficit stress significantly reduced plant growth indicated by reduction in number of leaves per tiller, plant height, roots per tiller, root-bearing phytomers. Moreover, PEG-induced drought stress significantly increased root dry weight by increasing the length of both primary and secondary roots as well as the density of root hairs and diameter of every single root. These variations in the root architecture traits under drought stress are essential as they provide breeders with diverse selection options for breeding climate resilient cultivars.

Since root architecture and other seedling traits are important in determining the plant stand and grain yield, research is now focused on evaluating the drought tolerance at seedling stage. For instance, several GWAS studies revealed the significant MTAs linked with shoot length, germination percentage (Maulana et al. 2020), seedling vigour (Maulana et al. 2021), coleoptile length (Ma et al. 2020) and drought tolerance index (Schierenbeck et al. 2023). Regardless of these achievements, research is still needed to focus on unravelling the plasticity of RSA and the genetic loci associated with seedling tolerance to drought stress in wheat.

Considering the importance of root architecture traits in plant adaptation to drought stress, Gudi et al. (2024) examined the effect of drought stress at seedling stage in a collection of 198 wheat germplasm lines. Drought tolerance of the material was evaluated by using Cigar roll method of seed germination and drought stress was induced by using 20% PEG. The genotypes were evaluated for coleoptile length, germination percentage, root length, shoot length, and seedling vigour. GWAS analysis was used to identify the candidate genes associated with the traits under study. Analysis of variance revealed significant variation among genotypes under both control and osmotic stress. The results of GWAS analysis identified 39 MTAs which were further analyzed and led to the identification of 83 candidate genes with functional association with drought tolerance. The findings of the study are significantly valuable for the wheat breeders in selecting plants with beneficial alleles to improve drought tolerance in wheat.

Furthermore, Sharma et al. (2022) conducted an experiment to evaluate the potential of 80 wheat synthetics developed by crossing *T. durum* with *Ae. tauschii*. The experiment was conducted under control conditions using PEG-induced water deficit stress and 10 controls were used to validate the tolerance of the genotypes. The synthetics were evaluated for shoot and root architecture traits, photosynthetic pigments and physiological indices such as chlorophyll content and chlorophyll fluorescence. Significant variations were recorded among the synthetics under both control and water stress for all the studied traits. All the studied traits showed decline with increase in PEG concentration. Based on the performance of synthetics for the studied traits, some promising synthetics were found that can be utilized in the future breeding programmes to develop drought tolerant wheat cultivars.

Wheat wild and landrace progenitors are considered an important source of tolerance to various environmental factors. With the aim of identifying some promising genetic material for breeding drought tolerant varieties, Pour-Aboughadareh et al. (2020), evaluated 50 genotypes of durum wheat including 18 Iranian landraces, 18 breeding lines and 3 local cultivars at seedling stage for physiological parameters (e.g. relative water content and photosynthetic pigments), and the role of several antioxidants such as catalase, ascorbate peroxidase, peroxidase and superoxide dismutase under control and drought stress induced by PEG. They recorded statistically significant variations in the studied traits under drought stress. PEG caused significant decline in the physiological parameters, whereas antioxidants showed significant uplift in the studied durum wheats. In conclusion, they identified several promising breeding lines, Iranian landraces and local cultivars that can be utilized in wheat breeding programmes to develop varieties with significant tolerance to drought.

Based on the importance of RSA, this experiment was also designed to study the root system architecture of *T. araraticum* under PEG-induced drought stress as the wheat wild relatives are shown to be the valuable source of genetic diversity and tolerance to abiotic stresses especially drought.

2.3. Wheat wild relatives and drought tolerance

The crops that feed the globe today are the consequence of plant domestication dating back to the Neolithic era. However, continuous selection during the process of domestication led to a great reduction in genetic diversity, which now bottlenecks the capability of the crops to further evolve (Tanksley and McCouch 1997; Van Heerwaarden et al. 2010). This situation is made worse by the need for high crop productivity under recurrent climate change. Wheat wild relatives offer incredible, untapped genetic diversity for any wheat breeding programme because of their potential to provide beneficial traits to the elite genepools (Pour-Aboughadareh et al. 2019).

Drought is the primary detrimental abiotic stress in plant agriculture, severely affecting crop growth, development, and yield (Gong et al. 2020). Wheat (*Triticum aestivum* L.) is the most widely grown cereal, but its yield is severely affected by biotic and abiotic stresses (Ge et al. 2024). In order

to develop stress tolerant wheat cultivars, wild relatives of wheat represent a potential source of tolerance to biotic and abiotic stresses (Pour-Aboughadareh et al. 2017). The first study on phenotypic diversity in wild wheat species and landraces referred to a study conducted by Percival (1921) which described diversity for plant height, spike length, number of spikelets per spike, and straw quality among landraces of bread wheat from Iran. The review of literature has shown that wild relatives of common wheat are an ideal source of genes related to biotic and abiotic stress resistance, and have a long history in wheat breeding, predominantly for salinity, drought, heat and cold tolerance (Zaharieva et al. 2001; Yesayan et al. 2009; Zamani Bangohari et al. 2013; Arabbeigi et al. 2014; Kiani et al. 2015; Masoomi-Aladizgeh et al. 2015).

For instance, Zaharieva et al. (2001) conducted a study to evaluate the potential of *Aegilops geniculata* under drought and heat stress. They used 157 accessions of *Ae. geniculata* originating from different ecogeographical conditions and studied for two successive years for several traits related to chlorophyll content, water status and plant thermal regulation under Mediterranean field conditions. The findings demonstrated that, *Ae. geniculata* possesses great potential for enhancing drought and high temperature stress tolerance in wheat. Likewise, Balbaki et al. (2006) assessed the drought tolerance of twenty-one populations of six different *Aegilops* species (*Ae. biuncialis, Ae. cylindrica, Ae. geniculata, Ae. markgrafi, Ae. triuncialis,* and *Ae. vavilovii*) by examining the structure and extent of variation in their quantitative attributes like dry weight, plant height, tillers per plant, days to maturity, productive tillering, spike length, kernels per spike, seed number, seed weight, and yield, under different levels of water stress. Based on the results of the examined traits, *Ae. geniculata* and *Ae. markgrafi* emerged as the most drought tolerant species.

Similarly, Sultan et al. (2012) assessed the drought tolerance of three wild species of the genus *Triticum* with different ploidy levels, i.e. *Triticum boeticum* (YS-1L), *Triticum dicoccoides* (YS-2L), and *Triticum araraticum* (ALLT), with two cultivated varieties of *Triticum durum* (MXLK and 87341), and two well-known old common wheat cultivars (SH6 and ZY1) based on their leaf relative water content, free proline content, and malondialdehyde accumulation under water deficit conditions. The order of water stress tolerance of these species according to the three parameters was: YS-1L > YS-2L > SH6 > 87341 > ZY1 > MXLK > ALLT.

Moreover, a comprehensive study conducted by Pour-Aboughadareh et al. (2017) evaluated a set of 180 accessions belonging to 12 wheat species including 11 wild (six diploid species i.e. *T. boeoticum* Bioss. *T. urartu* Gandilyan. *Ae. speltoides* Tausch. *Ae. tauschii* Coss. *Ae. caudata* L. and *Ae. umbellulata* Zhuk. and five tetraploid species i.e. *T. durum* Def. *Ae. neglecta* L. *Ae. cylindrica* Host. *Ae. crassa* Boiss. and *Ae. triuncialis*) and one domesticated hexaploid species (*T. aestivum L.*) along with two commercial tolerant and sensitive control varieties in terms of shoot dry mass and chlorophyll fluorescence parameters under two water regimes: optimum irrigation (FC = 100%) and drought stress (FC = 30%). A considerable number of wild wheat species such as *Ae. crassa* (DM genome), *T. urartu* (A^u genome), *Ae. cylindrica* (DC genome), and *Ae. caudata* (C genome) indicated

a higher tolerance to drought stress as compared to the domesticated genotypes and check varieties, reflecting greater drought adaptations in these species.

In case of tetraploid group of wild relatives of wheat, *T. dicoccoides* (Körn. ex Asch. & Graebn.), a wild tetraploid (2n=4x=28) species with the genome BBAA, offers breeders with rich allelic repertoire to develop drought tolerant cultivars in bread wheat (Peleg et al. 2007 and references therein). Wild emmer wheat, being a potential reservoir of drought-related research, has been the source of several candidate genes associated with drought that are further elaborated well with the development of "omics" approaches in the recent decades (Budak et al. 2013). A significant number of genes in wild emmer wheat related to drought have been identified, cloned and further characterized. Moreover, gene expression studies in this species identified more than 13,000 expressed sequence tags in response to water stress and among them 33 outlier loci for drought tolerance were recognized by single nucleotide polymorphisms marker (Ergen and Budak, 2009; Ren et al. 2013). Several studies have been conducted to evaluate the potential of *T. dicoccoides* for drought tolerance. For instance, Suneja et al. (2019) explored the water stress induced plasticity in 26 accessions of *T. dicoccoides* (BBAA-genome) and 56 accessions of *Aegilops tauschii* (DD-genome) along with bread and durum wheat cultivars for proline induction, early root-shoot development and cell membrane injury. The findings showed significant variation in two species in response to water stress and identified several accessions (*Ae. tauschii* 9816, 14109, 14128, and *T. dicoccoides* 5259, 7130) as potential donors for breeding drought-resistant wheat varieties, emphasizing the role of adaptive plasticity in improving crop resilience.

One another study conducted by Suneja et al. (2017), evaluated the activity of four antioxidant enzymes viz. catalase, superoxide dismutase, glutathione reductase and ascorbate peroxidase in the flag leaves of three *Triticum dicoccoides* and nine *Aegilops tauschii* accessions along with two bread wheat cultivars under irrigated and rain-fed conditions. The studied accessions were shortlisted from a previous study based on their field performance for several morpho-physiological traits. Significant variations were observed in these two species at anthesis under two environments. Based on the changes in the activity of the antioxidant enzymes under study and in spike length, plant height and grain weight, a cumulative tolerance index was deemed and ranked the accession for drought tolerance. The findings revealed that, *Ae. tauschii* accession 3769, 14096, 14113 (DD-genome) and *T. dicoccoides* accession 7054 (AABB-genome) could be used as donors to integrate beneficial stress adaptive alleles from all three sub-genomes into synthetic hexaploid for improving wheat drought tolerance.

There are several reports on the role of *T. dicoccoides* (wild ancestor of wheat) for wheat improvement, however, GGA^tA^t genome of timopheevii section of wheat (a distant relative of common bread wheat) has not been investigated intensively to date. However, *T. araraticum* and *T. timopheevii* have also contributed to the improvement of bread wheat, and the studies conducted so far have shown that these wheat wild relatives have great potential for improvement of bread and

durum wheat. For instance, Nsarellah et al. (2003) developed Hessian fly (an important insect pest in North America, North Africa and Southern Europe) resistant durum wheat cultivars by backcrossing with *T. araraticum.* Brown-Guedira et al. (1996) evaluated a collection of 301 wild timopheevii wheat accessions from Armenia, Azerbaijan, Iraq and Turkey for resistance to 6 foliar diseases and 2 arthropod pests. All the tested accessions were resistant to Septoria blotch (caused by *Septoria tritici* Roberge in Desmasz.) and a very high percentage of them were resistant to tan spot (caused by *Pyrenophora tritici-repentis* (Died.) Drechs.). Resistance to leaf rust was more frequent in the collection than resistance to stripe rust, stem rust, or powdery mildew.

Furthermore, stem rust resistance gene Sr40 was transferred to the short arm of common wheat chromosome 2B (Dyck, 1992) from *T. araraticum* chromosome 2G (Allard and Shands, 1954; McIntosh and Gyarfas, 1971). Recently, a study conducted by Zeibig et al. (2024) analyzed nutrient compositions of wild and domesticated diploid, tetraploid, and hexaploid wheats under field conditions in Germany, comparing them with modern bread (*Triticum aestivum*) and durum wheat (*Triticum durum*) cultivars. The research focused on grain iron and zinc concentrations, phytate molar ratios, grain protein content (GPC), and antioxidant activity across 125 genotypes. Results showed that *T. araraticum* exhibited high Fe accumulation and bioavailability, while *T. zhukovskyi* stood out for its high micronutrient concentrations and antioxidant activity. The findings suggest that the GGA^tA^t wheat lineage, particularly *T. araraticum* and *T. zhukovskyi,* possesses valuable traits for improving grain quality and could be leveraged in wheat breeding programs for enhanced nutritional traits.

Therefore, this study was designed to uncover the potential of neglected GGA^tA^t genome of *Triticum araraticum* for the drought tolerance at seedling stage and to assess the diversity for some morpho-physiological traits to utilize it in the wheat breeding of bread wheat under consistently changing climate.

3. MATERIALS AND METHOD

To evaluate the potential of the overlooked GGA^tA^t genome, two different experiments i.e. one seedling stage PEG (Polyethylene glycol-6000) induced drought stress experiment and a two-year field experiment under rainfed conditions, were conducted.

3.1. Plant materials

A collection of 90 *T. araraticum* along with 15 *T. dicoccoides* genotypes and 5 commercial cultivars of durum wheat (Kiziltan-91, C-1252, Inbar, Svevo and Iride) as control were used in the seedling stage drought stress experiment. However, in the field experiment, only *T. araraticum* genotypes along with two genotypes of its domesticated form, *T. timopheevii* were used. These genotypes were collected from different countries such as Iraq, Iran, Turkey, Azerbaijan, Armenia, Israel, Lebanon and Syria. All these genotypes are preserved in the gene banks within their respective countries. Detailed information about these genotypes such as accession number and location are provided in Table 3.

Table 3. 1. List of genotypes used in both drought and field experiment.

Genotype	Accession number	Location
T. araraticum-38	TR 62	Iraq, 53 km NW from Sulaymaniyah to Dukan Dam
T. araraticum-9	TR 98-1-1	Turkey, 39.9 km N from Elazig to Hozat
T. araraticum-74	TA 6	Turkey, 17 km S of Tunceli, 39 00'N, 39 30'E
T. araraticum-83	8593	Iraq, 35.3 km NE from Sulaymaniyah to Chuarta
T. araraticum-45	KU-8460	13.2 km S from Sulaymaniyah to Qara Dagh,
T. araraticum-25	TR 61 TP071	Iraq, 53 km NW from Sulaymaniyah to Surdash
T. araraticum-7	IG 117895	Syria, 4 km N of St. Simeon, road to Afrin
T. araraticum-97	8872	Iraq, 4.4 km NW from Amadiyah, Mazorka Gorge
T. araraticum-39	IG 116166	Turkey, between Tekirsin and Camurlu
T. araraticum-41	TRI 17419	7 km NE of Shaqlawah
T. araraticum-67	PI 427420	Iraq, between Zawita and Suara Tuka, 36 58'N, 43 11'E
T. araraticum-62	PI 538458	19 km east of Sulaimaniya towards Chuarta
T. araraticum-72	PI 538461	Iraq, Salahadin, 36 23'N, 44 17'E
T. araraticum-68	PI 427435	Iraq, 41 km NW Sulaimaniya, 35 47'N, 45 08'E
T. araraticum-19	KU-1986	Turkey, 45 km SE of Maras (Maras - Gaziantep),
T. araraticum-86	-	-
T. araraticum-64	-	-
T. araraticum-105	-	-
T. araraticum-13	2005-7-5-9-4	Turkey, 61 km SE from Türkoğlu (SW of Karadağ)
T. araraticum-58	PI 427407	21 km S of Harir; between Rawanduz and Shaqlawah
T. araraticum-91	8739	Iraq, ca. 2 km S from the position of 38.9 km from Rowanduz to Rayat
T. araraticum-102	8919	Turkey, 17.3 km E from Silvan to Bitlis
T. araraticum-81	8545	Iraq, 14 km S from Sulaymaniyah to Qara Dagh
T. araraticum-65	PI 427371	Iran, Bakhtaran, 34 18'N, 46 01'E
T. araraticum-23	IG 116165	Turkey, 1 km North of Akcaburc
T. araraticum-31	IG 116168	Turkey, 2 km West of Kavsak road Kuscu

Table 3.1. Continue.

Genotype	Accession number	Location
T. araraticum-92	8758	Iraq, ca. 2 km S from the position of 38.9 km from Rowanduz to Rayat
T. araraticum-17	KU-1982	Turkey, 45 km SE of Maras (Maras - Gaziantep),
T. araraticum-5	IG 116164	Turkey, Cibeker Village or Bagbasi (old village name)
T. araraticum-90	8733	Iraq, 33.2 km W from Shaqlawa to Rowanduz
T. araraticum-8	TR 96 SSD 2007+2009	Turkey, 17.3 km E from Silvan to Bitlis
T. araraticum-14	TR 101-1	Iran, 12.2 km NW from Karand to Qasri Shirin
T. araraticum-73	PI 596290	Turkey,Siirt, 37 43'N, 42 15'E
T. araraticum-70	PI 503294	Iraq, Salahadin, 36 24'N, 44 12'E
T. araraticum-44	PI 538508_2791, 3338	43 km NW of Sulaimaniya near Surdash
T. araraticum-28	TR 44-2	Turkey, 45 km SE of Maras (Maras-Gaziantep)
T. araraticum-1	TR 133-1	Iran
T. araraticum-52	KU-8824A	15.3 km ENE from Dohuk to Amadiyah
T. araraticum-20	TR 99 TP083-TP087	Turkey, 39.9 km N from Elazig to Hozat
T. araraticum-35	TR 94 TP077-TP079	Turkey, 26.3 km NE from Mardin to Midyat
T. araraticum-50	KU-8877	13.4 km W from Amadiyah to Bamarni
T. araraticum-53	PI 427322_2900, 3222	2 km NW of Salahadin
T. araraticum-103	-	-
T. araraticum-42	PI 538456_2788, 3308	44 km NW of Sulaimaniya
T. araraticum-71	PI 503295	Iraq, Shaqlawa, 36 25'N, 44 22'E
T. araraticum-43	TRI 18514	21 km S of Harir; between Rawanduz and Shaqlawah
T. araraticum-79	8529	Iraq, 19.3 km S from Sulaymaniyah to Qara Dagh
T. araraticum-59	PI 538426	2 km NW of Salahadin
T. araraticum-57	PI 427390	4 km NE of Shaqlawa
T. araraticum-4	TR 98-1-1	Turkey, 39.9 km N from Elazig to Hozat
T. araraticum-88	8709	Iraq, 10.6 km NE from Koi Sanjaq to Ranya

Table 3.1. Continue

Genotype	Accession number	Location
T. araraticum-18	IG 113297	Iran, Sardasht
T. araraticum-55	PI 427368	40 km northwest of Shahabad
T. araraticum-30	2006-6-20-2-2 D	Turkey, 36 km NE from Kilis to Gaziantep
T. araraticum-77	1914	Armenia, 5-10 km SE of Erevan
T. araraticum-12	2006-6-16-7-4 D	Turkey, 4 km SE from Musabeyli to Kilis
T. araraticum-95	8799A	Iraq, Shaqlawa
T. araraticum-80	8543	Iraq, 19.3 km S from Sulaymaniyah to Qara Dagh
T. araraticum-60	PI 538431	4 km NE of Shaqlawa
T. araraticum-34	TR 69 TP072-TP076	Iraq, 19.1 km W Shaqlawa to Arbil
T. araraticum-93	8774	Iraq, 4.8 km NE from Shaqlawa to Rowanduz
T. araraticum-22	IG 119456	Syria, Kafr Nabil, 2 km S
T. araraticum-40	IG 116166	Turkey, between Tekirsin and Camurlu
T. araraticum-56	PI 427381	1 km NE of Salahadin
T. araraticum-99	8885	Iraq, 21.9 km W from Amadiyah to Dohuk
T. araraticum-89	8715	Iraq, 17.9 km W Shaqlawa to Arbil
T. araraticum-15	2005-7-5-9-4	Turkey, 61 km SE from Türkoğlu (SW of Karadağ)
T. araraticum-11	KU-1960	Turkey, 45 km SE of Maras (Maras - Gaziantep),
T. araraticum-82	8561	Iraq, 14 km S from Sulaymaniyah to Qara Dagh
T. araraticum-69	PI 503292	Iraq, Salahadin, 36 23'N, 44 17'E
T. araraticum-37	KU-8944	Iran, 12.2 km NW from Karand to Qasri Shirin
T. araraticum-61	PI 538450	east of Suara Tuka; 3-4 km W of Mazorka Gorge
T. araraticum-26	TR 1	Armenia
T. araraticum-47	KU-8657	52.4 km SW from Sulaymaniyah to Surdash
T. araraticum-94	8788	Iraq, 7.6 km W Shaqlawa to Arbil
T. araraticum-21	2006-6-20-11-6 D	Turkey, 45 km NE from Kilis to Gaziantep

Table 3.1. Continue.

Genotype	Accession number	Location
T. araraticum-76	TA 873	Iraq, 17.9 km W of Shaqlawah to Irbil, 36 33'N, 44 112'E
T. araraticum-100	8908	Turkey, 26.3 km NE from Mardin to Midyat
T. araraticum-98	8884	Iraq, 21.9 km W from Amadiyah to Dohuk
T. araraticum-85	8639	Iraq, 52.4 km SW from Sulaymaniyah to Surdash
T. araraticum-84	8597	Iraq, 52.4 km SW from Sulaymaniyah to Surdash
T. araraticum-96	8861	Iraq, 4.4 km NW from Amadiyah, Mazorka Gorge
T. araraticum-49	KU-8822	15.3 km ENE from Dohuk to Amadiyah
T. araraticum-36	TR 122	Azerbaijan
T. timopheevii-27	TR 106 TP041-TP045	former Soviet Union
T. timopheevii-29	TR 104 TP031-TP034	former Soviet Union
T. dicoccoides-10	-	-
T. araraticum-51	KU-1908A	8 km W of Garni (Erevan - Garni)
T. araraticum-101	8909	Turkey, 26.3 km NE from Mardin to Midyat
T. araraticum-2	IG 116169	Turkey, between T. Karadut and Kizilkent Villages, 2 km before Kizilkent
T. araraticum-16	KU-1984B	Turkey, 45 km SE of Maras (Maras - Gaziantep),
T. araraticum-87	8706	Iraq, 11.4 km NE from Koi Sanjaq to Ranya
T. araraticum-54	PI 427355	41 km NW of Sulaimaniya towards Surdash
T. dicoccoides-030	-	44 km west of Diyarbakır in the Karacadag
T. dicoccoides-246	-	Afula-Tiberias
T. dicoccoides-062	-	1 to 2 km south of Pinna towards Safad
T. dicoccoides-073	-	Aiha-Kfarkouk, above 'sahlet'
T. dicoccoides-163	-	Kazrin
T. dicoccoides-232	-	51 km west of Diyarbakır in the Karacadag
T. dicoccoides-249	-	Afula-Tiberias
T. dicoccoides-395	-	North slope of Jabal Sinjar N of Kursi

Table 3.1. Continue.

Genotype	Accession number	Location
T. dicoccoides-399	-	58.8 km N from Kermanshah to Ravansar
T. dicoccoides-038	-	33.6 km west of Diyarbakır in the Karacadag
T. dicoccoides-012	-	36.2 km west of Diyarbakır in the Karacadag
T. dicoccoides-107	-	Bat Shelomo
T. dicoccoides-126	-	Mt. Dov
T. dicoccoides-010	-	12.9 km NW from Ovabag to Pirinclik

3.2. Methodology

3.2.1 Seedling stage drought stress experiment

A seedling stage PEG induced drought stress experiment was conducted to evaluate the potential of *T. araraticum*. A 15% concentration of PEG-6000 was used to stimulate drought conditions for the seedlings. The experiment was conducted using factorial completely randomized design with two replications. Drought tolerance of the genotypes was evaluated using the Cigar roll method of seed germination (Sharma et al. 2022). Briefly, 5 bold and uniform seeds of every single genotype were surface sterilized with 3% sodium hypochlorite (NaCLO) solution for 10 minutes and washed subsequently with sterile distilled water for three times. Seeds were then placed on moistened germination paper and the papers were then rolled and kept vertically in dark for two days. During this time period all the seeds were treated as control. However, after two days the control group continued to receive distilled water while the other set was treated as drought and seeds were treated with 15% PEG. Following the seed germination, the seedlings were grown in the growth chamber for 12 days at a day/night temperature of $\pm$ 22 ˚C and relative humidity of 60%. The photoperiod was adjusted to 16 hour of light period and 8 hours of dark mode as described by Gudi et al. (2024). The traits were measured using IMAJEJ software (Peršić et al.2022).

3.2.2. Data collection

The data for the traits under study was recorded on the 12^{th} day after germination on randomly selected three plants from each replication and are described below.

Germination percentage (%)

Germination percentage for every single genotype was calculated by dividing the number of germinated seeds by the total number of seeds tested for germination per replication and multiplying the result by 100.

Coleoptile length (cm)

The seedlings were photographed and finally the images were imported to IMAJEJ software to measure coleoptile length in centimeters from the embryo to the tip of this cylindrical sheath.

Shoot length (cm)

The seedlings were photographed and finally the images were imported to IMAJEJ software to measure the shoot length in centimeters from the base of the shoot to the end point.

Primary root length (cm)

The seedlings were photographed and finally the images were imported to IMAJEJ software to measure Primary root length in centimeters from the tip of the embryo to the end of the primary root.

Seminal root length (cm)

The seedlings were photographed and finally the images were imported to IMAJEJ software to measure seminal root length in centimeters from the tip of the embryo to the end of the longest seminal root.

Mean seminal root length (cm)

The seedlings were photographed and finally these images were imported to IMAJEJ software to calculate average seminal root length. The length of every single seminal root was measured in centimeters from the tip of the embryo to the end point.

Total root length (cm)

The total root length was calculated by summing up the primary root length and the seminal root length.

Total root number

The seedlings were photographed and finally the images were imported to IMAJEJ software to count total roots. Total roots were counted from five seedlings of every single genotype and the average was then calculated.

Seedling vigour index

Seedling vigour was estimated by using the formula given by Gudi et al. (2024) and is described below:

$$\text{Seedling vigour (SV)} = \frac{[\text{shoot length (cm)}]+[\text{root length (cm)}]* \text{ germination percentage (\%)}}{100}$$

3.3. Field experiment under rainfed conditions

3.3.1. Site description and meteorological data

The field trial was conducted at the research and experimental area of the Department of Field Crops, Faculty of Agriculture, Çukurova University during the growing seasons 2022-23 and 2023-2024. The Çukurova Delta, located in the eastern Mediterranean, was formed by the accumulation of alluvial soils along the coastline and consists of fertile, wide plains. Consequently, the flat terrain of the delta provides a significant advantage for conducting agricultural activities. The

field area was composed of sandy-loam, friable soils with moderate pH, which were formed by the accumulation of alluvium carried by the Seyhan River. These soils are highly fertile. The examination of the soil properties revealed that the soil is rich in minerals, high in lime content, has a normal pH value, easily tillable property, with a sandy-loam and clay texture, high groundwater level, and consists of flat or nearly flat terrain.

The experimental area is located in the Mediterranean climate zone, characterized by mild and rainy winters, and hot and dry summers. Weather data, i.e. monthly averages of maximum temperature, minimum temperature, average temperature, average relative humidity, and total rainfall for the experimental area during the growing season 2022-23 and 2023-2024, is presented in Table 3.2.

Table 3 2. Weather data of experimental site during the wheat growing seasons (2022-23&2023-24).

	Min Temp (°C)		**Max Temp (°C)**		**Ave Temp (°C)**		**Total RF (mm)**	
Months	2022-23	2023-24	2022-23	2023-24	2022-23	2023-24	2022-23	2023-24
December	7.26	10.46	21.17	20.2	12.52	14.01	24.8	75.8
January	3.5	9	18.74	15.51	9.91	11.77	19.9	71.2
February	1.91	9.39	17.38	19.74	8.67	13.72	82.5	29.7
March	9.45	10.5	21.82	21.85	14.81	15.56	81.4	79.9
April	11.03	16.48	24.95	28.72	17.19	21.75	47.8	29.0
May	13.48	18.02	30.48	27.73	21.58	22.47	13.9	92.4
June	18.37	24.75	31.88	36.58	25.05	30.17	22.9	4.90

Min Temp, minimum temperature; Max Temp, maximum temperature; Ave Temp, Average temperature

3.3.2. Experimental setup

A two-year field experiment during the growing seasons, 2022-23 and 2023-24, was carried out to explore the genetic diversity of GGA^tA^t genome under rainfed conditions. Ten good quality seeds of each genotype were first grown in the petri dishes and were transferred to refrigerator one day after sowing. The seeds were kept there at 4°C for one month for vernalization. After vernalization, the germinated seeds were transferred from petri dishes to the seed trays and kept under normal environmental conditions for adaptation. Finally, eight well-established seedlings were transplanted to the field on December 27, 2022, and December 21, 2023, in the first and second growing season, respectively. The genotypes were arranged in the field using randomized complete block design in four replications and each replication had two plants of each genotype. Row to row distance was maintained as 100 cm and plant to plant to distance was maintained 50 cm because of prostrate and semi-prostrate growth habit of wheat wild relatives. Nitrogenous fertilizers were applied solely to meet the basic requirements of the plants because the harvested seeds will be used for analyzing quality parameters i.e. micronutrients, protein, phenolics and phytate contents. The

experiment was conducted completely under rainfed conditions while solely one irrigation was done after transplantation to ensure uniform establishment of seedlings.

3.3.3. **Agronomical practices**

After transplantation, field inspections and other agronomical operations like weeding were done regularly for proper crop management. Because of the prostrate and semi-prostrate growth habit of wheat wild relatives, bamboo stakes were inserted at the corner of each plant and the plants were tied to these bamboo stakes to keep them upright. After heading, each plant was covered with microperforated polythene bags to avoid cross-pollination and to retain the spikelets that disarticulate on maturity in wheat wild relatives. Harvesting was done manually with the help of a sharp sickle when the plants had completely dried. All these agronomical approaches are shown in Figure 3.1.

Figure 3.1. Illustration of the agronomical approaches used.

3.3.4. Data collection

During the two-year field experiment, the data was recorded only for *T. araraticum* genotypes because *T. timopheevii* produced no spike. The following traits were measured on randomly selected five plants during the two-year field experiment and the obtained values were then averaged.

Plant height (cm)

Plant height was measured in centimeters from the base of the plant to the top of the spike excluding awns, for every individual plant within each replication and the average was taken to calculate the plant height.

Days to heading

Days to heading were recorded from the date of transplantation to the field till 50% of the plants of a genotype had spike emerged from the flag leaf sheath. The average was then taken to calculate the days to heading for every single genotype.

Number of spikelets per spike

Number of spikelets per spike were determined when the plants were in the field and spikes were green because the spikelets disarticulate on maturity in wheat wild relatives, a characteristic called brittleness of spike. Spikelets were counted on three spikes of the first plant and two spikes of the second plant for each genotype within each replication and then the average was taken to determine the number of spikelets per spike for each genotype.

Spike length (cm)

Spike length was measured in centimeters on three spikes of the first plant and two spikes of the second plant for each genotype withing each replication from the base of the spike to the topmost spikelet excluding awns. Then the average was taken for each genotype to calculate the spike length.

Spikelet yield per plant (g)

After harvesting, the spikelets collected from each plant of a genotype were weighed and the average was taken to calculate the spikelet yield per plant (SY) for a genotype.

Grain yield per plant

To measure the grain yield (GY), a sample of weight 3-4 grams of spikelets was taken from each plant of a genotype and dehusked and the grain weight was measured. Then the obtained grain weight was multiplied with the spikelet yield and finally divided by the sample weight of the respective plant to estimate grain yield per plant.

Thousand kernel weight (g)

The seeds obtained by dehusking the samples of every single plant of a genotype were counted, weighed and used to estimate the thousand kernel weight for the genotypes under study.

Physiological parameters

Some physiological parameters such as stomatal conductance and maximum quantum yield of photosystem II were measured to get insights into the physical health of the plants. These parameters were measured only in the second growing season (2023-24) because of earthquake in the first growing season. The following physiological characteristics were measured:

Stomatal conductance (mol $m^{-2}s^{-1}$)

Stomatal conductance was measured at two distinct time periods on two different leaves by using Licor-600 handheld instrument at midday between 10:00 and 12:00 (Figure 3.2). The first measurement ($gsw_{1)}$ was performed on the third basal leaf, while the second measurement (gsw_2) was recorded after two weeks of first reading, on the flag leaf of each plant within each replication. Then the average was taken at each stage to calculate the stomatal conductance for each genotype.

Quantum yield of photosystem II

Quantum yield of photosystem II was measured at two different time points on two different leaves at midday by using Licor-600 instrument (Figure 3.2). The first reading ($PhiPSII_1$) was performed on the third leaf from the base of the plant, followed by a second measurement ($PhiPSII_2$) on the flag leaf of each plant within each replication with a time interval of two weeks. Then data was averaged at each stage to measure the quantum yield.

Figure 3.2. Measurement of Physiological parameters.

3.4. Data analysis

Phenotypic data collected from both the field and PEG-induced drought stress experiment was first averaged and subjected to basic descriptive statistics in MS Excel. Analysis of variance (ANOVA) was conducted within the statistical software R studio version 4.4.1 (R Core Team 2024). Histogram and Box and whisker plots were drawn by JASP software (version 0.18.3.0) to show the graphical distribution of the studied traits. Correlation analysis was carried out by JASP software to uncover the relationship between the studied traits under both rainfed and PEG-induced drought stress conditions. Moreover, Principal component analysis was performed using Originpro software, 2024 (Origin Lab Corporation, Northampton, MA, USA), to reveal the contribution of statistically significant traits to the total variations.

4. RESULTS AND DISCUSSIONS

4.1. PEG-induced drought stress experiment

4.1.1. Coleoptile length (cm)

The results of the analysis of variance showed statistically significant differences among genotypes for coleoptile length (CL), and drought stress also had significant effect on coleoptile length at probability level of P <0.001 (Table 4.1). However, the interaction between genotype and drought stress was not significant, indicating that the genotypic response to drought stress was consistent for coleoptile length. Under control conditions, CL ranged from 2.43 to 4.65 cm in *T. araraticum* genotypes with average CL of 3.78 cm, while from 3.34 to 4.94 cm in *T. dicoccoides* genotypes with average CL of 4.94 cm, and 3.26 to 3.82 cm in *T. durum* cultivars with average CL of 3.82 cm (Table 4.2). On the other hand, CL was reduced under water stress conditions and ranged from 2.18 to 4.78 cm in *T. araraticum* genotypes with a mean of 3.25 cm and 2.32 to 3.91 cm in *T. dicoccoides* genotypes with a mean of 3.19 cm and 3.05 to 3.46 cm in *T. durum* cultivars with average CL of 3.27 cm. The reduction percentage in CL was higher (20.99%) in *T. dicoccoides* followed by *T. araraticum* (14.00%) and *T. durum* (8.76%). The graphical distribution of CL with some outliers under both control and water deficit conditions is shown by Box and Whisker plot (Figure 4.1). The mean data for coleoptile length under both control and drought stress is given in the supplementary Table 1 and Table 2, respectively.

Coleoptile length is considered as an important plant trait for plant adaptation to limited water conditions and is found to be significantly affected by water deficit stress. Gudi et al. (2024) conducted a study to evaluate the effect of drought stress on seedling traits of 198 germplasm lines of wheat under PEG-stimulated drought stress (20%). They reported that coleoptile length ranged from 2.64-6.97 cm under control conditions, while 0-6.93 cm under drought stress and exhibited a reduction of 12.75% under drought stress. Moreover, a study conducted to examine the potential of 80 wheat synthetics developed by crossing *T. durum* and *Ae. tauschii* under PEG induced drought stress (14, 19 and 23% PEG) recorded coleoptile length between 2.5 to 6.3 cm with a mean of 3.76 under control conditions and 0.9 to 5.5 cm with a mean of 2.91, 1.86 and 1.31 cm under 14, 19 and 23% PEG-induced drought stress, respectively. These results align with our study along with some variations because of the different stress levels applied and different wheat species under study. However, the results indicate the presence of significant variations that can be utilized in future wheat breeding programs to develop drought tolerant cultivars.

Table 4.1. Analysis of variance (ANOVA) for coleoptile length of genotypes under study.

Source of variation	DF	Sum Sq	Mean Sq	F value	Pr(>F)
Genotype (A)	109	57.16	0.52	1.771	0.000189***
Water stress (B)	1	34.76	34.76	117.391	<2e-16***
A × B	109	31.31	0.29	0.97	0.565257^{ns}
Residuals	220	65.14	0.3		
CV	15.43%				

^{ns} P >0 .05* P <0.05, ** P <.01, *** P <0.001, level of significance DF, degrees of freedom; Sum Sq, sum of squares; Mean Sq, mean sum of squares.

Table 4.2. Minimum, maximum and Mean coleoptile length for three wheat species under control and drought stress conditions.

	Coleoptile length (cm)					
	Control			Drought		
	T. ara	***T. dic***	***T. dur***	***T. ara***	***T. dic***	***T. dur***
Minimum	2.43	3.34	3.26	2.18	2.32	3.05
Maximum	4.65	4.94	3.82	4.78	3.91	3.46
Mean	3.78	4.03	3.58	3.25	3.19	3.27
Standard dev.	0.42	0.45	0.19	0.48	0.46	0.15
Reduction (%)				14.00	20.99	8.76

T. ara, T. araraticum; *T. dic*, *T. dicoccoides*; *T. dur*, *T. durum*.

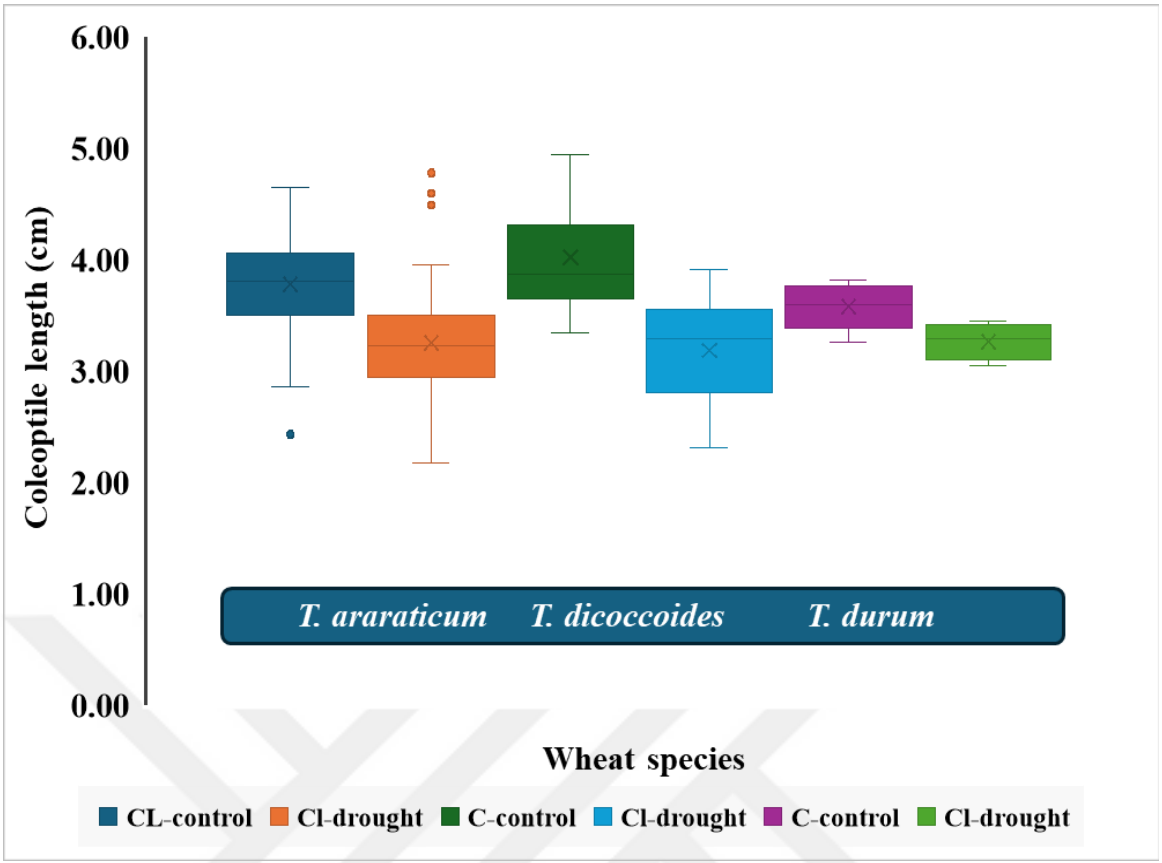

Figure 4.1. Box and Whisker plots of Coleoptile length for three wheat species under control and drought conditions.

4.1.2. Shoot length (cm)

The results of analysis of variance revealed statistically significant differences among genotypes for shoot length (SL) indicating valuable genetic diversity, and drought stress also significantly affected shoot length at probability level of P <0.001 (Table 4.3). However, the interaction between genotype and drought stress was not significant indicating that the genotypes responded in the same manner to drought stress in terms of shoot length. Under control conditions, SL varied from 10.87 to 21.02 cm in *T. araraticum* genotypes with average SL of 15.63 cm, while from 12.62 to 22.96 cm in *T. dicoccoides* genotypes with average SL of 18.63 cm and from 15.39 to 18.29 cm in *T. durum* cultivars with average SL of 16.55 cm (Table 4.4). On the other hand, SL was reduced under water stress conditions and ranged from 3.91 to 16.18 cm in *T. araraticum* genotypes with a mean of 9.33 cm, while from 6.37 to 15.74 cm in *T. dicoccoides* genotypes with a mean of 11.29 cm and 13.02 to 14.87 cm in *T. durum* cultivars with average SL of 13.62 cm. The reduction in SL was higher (40.39%) in *T. araraticum* followed by *T. dicoccoides* (39.39%) and T. durum (17.66%). The graphical distribution of SL with some outliers under both control and water deficit conditions is shown by Box and Whisker plot (Figure 4.2). The mean data for shoot length under both control and drought stress is given in the supplementary Table 1 and Table 2, respectively.

Table 4.3. Analysis of variance (ANOVA for shoot length of genotypes under study

Source of variation	DF	Sum Sq	Mean Sq	F value	Pr(>F)
Genotype (A)	109	2263	21	1.617	0.00143 **
Water stress (B)	1	4358	4358	339.452	< 2e-16 ***
A × B	109	1057	10	0.756	0.94972^{ns}
Residuals	220	2825	13		
CV	27.70%				

^{ns} P >0 .05* P <0.05, ** P <0.01, *** P <0.001, level of significance DF, degrees of freedom; Sum Sq, sum of squares; Mean Sq, mean sum of squares.

Table 4.4. Minimum, maximum and mean shoot length for three wheat species under control and drought stress conditions.

	Shoot length (cm)					
	Control			Drought		
	T. ara	***T. dic***	***T. dur***	***T. ara***	***T. dic***	***T. dur***
Minimum	10.87	12.62	15.39	3.91	6.37	13.02
Maximum	21.02	22.96	18.29	16.18	15.74	14.87
Mean	15.63	18.63	16.55	9.33	11.29	13.62
Standard dev.	2.38	3.06	1.13	2.76	2.28	0.67
Reduction (%)				40.34	39.39	17.66

T. ara, T. araraticum; T. dic, T. dicoccoides; T. dur, T. durum.

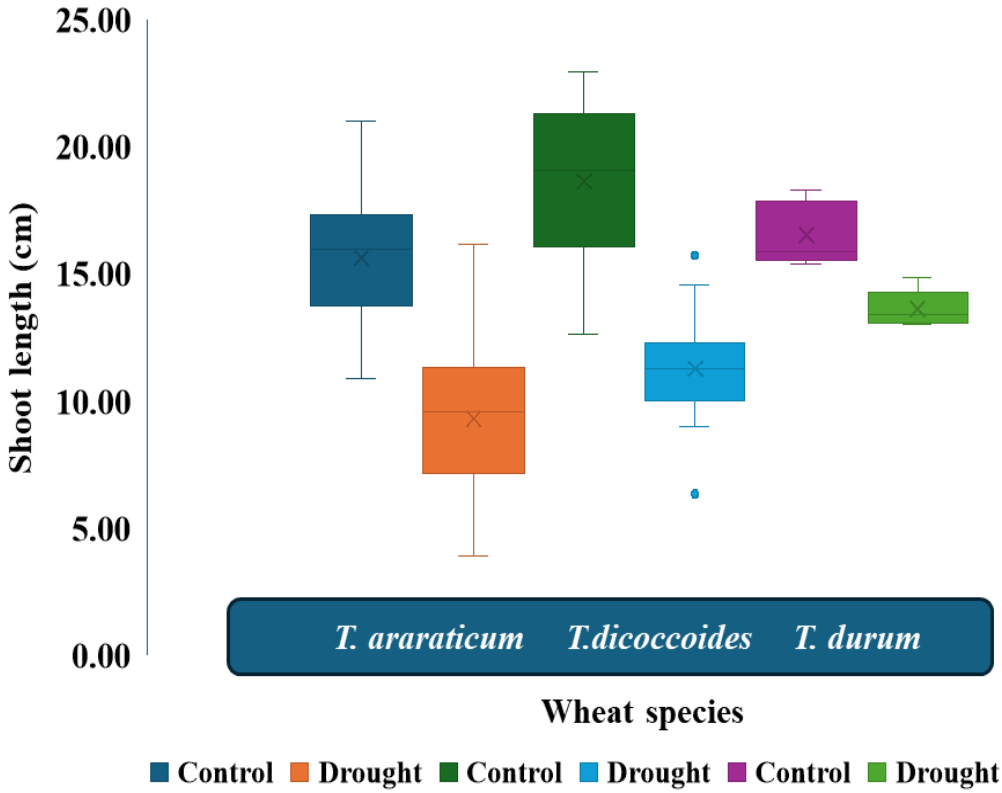

Figure 4.2. Box and Whisker plots of shoot length for three wheat species under control and drought conditions.

Wild relatives of wheat have not been utilized widely as source of tolerance to abiotic stresses though *Ae. tauschii* (Kurahashi et al. 2009) and *T. dicoccoides* (Peleg et al. 2005) have been studied for high temperature (Pradhan et al. 2012), drought (Peleg et al. 2005) and salinity stress (Saisho et al. 2016). However, GGA^tA^t genome of *T. araraticum* is studied even less in terms of abiotic stresses. A study conducted by Suneja et al. (2019) to evaluate the plasticity induced by water stress in root-shoot traits of *Ae. tauschii* and *T. dicoccoides* accession under PEG-induced water stress (25%) recorded shoot length between 9.90–27.72 cm and 7.17–16.75 cm in *Ae. tauschii*, while between 12.35–23.57 cm and 9.23–16.43 cm in *T. dicoccoides* under control and water stress conditions, respectively. The stress was induced after one week of sowing on Murashige and Skoog solution and the experiment was conducted in propagation trays. Furthermore, Gudi et al. (2024), examined the effect of PEG-induced drought stress on seedling traits of 198 bread wheat genotypes and found that drought stress significantly reduced shoot length (50.93%) and ranged between 12.1- 28.74 cm and 0-23.9 cm under control and water deficit conditions, respectively.

4.1.3. Primary root length (cm)

The results of analysis of variance revealed statistically significant differences among genotypes for primary root length (PRL) indicating the presence of valuable genetic diversity, and PEG-stimulated drought stress had also significantly affected primary root length at probability level

of P <0.001 (Table 4.5). However, the interaction between genotype and drought stress was not significant indicating that the genotypic response was constant to drought stress in terms of primary root length. Under control conditions, PRL varied from 16.67 to 29.74 cm in *T. araraticum* genotypes with average PRL of 21.94 cm, while from 17.11 to 34.09 cm in *T. dicoccoides* genotypes with average PRL of 22.94 cm and from 26.92 to 33.11 cm in *T. durum* cultivars with average PRL of 30.04 cm (Table 4.6). On the other hand, PRL was reduced under water stress conditions and ranged from 6.59 to 24.67 cm in *T. araraticum* genotypes with a mean of 14.81 cm, while from 8.96 to 21.28 cm in *T. dicoccoides* genotypes with a mean of 16.32 cm and from 17.49 to 21.97 cm in *T. durum* cultivars with average PRL of 19.56 cm. The reduction in PRL was highest in *T. durum* (34.89%) followed by *T. araraticum* (32.49%) and *T. dicoccoides* (28.88). The graphical distribution of PRL with some outliers under both control and water deficit conditions is shown by Box and Whisker plot (Figure 4.3). The mean data for primary root length under both control and drought stress is given in the supplementary Table 1 and Table 2, respectively.

Plant roots play a vital role in water and minerals uptake as well as anchoring the plant to the soil with several primary roles in plant adaptation to water limited conditions. The research was not focused on root system for a long time, but the trend has changed recently over the last few years (Bektaş and Waines, 2020). A study conducted to examine the effect of grain size on root architecture traits of ten bread wheat cultivars recorded primary root length between 20.36 and 29.15 cm under normal irrigation (Bektaş and Waines, 2020). Moreover, a study conducted to identify the quantitative trait loci (QTLs) associated with seminal root morphology in 142 recombinant inbred lines derived by crossing two Chinese winter wheat cultivars (Xiaoyan 54 and Jing 411) recorded primary root length between 10.5 and 31.5 cm with average PRL of 18.9 cm under normal irrigation (Ren et al. 2012). Furthermore, Gudi et al. (2024), examined the effect of PEG-induced drought stress on seedling traits of 198 bread wheat genotypes and found that drought stress reduced root length (23.93%) and ranged between 13.75- 35.64 cm and 5.55-32.8 cm under control and water deficit conditions, respectively. The reduction in our study is higher as compared to the reported studies that may have resulted from the differences in the environment and the ploidy level of the wheat species under study.

Table 4. 5. Analysis of variance (ANOVA) for primary root length of genotypes under study.

Source of variation	DF	Sum Sq	Mean Sq	F value	Pr(>F)
Genotype (A)	109	3227	30	1.598	0.00183 **
Water stress (B)	1	5749	5749	310.202	< 2e-16 ***
A × B	109	2223	20	1.101	0.27458^{ns}
Residuals	220	4077	19		
CV	22.86%				

^{ns} P >0 .05* P <0.05, ** P <0.01, *** P <0.001, level of significance DF, degrees of freedom; Sum Sq, sum of squares; Mean Sq, mean sum of squares.

Table 4.6. Minimum, maximum and mean of primary root length for three wheat species under control and drought stress conditions .

	Primary root length (cm)					
	Control			Drought		
	T. ara	***T. dic***	***T. dur***	***T. ara***	***T. dic***	***T. dur***
Minimum	16.67	17.11	26.95	6.59	8.96	17.49
Maximum	29.74	34.09	33.11	24.67	21.28	21.97
Mean	21.94	22.94	30.04	14.81	16.32	19.56
Standard dev.	2.67	3.79	2.18	3.72	3.14	1.61
Reduction (%)				32.49	28.88	34.89

T. ara, T. araraticum; T. dic, T. dicoccoides; T. dur, T. durum.

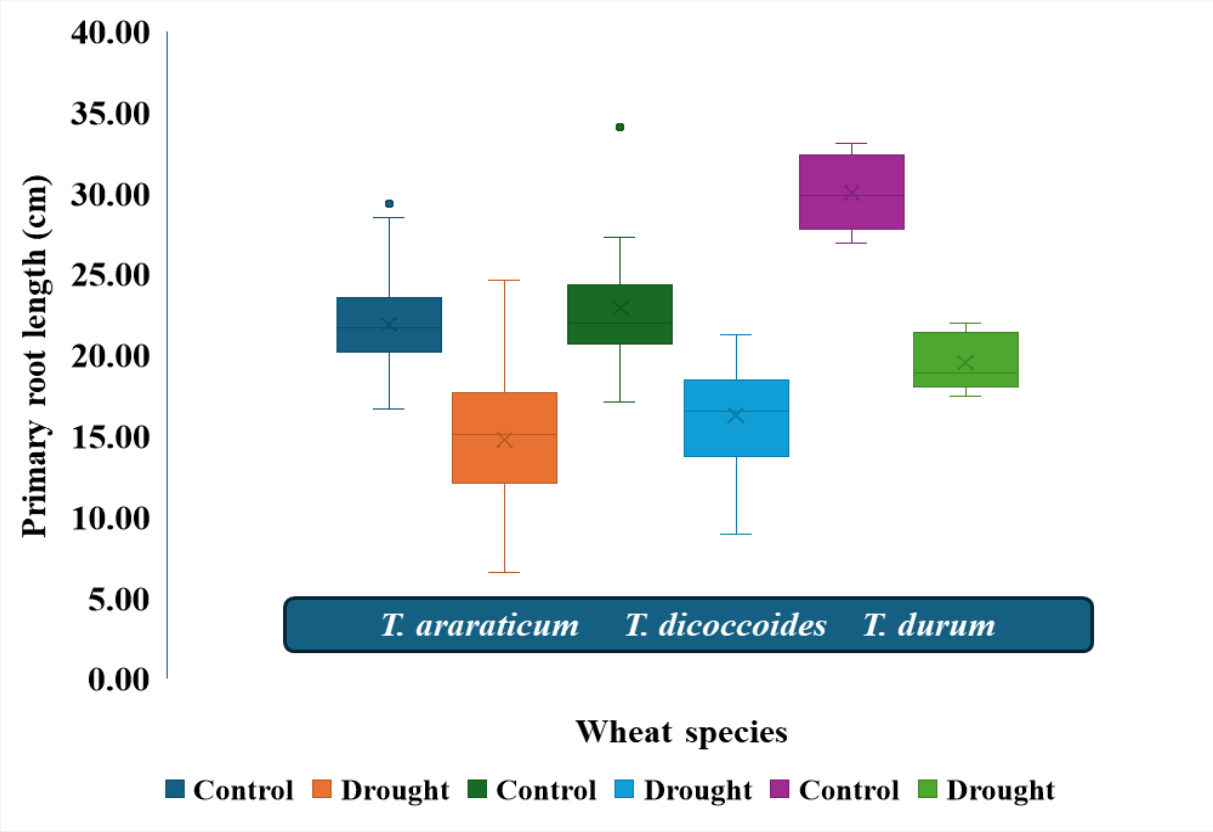

Figure 4.3. Box and Whisker plots of primary root length for three wheat species under control and drought conditions.

4.1.4. Seminal root length (cm)

The results of analysis of variance (ANOVA) showed statistically significant variations among genotypes for seminal root length (SRL), and PEG-stimulated drought stress had also significantly affected seminal root length at probability level of P <0.001 (Table 4.7). However, the interaction between genotype and water stress was not significant indicating that the genotypic response was constant to drought stress in terms of seminal root length. Under control conditions, SRL ranged from 14.77 to 25.58 cm in *T. araraticum* genotypes with average SRL of 20.56 cm, while from 13.56 to 34.42 cm in *T. dicoccoides* genotypes with average SRL of 21.43 cm and from 24.85 to 29.07 cm in *T. durum* cultivars with average SRL of 27.53 cm (Table 4.8). On the other hand, SRL was reduced under water stress conditions and ranged from 6.03 to 23.80 cm in *T. araraticum* genotypes with a mean of 12.65 cm, while from 7.14 to 19.21 cm in *T. dicoccoides* genotypes with a mean of 14.01 cm and from 15.50 to 20.30 cm in *T. durum* cultivars with average SRL of 18.31 cm. The reduction in SRL was highest in *T. araraticum* (38.49%) followed by *T. dicoccoides* (34.64) and *T. durum* (33.47%). The graphical distribution of PRL with some outliers under both control and water deficit conditions is shown by Box and Whisker plot which clearly illustrates the reduction in seminal root length of all three wheat species under study (Figure 4.4). The mean data for seminal root length under both control and drought stress is given in the supplementary Table 1 and Table 2, respectively.

Seminal roots in wheat have been proved to linked with higher yields and plant adaptation to environmental conditions (Cope et al. 2024). Moreover, seminal roots are known to play an important role in crop performance under drought conditions (Boudiar et al. 2020), but only few studies have targeted the seminal root traits (Kang et al. 2024). Rahnama et al. (2024) conducted a study to identify the variations in root architecture and leaf traits of eight bread wheat cultivars under drought conditions at seedling stage and reported significant reduction (38-41%) in total seminal root length of drought sensitive cultivars, while the reduction was lower in drought tolerant cultivars. Our findings related to seminal root angle indicates the presence of significant variations among genotypes that can be used to develop drought tolerant wheat breeding programmes. Based on the findings of the current study, no significant differences among three wheat species in terms of reduction percentage in SRL. Therefore, *T. dicoccoides* and *T. araraticum* serve as potential source for developing drought tolerant cultivars with longer seminal roots.

Table 4. 7. Analysis of variance (ANOVA) for seminal root length of genotypes under study.

Source of variation	DF	Sum Sq	Mean Sq	F value	Pr(>F)
Genotype (A)	109	3623	33	2.184	5.22e-07 ***
Water stress (B)	1	6882	6882	452.275	< 2e-16 ***
A × B	109	2055	19	1.239	0.0927^{ns}
Residuals	220	3348	15		
CV	22.88 %				

^{ns} P >0 .05* P <0.05, ** P <0.01, *** P <0.001, level of significance DF, degrees of freedom; Sum Sq, sum of squares; Mean Sq, mean sum of squares.

Table 4.8. Minimum, maximum and mean of seminal root length for three wheat species under control and drought stress.

	Seminal root length (cm)					
	Control			Drought		
	T. ara	***T. dic***	***T. dur***	***T. ara***	***T. dic***	***T. dur***
Minimum	14.77	13.56	24.85	6.03	7.14	15.50
Maximum	25.58	34.42	29.07	23.80	19.21	20.30
Mean	20.56	21.43	27.53	12.65	14.01	18.31
Standard dev.	2.57	4.57	1.86	3.79	3.66	1.79
Reduction (%)				38.49	34.64	33.47

T. ara, T. araraticum; *T. dic*, *T. dicoccoides*; *T. dur*, *T. durum*.

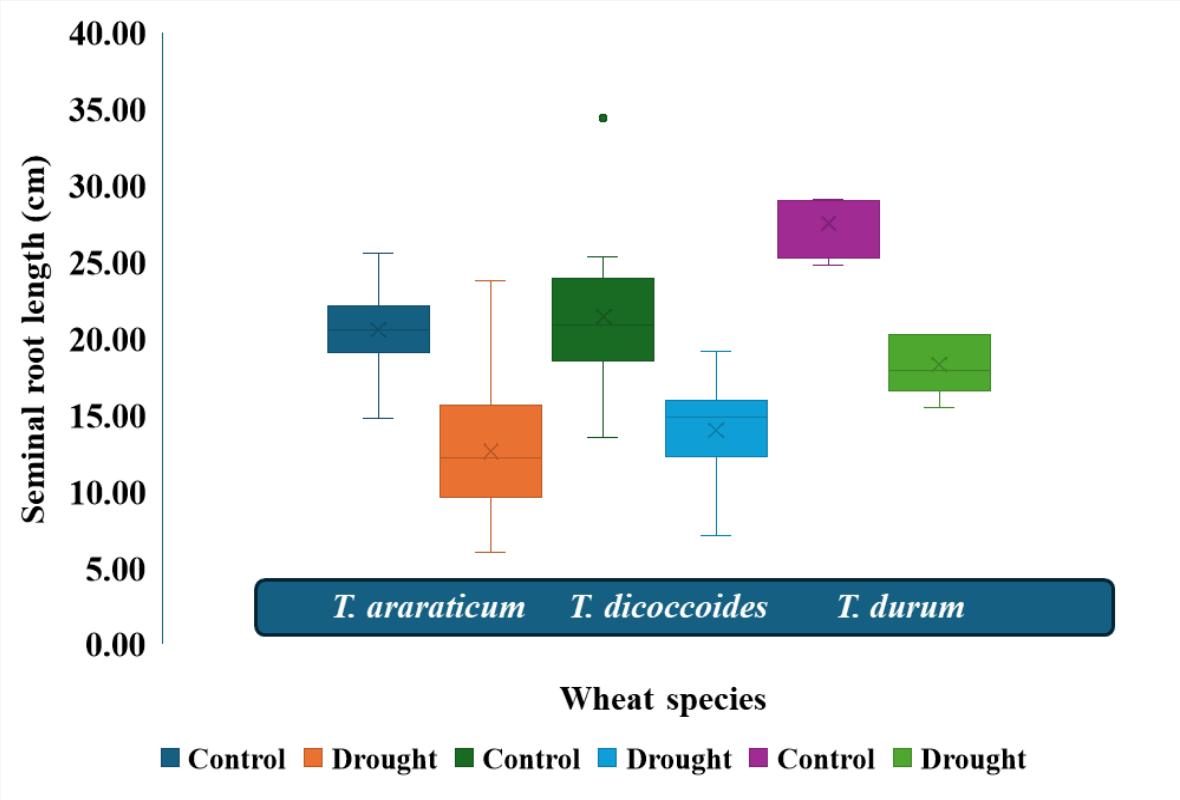

Figure 4.4. Box and Whisker plots of seminal root length for three wheat species under control and drought conditions.

4.1.5. Mean seminal root length (cm)

Analysis of variance (ANOVA) showed the existence of statistically significant variations among genotypes for mean seminal root length (MSRL), and water stress had significant effect on MSRL at probability level of $P < 0.001$ (Table 4.9). Moreover, the interaction between genotypes and water stress was also found statistically significant indicating that the genotype response to water stress for MSRL was not constant. Among three wheat species under control conditions, MSRL ranged from 13.40 to 25.36 cm in *T. araraticum* with a mean of 19.28 cm, while from 12.82 to 34.03 cm in *T. dicoccoides* with a mean of 20.44 cm and from 24.44 to 28.21 cm in *T. durum* with a mean of 26.52 cm. On the other hand, under drought conditions, MSRL was reduced significantly and ranged from 5.29 to 19.72 cm in *T. araraticum* with a mean of 11.13 cm, while from 6.78 to 18.38 cm for *T. dicoccoides* and from 13.50 to 19.64 cm for *T. durum* with a mean of 16.73 cm (Table. 4.10). The reduction in MSRL among three wheat species was highest in *T. araraticum* (42.26%) followed by *T. dicoccoides* (39.76%) and *T. durum* (36.92%). Box and whisker plots were drawn to show the graphical distribution and reduction percentage in all three wheat species under study (Figure 4.5). The raw data for MSRL under both control and drought stress conditions is given in the supplementary Table 1 and Table 2, respectively.

Root architecture of plants is directly involved in adaptation of plants to water limited conditions. The root architecture of mature plants is closely associated with growth of seminal roots

at seedling stage. Therefore, selections at seedling stage for roots specifically seminal roots can be effective for identification of genotypes suitable for drought conditions (Bektaş and Hohn, 2020). However, only a few studies have focused on seminal root length under drought conditions, even less on the mean seminal root length. Rahnama et al. (2024) investigated the genotypic differences in shoot and root architecture of 21 day old seedlings of the eight bread wheat cultivars under drought stress in the polyvinyl chloride tubes filled with soil. They recorded total seminal axile root length between (TSARL) 130 and 144 cm in drought tolerant cultivars, while between 121 and 141 cm in drought sensitive cultivars under control conditions. On the other hand, TSARL ranged from 101-108 cm for drought tolerant cultivars and 79-89 cm in drought sensitive cultivars. The reduction percentage in TSARL was recorded as 22-41% for all the cultivars. The reduction percentage shows harmony to the reduction percentage in our study with some variations that may be resulted from difference in the ploidy level of the species under study or due to the environmental conditions.

Table 4.9. Analysis of variance (ANOVA) for mean seminal root length of genotypes under study.

Source of variation	DF	Sum Sq	Mean Sq	F value	Pr(>F)
Genotype (A)	109	3293	30	2.538	2.65e-09 ***
Water stress (B)	1	7473	7473	627.764	< 2e-16 ***
A × B	109	1788	16	1.378	0.0238 *
Residuals	220	2619	12		
CV	22.05%				

ns P >0 .05* P <0.05, ** P <0.01, *** P <0.001, level of significance DF, degrees of freedom; Sum Sq, sum of squares; Mean Sq, mean sum of squares.

Table 4.10. Minimum, maximum and mean seminal root length for three wheat species under control and drought stress.

Mean Seminal root length (cm)						
	Control			Drought		
	T. ara	*T. dic*	*T. dur*	*T. ara*	*T. dic*	*T. dur*
Minimum	13.40	12.82	24.44	5.29	6.78	13.50
Maximum	25.36	34.03	28.21	19.72	18.38	19.64
Mean	19.28	20.44	26.52	11.13	12.31	16.73
Standard dev.	2.44	4.80	1.53	3.36	3.44	2.34
Reduction (%)				42.26	39.76	36.92

T. ara, T. araraticum; T. dic, T. dicoccoides; T. dur, T. durum

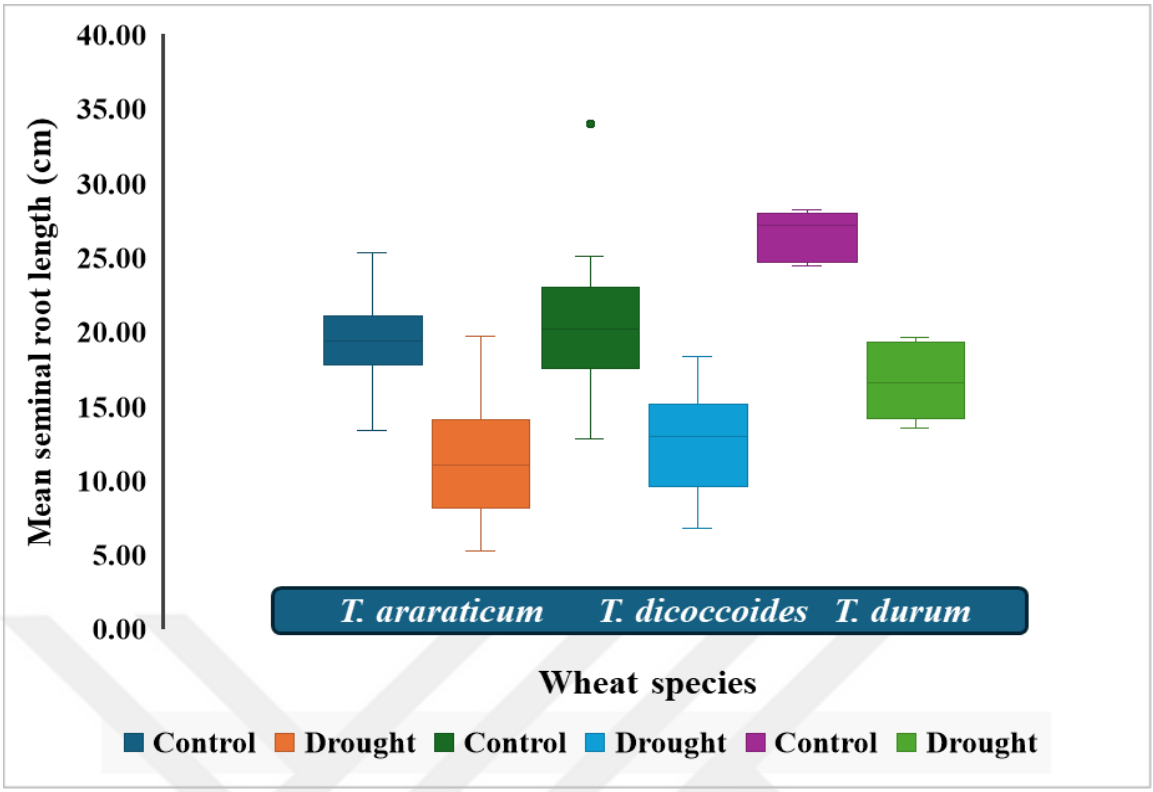

Figure 4.5. Box and Whisker plots of mean seminal root length for three wheat species under control and drought conditions.

4.1.6. Total root length (cm)

Analysis of variance (ANOVA) revealed statistically significant variations among genotypes for total root length (TRL), and water stress had significant effect on TRL at probability level of P <0.001 (Table 4.11). Moreover, the interaction between genotypes and water stress was also significant (P <.05) indicating that the genotypes responded in the different manner to drought conditions in terms of total root length. Among three wheat species under control conditions, TRL ranged from 39.94 to 80.09 cm in *T. araraticum* with a mean of 60.44 cm, while from 42.56 to 102.15 cm in *T. dicoccoides* with a mean of 63.83 cm and 75.83 to 88.72 with a mean of 83.08 cm. On the other TRL reduced significantly under drought stress and ranged from 9.18 to 61.77 cm in *T. araraticum* with an average of 36.07 cm, while in *T. dicoccoides* ranged from 15.24 to 53.35 cm with average TRL of 39.79 cm and 45.62 to 61.26 cm in *T. durum* with a mean of 53.02 cm. Drought stress caused a significant reduction in TRL of three wheat species and the percentage was highest in *T. araraticum* (40.32%) followed by *T. dicoccoides* (37.67%) and T. *durum* (36.18%). Box and whisker plots were drawn to show the graphical distribution and reduction percentage in all three wheat species under study (Figure 4.6). The raw data for TRL under both control and drought stress conditions is given in the supplementary Table 1and Table 2, respectively.

Total root length varied significantly among three wheat species under study ranging from shallow to deepest roots under both control and drought conditions. However, only few studies have targeted total root length under normal irrigation and even less under drought stress. Cane et al.

(2014) conducted a study on 183 elite accessions of durum wheat for association mapping of root traits under normal irrigation and recorded total root length in 9 days old plants ranging from 52.8 to 144.7 cm with an average of 94.6 cm. The range for total root length reported by Cane et al. (2014) is superior to the total root length reported in the current study that may be due to the difference in the environmental conditions. However, the findings of the current study support the existence of significant differences among the genotypes in terms of total root length that can be utilized in the future wheat breeding programmes to develop drought tolerant cultivars.

Table 4.11. Analysis of variance (ANOVA) for total root length of genotypes under study.

Source of variation	DF	Sum Sq	Mean Sq	F value	Pr(>F)
Genotype (A)	109	28226	259	2.495	5.06e-09 ***
Water stress (B)	1	61561	61561	593.125	< 2e-16 ***
A × B	109	15007	138	1.327	0.0404 *
Residuals	220	22834	104		
CV	20.33%				

ns P > .05* P <.05, ** P <.01, *** P <.001, level of significance DF, degrees of freedom; Sum Sq, sum of squares; Mean Sq, mean sum of squares.

Table 4.12. Minimum, maximum and mean of total root length for three wheat species under control and drought stress.

	Total root length (cm)					
	Control			Drought		
	T. ara	*T. dic*	*T. dur*	*T. ara*	*T. dic*	*T. dur*
Minimum	39.94	42.76	75.83	9.18	15.24	45.62
Maximum	80.09	102.15	88.72	61.77	53.35	61.26
Mean	60.44	63.83	83.08	36.07	39.79	53.02
Standard dev	7.29	13.17	5.13	10.74	11.13	6.15
Reduction (%)				40.32	37.67	36.18

T. ara, T. araraticum; T. dic, T. dicoccoides; T. dur, T. durum.

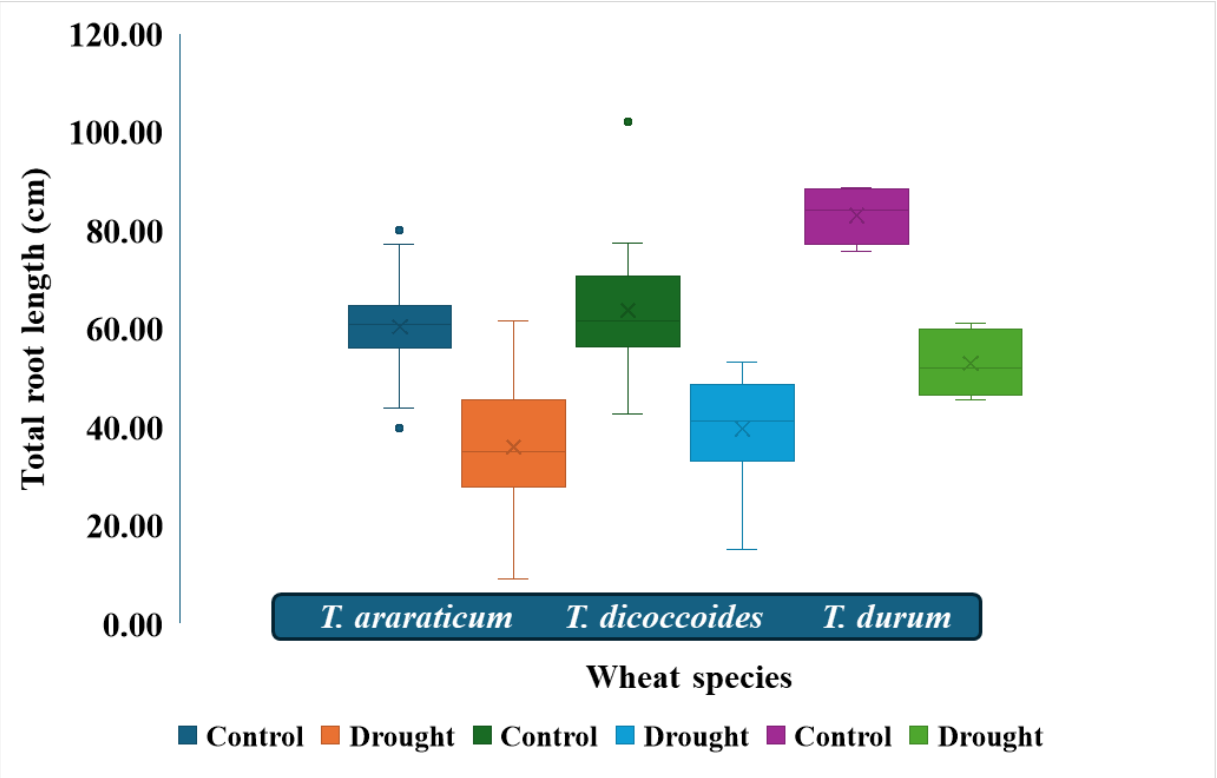

Figure 4.6. Graphical distribution of total root length for three wheat species under control and drought stress.

4.1.7. Total root number

Analysis of variance (ANOVA) revealed statistically significant variations among genotypes for total root number (TRN), and water stress had significant effect on TRN at probability level of P <0.001 (Table 4.13). However, the interaction between genotype and water stress was non-significant, indicating that the genotypic response to water stress for TRN was consistent. Among three wheat species, under control conditions TRN ranged from 2.58 to 4.15 in *T. araraticum* with an average number of 3.29, while from 2.80 to 5.30 and from 3.78 to 5.90 with average values of 3.33 and 4.67 in *T. dicoccoides* and *T. durum*, respectively (Table 4.14). On the other hand, under drought stress TRN recorded between 2.30 and 3.79 in *T. araraticum* with an average of 2.98, while ranged from 2.50 to 4.00 and 3.30 to 4.80 with average values of 2.90 and 3.98 in *T. dicoccoides* and *T. durum*, respectively. Moreover, the descriptive statistics showed that drought stress caused a reduction of 9.50 % in TRN of *T. araraticum*, while the reduction was higher in *T. dicoccoides* (13.30%), followed by *T. durum* (14.78%). The raw data for TRN under both control and drought stress conditions is given in the supplementary Table 1 and Table 2, respectively.

Root traits like total root number is a crucial root trait as it greatly influences plant growth, water absorption and nutrient uptake and helps plant adaptation to water limited conditions (Alemu et al. 2021). The studies conducted to phenotype wheat for root architecture traits reported total root number in 192 Ethiopian wheat accession between 3.4 and 6.7 with average number of 5.1 under normal irrigation (Alemu et al. 2021). Moreover, a study conducted by Sallam et al. (2024) on 142

highly diverse wheat accessions representing 28 countries, reported total root number between 2 and 5.25 with average number of 3.98 under water deficit conditions. These results show alignment with the findings of the current study with slight variations that may have resulted from environmental conditions or the different wheat species under study. However, the results of the current study indicate great variations among genotypes for total root number that can be utilized in the wheat breeding programmes to develop drought tolerant cultivars.

Table 4.13. Analysis of variance (ANOVA) for total root number levels of genotypes under study.

Source of variation	DF	Sum Sq	Mean Sq	F value	Pr(>F)
Genotype (A)	109	75.6	0.694	3.837	< 2e-16 ***
Water stress (B)	1	13.09	13.093	72.436	2.7e-15 ***
A × B	109	16.13	0.148	0.819	0.88^{ns}
Residuals	220	39.77	0.181		
CV	13.32%				

^{ns} P >0 .05* P <0.05, ** P <0.01, *** P <0.001, level of significance DF, degrees of freedom; Sum Sq, sum of squares; Mean Sq, mean sum of squares.

Table 4.14. Minimum, maximum and mean of total root number for three wheat species under control and drought stress.

	Total root number (cm)					
	Control			Drought		
	T. ara	***T. dic***	***T. dur***	***T. ara***	***T. dic***	***T. dur***
Minimum	2.58	2.80	3.78	2.30	2.50	3.30
Maximum	4.15	5.30	5.90	3.79	4.00	4.80
Mean	3.29	3.33	4.67	2.98	2.90	3.98
Standard dev.	0.36	0.61	0.78	0.30	0.36	0.64
Reduction (%)				9.50	13.03	14.78

T. ara, T. araraticum; T. dic, T. dicoccoides; T. dur, T. durum.

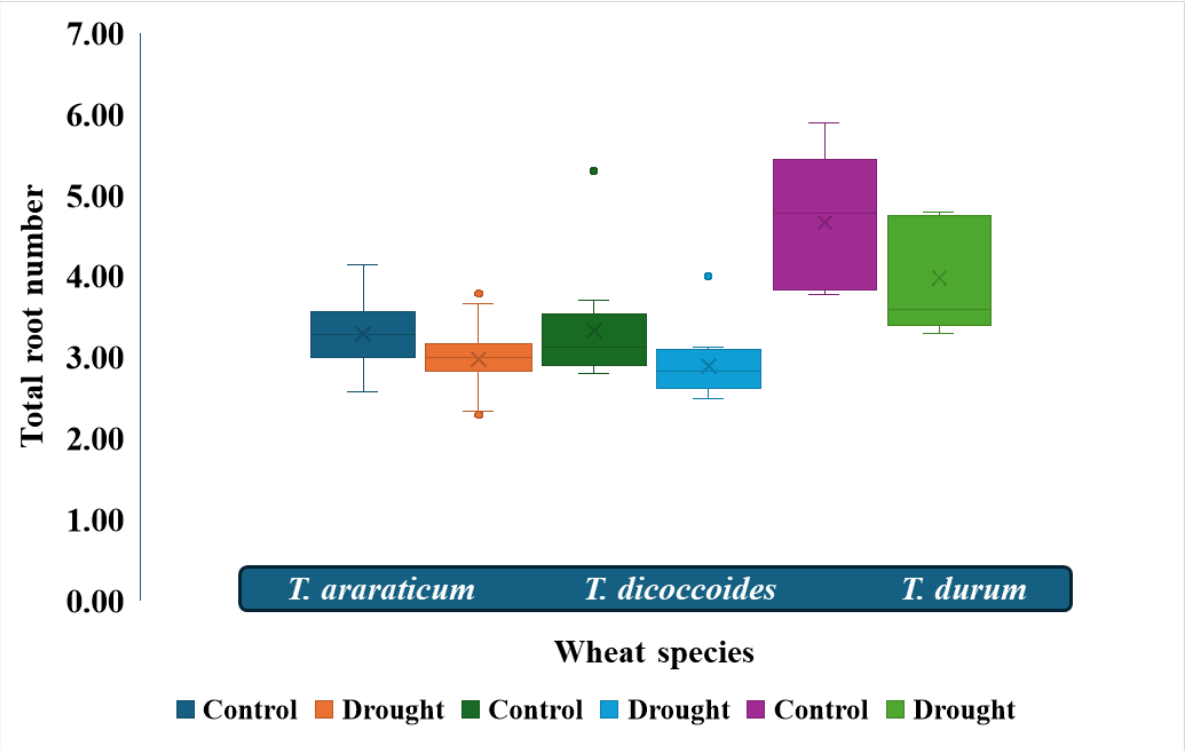

Figure 4.7. Graphical distribution of total root number for three wheat species under control and drought stress.

4.1.8. Germination percentage (%)

The results of analysis of variance (ANOVA) revealed that the variations among genotypes in germination percentage were not significant (Table 4.15). However, the drought had significant effect on germination percentage at probability level of P <0.001, while the interaction between genotype and water stress was non-significant indicating that the genotypic response to drought stress was constant in terms of germination percentage (Table 4.15). Among three wheat species, under control conditions germination percentage ranged from 70 to 100 % in *T. araraticum* and *T. dicoccoides* with average values of 91.78 and 92.67 %, respectively. However, the germination percentage was higher in *T. durum* and ranged from 90 and 100 % with average percentage of 98.23 % (Table 4.16). On the other hand, germination percentage was reduced under drought conditions and ranged from 40-100 percent in *T. araraticum* with a mean value of 71.56% and from 50-100 % in *T. dicoccoides* with a mean value of 73.33 %. Moreover, in T. durum germination percentage showed no reduction and ranged from 90-100 % with an average percentage of 98 %. Reduction percentage was comparable in both *T. araraticum* and *T. dicoccoides* (Table 4.16). The raw data for GP under both control and drought stress conditions is given in the supplementary Table 1and Table 2, respectively.

Seedling stage of a crop plant is an important determinant of plan stature and is highly vulnerable to water limited conditions. Seed germination is a crucial stage in the transition of plants from seed to seedlings and finally to the mature plant (Mahpara et al. 2022). Therefore, the

development of cultivars with high germination percentage even under water deficit conditions is a crucial parameter in wheat breeding. The studies conducted to evaluate the potential of bread wheat under drought stress at seedling stage reported germination percentage ranging from 70-100 % with a mean 97.44 % for control conditions, while from 10-100 % with average percentage of 89.75 % under PEG-induced drought stress (Gudi et al. 2024). Furthermore, Mahpara et al. (2022) conducted a study to explore the potential of eight bread wheat genotypes under PEG-induced (-0.6 and-1.2 MPa) drought stress and reported average germination percentage as 100 % under control, while as 70.08 and 40.75% under -0.6 and -1.2 MPa osmotic potentials, respectively. In the current study, drought stress was applied two days after sowing and germination percentage was still calculated to investigate the effect of drought stress on germination and further seed growth because some of the seeds could not grow further after having a tiny radicle. Moreover, it is assumed that germination percentage is low in wheat wild relatives. Therefore, this study ensures the good germination percentage even under drought conditions and align perfectly with the studies mentioned above.

Table 4.15. Analysis of variance (ANOVA) for germination percentage of genotypes under study.

Source of variation	**DF**	**Sum Sq**	**Mean Sq**	**F value**	**Pr(>F)**
Genotype (A)	109	47619	437	1.288	0.0587^{ns}
Water stress (B)	1	36728	36728	108.314	<2e-16 ***
A × B	109	33372	306	0.903	0.7235^{ns}
Residuals	220	74600	339		
CV	22.87%				

^{ns} P >0 .05* P <0.05, ** P <0.01, *** P <0.001, level of significance DF, degrees of freedom; Sum Sq, sum of squares; Mean Sq, mean sum of squares.

Table 4. 16. Minimum, maximum and mean germination percentage for three wheat species under control and drought stress.

Germination percentage (%)						
	Control			**Drought**		
	T. ara	***T. dic***	***T. dur***	***T. ara***	***T. dic***	***T. dur***
Minimum	70	70	90	40	50	90
Maximum	100	100	100	100	100	100
Mean	91.78	92.67	98.23	71.56	73.33	98
Standard dev.	9.14	8.54	4.13	16.32	16.19	4
Reduction (%)				22.03	20.86	0.00

T. ara, T. araraticum; T. dic, T. dicoccoides; T. dur, T. durum.

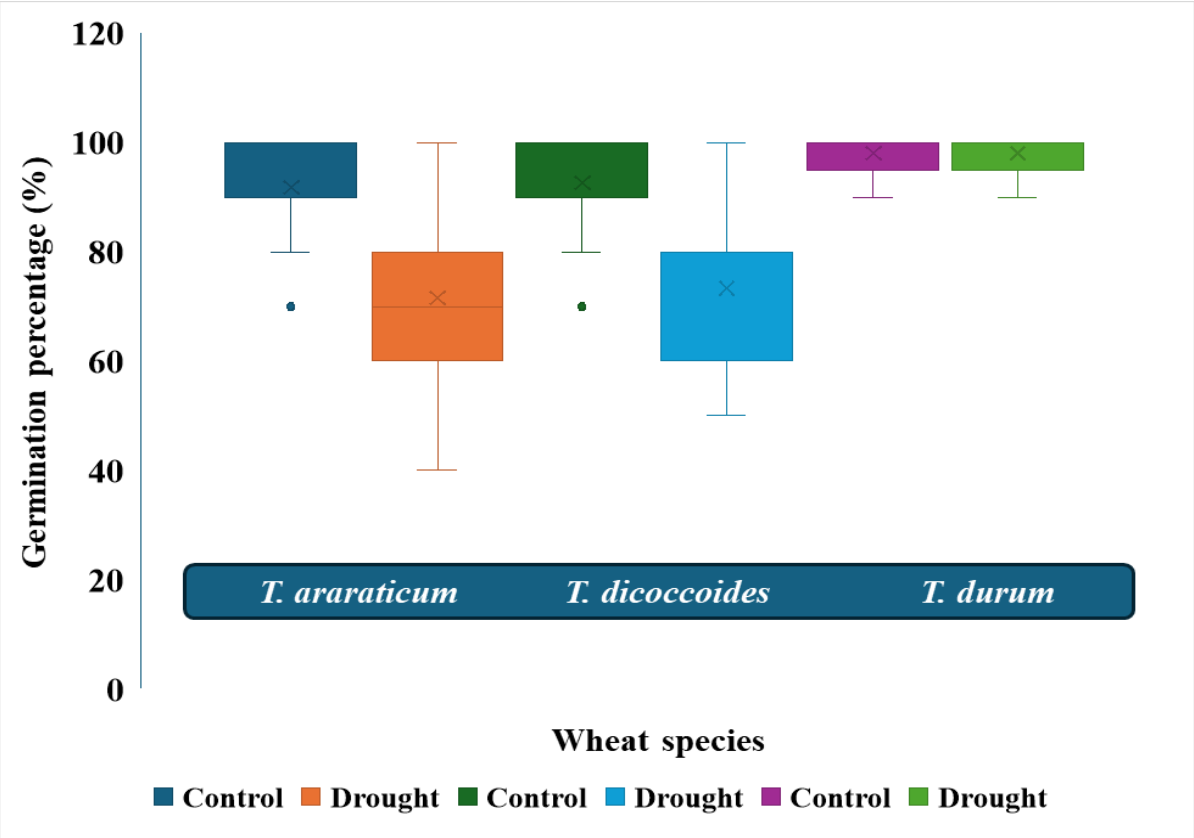

Figure 4.8. Graphical distribution of germination percentage for three wheat species under control and drought stress.

4.1.9. Seedling vigour index

Analysis of variance showed statistically significant variation among genotypes in terms of seedling vigour index (SVI) at probability level of P <0.001 (Table 4.17). Moreover, water stress had a significant effect on seedling vigour index of genotypes at probability level of P <0.001, but the interaction between water stress and genotype was not significant indicating constant genotypic response in terms of seedling vigour index (Table 4.17). Among three wheat species, SVI under control conditions ranged from 19.74-47.47 in *T. araraticum* with average index of 35.08, while from 28.10-56.99 and 41.36-48.97 in *T. dicoccoides* and *T. durum* with average values of 38.99 and 45.65, respectively (Table 4.18). On the other hand, under drought stress SVI varied from 6.15 to 32.05 in *T. araraticum* with average index of 17.71, while from 10.03 to 33.42 and 30.23 to 36.45 in *T. dicoccoides* and *T. durum* with average index values of 22.12 and 33.40, respectively (Table 4.18). Descriptive figures for reduction percentage showed significant decrease in seedling vigour index. However, the reduction percentage was highest in *T. araraticum* (49.52%) followed by T. *dicoccoides* (43.27%) and T. *durum* (26.83%) as shown by the Table 4.18. The raw data for SVI under both control and drought stress conditions is given in the supplementary Table 1and Table 2, respectively.

Table 4.17. Analysis of variance for seedling vigour index of genotypes under study.

Source of variation	DF	Sum Sq	Mean Sq	F value	Pr(>F)
Genotype (A)	109	13056	120	2.067	2.91e-06 ***
Water stress (B)	1	32037	32037	552.818	< 2e-16 ***
A × B	109	5786	53	0.916	0.694^{ns}
Residuals	220	12749	58		
CV	27.62%				

^{ns} P >0 .05* P <0.05, ** P <0.01, *** P <0.001, level of significance DF, degrees of freedom; Sum Sq, sum of squares; Mean Sq, mean sum of squares.

Table 4.18. Minimum, maximum and mean seedling vigour index for three wheat species under control and drought stress.

	Seedling vigour index					
	Control			Drought		
	T. ara	***T. dic***	***T. dur***	***T. ara***	***T. dic***	***T. dur***
Minimum	19.74	28.10	41.36	6.15	10.03	30.23
Maximum	47.47	56.99	48.97	32.05	33.41	36.45
Mean	35.08	38.99	45.65	17.71	22.12	33.40
Standard dev.	5.67	7.39	3.05	5.78	6.43	2.36
Reduction (%)				49.52	43.27	26.83

T. ara, T. araraticum; T. dic, T. dicoccoides; T. dur, T. durum.

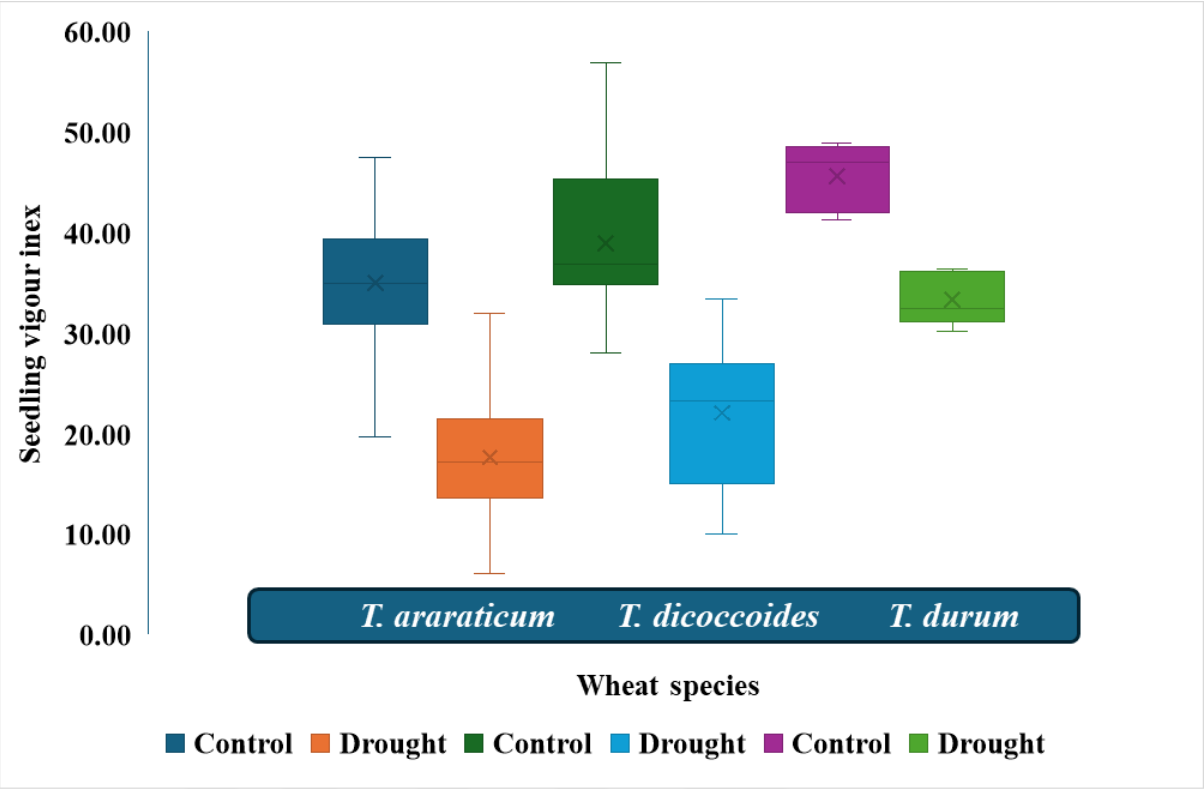

Figure 4.9. Graphical distribution of seedling vigour index for three wheat species under control and drought stress.

Seedling vigour is an important trait indicates seedling's ability to intercept light and the ability to compete for soil water and nutrients and could act as an important determinant of tolerance under drought stress (Maulana et al. 2021). The genotypes with higher seedling vigour index indicate tolerance to drought stress. A study conducted to investigate the potential of wheat for drought tolerance reported seedling vigour index between 21.85-54.03 with average index value of 43.83 under control conditions, while between 1.11-46.6 with average index value of 26.88 under PEG-induced (%20) drought stress (Gudi et al. 2024). Moreover, a study conducted to explore the potential of eighty wheat synthetics under PEG-induced drought stress reported a significant decrease in seedling vigour index of wheat synthetics under different osmotic potentials developed by using different concentrations of PEG (13,19 and 23%). The findings of the current study show harmony with the above-mentioned studies and indicate the presence of some promising genotypes that can be utilized in the future wheat breeding programmes to develop drought tolerant wheat varieties.

4.2. Correlation among seedlings traits under control and drought stress

Correlation analysis was carried out to uncover the relationship among seedling traits under both control and water deficit stress (Figure 4.10). Among seedling traits, coleoptile length had significant positive correlation with all the traits except total root number (TRN) under both control and drought stress conditions. Likewise, shoot length (SL) was positively associated with the all the

traits except TRN under control condition, while it had also significant positive correlation with TRN under drought stress. Furthermore, primary root length (PRL), seminal root length (SRL), mean seminal root length (MSRL), TRL and SVI had significant positive correlation with each other under both control and water limited conditions. TRN had significant positive correlation with all traits except CL and SL under control conditions, while the trend was similar under drought stress with only non- significant correlation with CL. Our results show complete harmony with Gudi et al. (2024), who reported significant positive correlation between all seedling traits under drought conditions, while the trend was similar under control conditions except traits like coleoptile length, germination percentage and seedling vigour, which had negative and non-significant correlation.

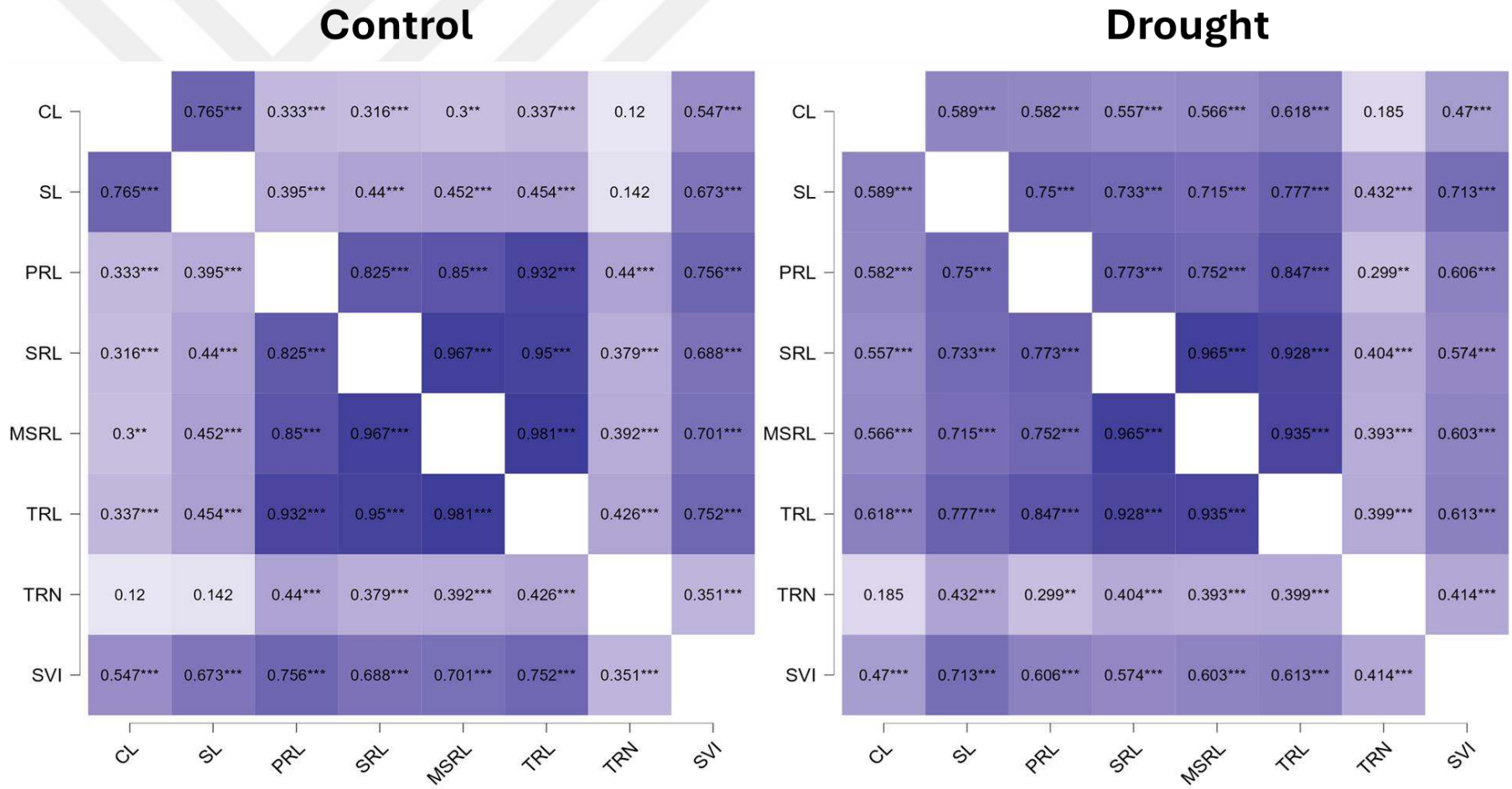

Figure 4.10. Correlation between seedling traits under control and drought stress.

4.3. Principal component analysis of seedlings traits

Principal component analysis (PCA) was used to analyze average data which is a form of multivariate analysis and reflects the key contributors of the total variations present in a dataset. The eigenvalues obtained because of PCA reveal the variance explained by each component and the sum of their eigenvalues is usually equal to the number of the variables (Sharma, 1998). In the current study the variations were identified for nine different seedling traits under both control and drought conditions. As a result of PCA analysis, the first two principal components explained the largest proportion of the variations i.e. 74.25 and 76.46 % under both control and drought stress, respectively (Table 4.19). Briefly, PC1 explained 58.35 and 61.27 % of the total variation under control and water stress conditions, respectively. On the other hand, PC2 explained 15.91 and 15.19 % of the total variation under control and drought stress, respectively. However, among traits the occurrence of positive and negative loadings indicates the positive and negative relationship between principal components and variables. Therefore, the variables in Table 4.19 with high positive loadings are the key contributors of PC1 and PC2. Accordingly, traits like total root length (TRL), seminal root length (SRL), mean seminal root length (MSRL), primary root length (PRL) and seedling vigour index (SVI) are the key contributors of PC1 under both control and drought stress. On the other hand, coleoptile length (CL), shoot length (SL), and germination percentage are the key contributors of PC2 under control, while GP and SVI contributed the most to the PC2 under drought stress (Table 4.19). Biplot analysis

Table 4.19. Eigenvalues of PC1 and PC2 with contribution of each variable to PC1 and PC2 under control and drought stress.

	Control		**Drought**	
Traits	**PC1**	**PC2**	**PC1**	**PC2**
CL	0.23	0.56	0.30	-0.04
SL	0.28	0.49	0.37	-0.01
PRL	0.39	-0.20	0.37	-0.19
SRL	0.39	-0.25	0.39	-0.19
MSRL	0.40	-0.25	0.39	-0.16
TRL	0.41	-0.23	0.40	-0.17
TRN	0.21	-0.23	0.21	0.18
GP	0.16	0.33	0.12	0.78
SVI	0.39	0.25	0.33	0.47
Eigenvalue	5.25	1.43	5.51	1.36
Percentage of variance (%)	58.35	15.91	61.27	15.19
Cumulative (%)	58.35	74.25	61.27	76.46

PC1, principal component 1; PC2, principal component 2.

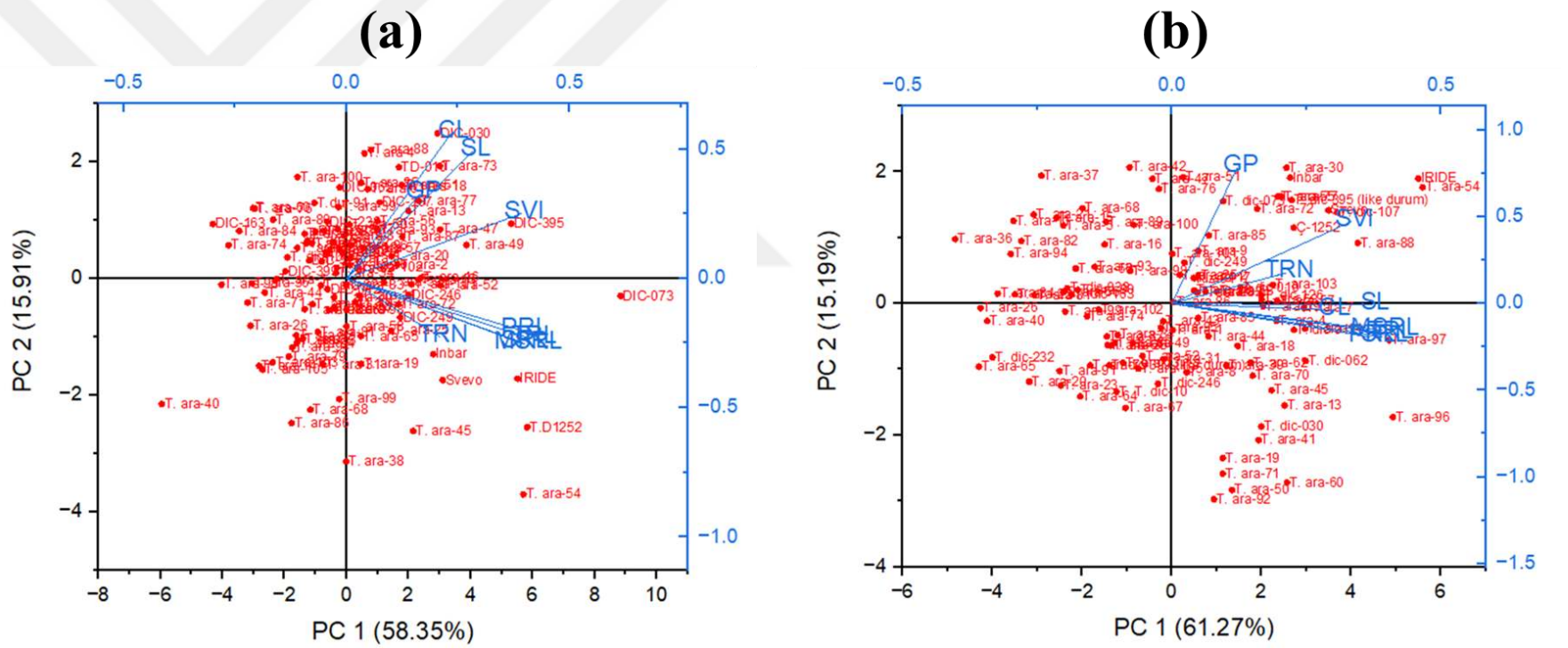

Figure 4.11. Biplot of nine seedling traits under (a) control and (b) drought stress.

4.4. Field experiment

4.4.1. Pre-harvest parameters

Analysis of variance revealed statistically significant variations among genotypes for agro-morphological traits such as plant height, days to heading, spike length and number of spikelets per spike at probability level of P <.001 (Table 4.19). Moreover, environment had a significant effect on all the traits and the interaction between genotype and environment was also significant indicating the variation in the response of genotypes to the environment for all the abovementioned traits. Among the agro-morphological parameters, days to heading ranged from 72 to 134 in the first growing season indicating the most early maturing and late maturing genotypes, with an average of 112 days. (Table 4.20). However, in the second growing season days to heading varied from 97 to 134 with average days to heading of 113 days. On the other hand, plant height ranged from 81.4 to 139.9 cm in the first growing season with an average plant height of 109.6 cm, while in the second growing season recorded between 78.3 and 129.5 cm with a mean of 98.5 cm.

Among yield components, spike length varied between 8.7 and 15.1 cm in the first growing season with a mean of 12.1 cm (Table 4.21). On the other hand, in the second growing season spike length was recorded between 10.2 and 17.0 cm with average spike length of 12.9 cm. The number of spikelets per spike ranged from 15.5-33.1 in the first growing season and from 14.0-34.0 in the second growing season, with mean values of 19.4 and 20.8, respectively. Moreover, Graphical distribution of preharvest traits also supports the existence of valuable diversity among genotypes and is shown for both first and second growing season along with their mean in the Figure 4.10. The raw data for all pre-harvest parameters in the first and second growing season along with their mean and standard deviation is given in the Table 4.20 and 4.21, respectively.

Wheat wild relatives serve as potential source of tolerance to biotic and abiotic stresses. Therefore, the agro-morphological characterization of these wild species is an essential aspect to harness their promising genetic diversity. The studies have long been focused on *T. dicoccoides* because of its primary role in the evolution of bread wheat. However, *T. araraticum* is also reported to have great potential for both quality parameters and stress tolerance (Frederike et al. 2023, 2024). Regardless of its great potential only few studies are conducted to explore its potential for biotic and abiotic stress factors to date. The studies conducted for agro-morphological characterization of *T. araraticum* reported days to heading between 90 and 130 days (Gabal et al. 2023). Furthermore, a study conducted on its most closely related tetraploid wheat i.e. *T. dicoccoides,* reported days to heading between 98 and 114 days with a mean of 77 days (Bonfil and Kafkafi, 2000; Gurcan et al. 2017).

In case of wheat wild relatives, plant height refers to the height from the earth surface till the tip of the spike excluding awns or stem height because they have different growth habits (Prostrate or semi-prostrate) as compared to bread wheat. A study conducted by Frederike et al. (2024) phenotyped various wild relatives including *Triticum araraticum* and recorded plant height between

75 cm and 120 cm with a mean of 91.5 cm in *T. araraticum*. The findings of the current study are in accordance with the one reported by Frederike et al. (2023). Plant height is a crucial phenotypic parameter in wheat breeding because it shows the ability of a plant to withstand lodging. Therefore, the development of wheat cultivars with moderate plant height is a crucial breeding objective and requires germplasm with diverse plant height. The current study offers great variation among genotypes in terms of plant height that can be used to develop wheat cultivars with optimum plant height.

To date, a few studies are conducted to phenotypes *T. araraticum* for spike length and even none for spikelets per spike. Our results align with Gabal et al. (2021), who phenotyped *T. araraticum* genotypes under field conditions and recorded spike length ranging from 8-15 cm with an average spike length of 11.5 cm. Additionally, some preliminary studies conducted on its most closet wild relative i.e. *T. dicoccoides* reported spikelets per spike between 8.7 and 21.2 (Bonfil and Kafkafi, 2000), and between 12.00 and 26.33 with an average of 20.69 (Çakır, 2015). These findings show harmony with our results with some variation that may have arisen from the variations in the environmental conditions or different species involved in the study. Our results present great variations among genotypes for all pre-harvest traits that could be utilized in the future wheat breeding programmes.

Table 4.20. Analysis of variance of genotypes under study for pre-harvest parameters.

		Pre-harvest parameters			
Source of variation	**df**	**DTH**	**PH**	**SL**	**SPS**
Genotype (G)	89	682.3***	522***	9.4***	45.6***
Environment (E)	1	38.1*	22339***	423.9***	335***
Replication	6	9.3	269***	5.7***	19.8
G X E	89	179.1***	304***	4.2***	11.5***
Residuals	534	9.3	67	0.9	2.6

* P <.05, ** P <.01, *** P <.001, level of significance; df, degrees of freedom; DTH, days to heading, PH, plant height; SL, spike length, SPS, spikelets per spike.

Table 4.21. Mean data of days to heading and plant height across two growing seasons and their mean.

	Days to heading			Plant height (cm)		
Genotype	**2022-23**	**2023-24**	**Mean**	**2022-23**	**2023-24**	**Mean**
TR38	112	106	108.8 ± 2.8	100.2	102.0	101.1 ± 0.9
TR9	124	134	128.8 ± 5.2	109.6	100.0	104.8 ± 4.8
TR74	122	121	121.6 ± 0.6	136.1	97.1	116.6 ± 19.5
TR83	115	109	111.9 ± 2.9	105.5	108.8	107.2 ± 1.6
TR45	103	102	102.2 ± 0.2	113.4	123.1	118.3 ± 4.8
TR25	108	104	105.9 ± 1.9	109.8	109.1	109.4 ± 0.3
TR7	117	114	115.4 ± 1.4	95.1	101.3	98.2 ± 3.1
TR97	117	112	114.4 ± 2.4	115.4	98.8	107.1 ± 8.3
TR39	120	125	122.2 ± 2.8	104.6	90.8	97.7 ± 6.9
TR41	110	110	110.1 ± 0.1	108.0	98.0	103.0 ± 5.0
TR67	126	119	122.6 ± 3.6	119.3	95.5	107.4 ± 11.9
TR62	109	106	107.2 ± 1.2	110.8	108.4	109.6 ± 1.2
TR72	109	106	107.6 ± 1.6	121.8	108.3	115.0 ± 6.7
TR68	111	109	110.1 ± 1.1	125.1	110.1	117.6 ± 7.5
TR19	128	126	127.1 ± 1.1	139.9	97.8	118.9 ± 21.1
TR86	110	104	107.1 ± 3.1	104.9	121.6	113.2 ± 8.4
TR64	106	102	103.8 ± 1.8	110.7	129.5	120.1 ± 9.4
TR105	113	107	109.8 ± 2.8	116.0	98.4	107.2 ± 8.8
TR13	117	118	117.6 ± 0.4	109.0	89.1	99.1 ± 10.0
TR58	118	118	117.8 ± 0.2	128.3	95.8	112.1 ± 16.3
TR91	116	114	115.1 ± 1.1	106.9	91.8	99.3 ± 7.5
TR102	114	110	112.1 ± 2.1	112.0	106.5	109.3 ± 2.8
TR81	117	114	115.2 ± 1.2	110.1	101.0	105.6 ± 4.6
TR65	104	106	105.0 ± 1.0	113.9	112.1	113.0 ± 0.9
TR23	117	115	116.1 ± 1.1	98.8	88.6	93.7 ± 5.1
TR31	124	119	121.5 ± 2.5	101.9	84.8	93.3 ± 8.5
TR92	115	114	114.6 ± 0.6	108.4	98.5	103.4 ± 4.9
TR17	112	111	111.4 ± 0.4	102.6	100.9	101.8 ± 0.9
TR5	117	118	117.5 ± 0.5	125.1	90.8	107.9 ± 17.1
TR90	123	120	121.4 ± 1.4	108.8	85.0	96.9 ± 11.9
TR8	118	112	114.8 ± 2.8	103.9	98.0	100.9 ± 2.9
TR14	114	106	110.0 ± 4.0	116.7	100.0	108.3 ± 8.3
TR73	128	126	127.1 ± 1.1	116.0	91.5	103.8 ± 12.3
TR70	110	110	110.1 ± 0.1	117.3	102.9	110.1 ± 7.2
TR44	112	115	113.5 ± 1.5	98.4	99.0	98.7 ± 0.3
TR28	129	127	128.0 ± 1.0	103.5	95.5	99.5 ± 4.0
TR1	113	105	108.8 ± 3.8	111.1	95.0	103.1 ± 8.1
TR52	113	111	111.8 ± 0.8	110.6	99.0	104.8 ± 5.8
TR20	131	127	129.0 ± 2.0	125.6	92.3	109.0 ± 16.7
TR35	129	126	127.2 ± 1.2	110.8	92.0	101.4 ± 9.4
TR50	127	116	121.2 ± 5.2	110.4	96.3	103.3 ± 7.0
TR53	102	102	102.1 ± 0.1	113.3	110.3	111.8 ± 1.5

Table 4.21 Continue

TR103	106	110	108.1 ± 1.9	107.9	96.3	102.1 ± 5.8
TR42	111	110	110.2 ± 0.2	114.3	98.0	106.1 ± 8.1
TR71	126	124	124.8 ± 0.8	129.5	87.7	108.6 ± 20.9
TR43	109	110	109.5 ± 0.5	112.9	96.8	104.8 ± 8.0
TR79	110	107	108.4 ± 1.4	119.4	102.5	110.9 ± 8.4
TR59	110	109	109.4 ± 0.4	113.1	103.4	108.3 ± 4.9
TR57	115	115	115.1 ± 0.1	116.9	100.7	108.8 ± 8.1
TR4	134	126	129.9 ± 3.9	127.5	94.5	111.0 ± 16.5
TR88	108	107	107.6 ± 0.6	114.6	109.8	112.2 ± 2.4
TR18	125	119	121.8 ± 2.8	134.4	94.7	114.5 ± 19.8
TR55	110	107	108.2 ± 1.2	113.1	103.8	108.5 ± 4.7
TR30	117	107	112.0 ± 5.0	104.1	90.7	97.4 ± 6.7
TR77	125	121	123.1 ± 2.1	113.4	91.9	102.6 ± 10.7
TR12	118	116	116.9 ± 0.9	100.8	86.2	93.5 ± 7.3
TR95	114	108	110.8 ± 2.8	108.4	101.5	105.0 ± 3.5
TR80	123	123	123.1 ± 0.1	108.6	91.0	99.8 ± 8.8
TR60	111	109	109.8 ± 0.8	110.9	110.3	110.6 ± 0.3
TR34	109	105	106.8 ± 1.8	116.8	104.3	110.5 ± 6.2
TR93	115	111	113.1 ± 2.1	115.9	102.9	109.4 ± 6.5
TR22	128	122	125.1 ± 3.1	100.5	86.6	93.6 ± 7.0
TR40	98	123	110.5 ± 12.5	120.8	117.4	119.1 ± 1.7
TR56	112	113	112.4 ± 0.6	110.6	102.5	106.6 ± 4.1
TR99	130	129	129.6 ± 0.6	104.1	87.0	95.6 ± 8.6
TR89	119	116	117.5 ± 1.5	115.4	92.9	104.1 ± 11.2
TR15	118	119	118.6 ± 0.4	107.6	88.8	98.2 ± 9.4
TR11	122	117	119.4 ± 2.4	105.8	92.5	99.1 ± 6.6
TR82	107	107	107.0 ± 0.0	116.5	117.5	117.0 ± 0.5
TR69	116	110	112.9 ± 2.9	117.0	102.9	109.9 ± 7.1
TR37	114	106	109.8 ± 3.8	108.8	99.5	104.1 ± 4.6
TR61	104	108	105.8 ± 2.2	81.4	96.0	88.7 ± 7.3
TR26	116	124	120.1 ± 3.9	94.9	98.8	96.8 ± 2.0
TR47	106	102	104.0 ± 2.0	104.1	104.7	104.4 ± 0.3
TR94	113	109	110.9 ± 1.9	120.6	105.5	113.1 ± 7.6
TR21	129	124	126.5 ± 2.5	102.8	121.8	112.3 ± 9.5
TR76	112	108	109.9 ± 1.9	110.9	93.4	102.1 ± 8.7
TR100	94	113	103.7 ± 9.3	95.1	91.9	93.5 ± 1.6
TR98	98	112	105.2 ± 6.8	95.9	83.8	89.8 ± 6.0
TR85	78	97	87.3 ± 9.7	93.3	96.5	94.9 ± 1.6
TR84	74	103	88.7 ± 14.3	97.4	102.0	99.7 ± 2.3
TR96	113	104	108.4 ± 4.4	110.1	93.0	101.6 ± 8.6
TR49	110	101	105.2 ± 4.2	97.1	91.3	94.2 ± 2.9
TR36	72	115	93.5 ± 21.5	98.5	83.7	91.1 ± 7.4
TR51	108	108	108.0 ± 0.0	84.9	84.0	84.4 ± 0.4
TR101	80	112	96.2 ± 15.8	97.4	89.4	93.4 ± 4.0
TR2	100	110	105.2 ± 4.8	90.0	86.5	88.3 ± 1.8

Table 4.21 Continue

TR16	101	120	110.3 ± 9.7	86.1	78.3	82.2 ± 3.9
TR87	86	103	94.7 ± 8.3	101.1	94.6	97.9 ± 3.3
TR54	76	99	87.5 ± 11.5	104.3	95.8	100.0 ± 4.2
Min	72	97	87	81.4	78.3	82.2
Max	134	134	130	139.9	129.5	120.1
Mean	112	113	113	109.6	98.5	104.0

TR, *Triticum araraticum*; Min, minimum; Max, maximum.

Table 4.22. Mean data of spike length and spikelets per spike across two growing seasons and their mean.

Spike length (cm)				**Spikelets per spike**		
Genotype	**2022-23**	**2023-24**	**Mean**	**2022-23**	**2023-24**	**Mean**
TR38	12.1	14.8	13.5 ± 1.4	19	20	20 ± 0.5
TR9	12.7	12.1	12.4 ± 0.3	22	17	19 ± 2.3
TR74	15.1	16.2	15.6 ± 0.6	22	25	23 ± 1.6
TR83	11.7	14.7	13.2 ± 1.5	19	22	20 ± 1.7
TR45	10.8	13.8	12.3 ± 1.5	17	21	19 ± 2.1
TR25	12.5	14.3	13.4 ± 0.9	19	21	20 ± 1.2
TR7	12.3	14.3	13.3 ± 1.0	16	20	18 ± 2.3
TR97	13.9	15.4	14.7 ± 0.7	23	25	24 ± 0.8
TR39	11.6	12.9	12.3 ± 0.7	20	21	20 ± 0.6
TR41	11.7	15.0	13.4 ± 1.6	19	21	20 ± 1.1
TR67	13.2	17.0	15.1 ± 1.9	21	25	23 ± 1.9
TR62	11.9	15.3	13.6 ± 1.7	22	23	22 ± 0.6
TR72	12.1	14.0	13.1 ± 1.0	21	22	21 ± 0.8
TR68	12.1	13.4	12.7 ± 0.7	20	20	20 ± 0.2
TR19	15.1	13.6	14.3 ± 0.7	24	22	23 ± 0.9
TR86	11.1	14.7	12.9 ± 1.8	17	20	19 ± 1.4
TR64	10.1	13.0	11.6 ± 1.4	18	21	19 ± 1.5
TR105	12.0	13.1	12.6 ± 0.6	18	20	19 ± 1.1
TR13	12.1	12.3	12.2 ± 0.1	18	18	18 ± 0.1
TR58	11.7	13.2	12.5 ± 0.7	18	19	19 ± 0.4
TR91	11.0	10.2	10.6 ± 0.4	17	14	16 ± 1.6
TR102	13.6	16.1	14.9 ± 1.3	22	23	23 ± 0.3
TR81	13.7	16.1	14.9 ± 1.2	21	23	22 ± 1.1
TR65	12.2	13.3	12.7 ± 0.6	17	19	18 ± 0.8
TR23	12.2	13.3	12.8 ± 0.5	18	19	18 ± 0.6
TR31	12.6	13.1	12.8 ± 0.3	17	20	19 ± 1.3
TR92	10.7	11.5	11.1 ± 0.4	19	17	18 ± 0.8
TR17	13.4	12.9	13.1 ± 0.2	18	18	18 ± 0.1
TR5	14.1	15.2	14.7 ± 0.5	33	28	31 ± 2.6
TR90	12.5	15.4	13.9 ± 1.5	19	23	21 ± 1.8
TR8	12.2	15.6	13.9 ± 1.7	20	21	21 ± 0.5
TR14	11.4	13.0	12.2 ± 0.8	18	20	19 ± 1.0
TR73	14.4	14.4	14.4 ± 0.0	23	22	22 ± 0.4

Table 4.22 Continue

TR70	11.7	14.4	13.1 ± 1.3	19	23	21 ± 2.1
TR44	10.9	11.9	11.4 ± 0.5	17	19	18 ± 1.1
TR28	10.8	13.5	12.1 ± 1.4	19	22	21 ± 1.5
TR1	12.4	12.8	12.6 ± 0.2	18	20	19 ± 0.9
TR52	12.0	14.9	13.5 ± 1.5	19	23	21 ± 2.2
TR20	13.7	12.7	13.2 ± 0.5	22	20	21 ± 1.2
TR35	13.8	13.5	13.7 ± 0.2	22	23	23 ± 0.3
TR50	13.0	15.4	14.2 ± 1.2	22	23	22 ± 0.6
TR53	11.3	13.7	12.5 ± 1.2	20	22	21 ± 1.3
TR103	11.9	12.1	12.0 ± 0.1	17	19	18 ± 1.0
TR42	12.4	14.2	13.3 ± 0.9	19	20	20 ± 0.5
TR71	15.0	16.4	15.7 ± 0.7	21	24	22 ± 1.6
TR43	12.1	13.6	12.8 ± 0.8	18	19	18 ± 0.6
TR79	12.4	13.0	12.7 ± 0.3	18	19	18 ± 0.7
TR59	12.6	14.9	13.7 ± 1.2	21	23	22 ± 1.2
TR57	12.4	15.3	13.8 ± 1.5	20	22	21 ± 0.9
TR4	14.0	14.5	14.2 ± 0.3	24	23	23 ± 0.3
TR88	11.7	14.3	13.0 ± 1.3	19	21	20 ± 1.0
TR18	12.7	14.4	13.6 ± 0.9	21	23	22 ± 0.8
TR55	11.2	13.0	12.1 ± 0.9	17	18	18 ± 0.3
TR30	12.4	12.7	12.6 ± 0.1	21	21	21 ± 0.1
TR77	11.9	13.2	12.6 ± 0.6	19	22	21 ± 1.3
TR12	12.8	12.5	12.6 ± 0.1	18	18	18 ± 0.1
TR95	11.4	13.9	12.6 ± 1.3	19	20	19 ± 0.7
TR80	13.2	15.7	14.4 ± 1.3	19	24	22 ± 2.5
TR60	11.3	13.8	12.6 ± 1.3	17	20	19 ± 1.4
TR34	11.8	12.9	12.3 ± 0.6	17	20	19 ± 1.4
TR93	11.4	12.7	12.0 ± 0.7	17	17	17 ± 0.2
TR22	12.1	12.0	12.0 ± 0.0	18	20	19 ± 0.9
TR40	11.6	13.3	12.4 ± 0.9	25	34	30 ± 4.3
TR56	11.8	13.5	12.7 ± 0.8	17	17	17 ± 0.3
TR99	14.3	15.7	15.0 ± 0.7	22	24	23 ± 0.9
TR89	12.7	14.2	13.5 ± 0.8	20	21	20 ± 0.5
TR15	12.5	10.8	11.7 ± 0.9	17	16	16 ± 0.4
TR11	12.6	12.8	12.7 ± 0.1	21	21	21 ± 0.1
TR82	11.3	11.7	11.5 ± 0.2	17	18	17 ± 0.7
TR69	12.8	13.4	13.1 ± 0.3	18	21	20 ± 1.3
TR37	11.7	12.2	11.9 ± 0.3	18	19	19 ± 0.3
TR61	12.3	13.5	12.9 ± 0.6	18	20	19 ± 0.8
TR26	12.0	11.9	11.9 ± 0.0	22	21	22 ± 0.5
TR47	10.4	11.6	11.0 ± 0.6	17	18	17 ± 0.7
TR94	10.6	12.9	11.8 ± 1.1	17	19	18 ± 1.1
TR21	13.5	13.2	13.4 ± 0.2	19	21	20 ± 1.0
TR76	13.4	13.3	13.3 ± 0.0	20	21	21 ± 0.4
TR100	12.9	16.3	14.6 ± 1.7	20	24	22 ± 2.0

Table 4.22 Continue

TR98	12.8	15.1	13.9 ± 1.2	21	20	20 ± 0.5
TR85	10.9	12.6	11.8 ± 0.9	17	17	17 ± 0.2
TR84	10.6	14.8	12.7 ± 2.1	17	23	20 ± 3.1
TR96	12.1	11.8	12.0 ± 0.1	21	18	20 ± 1.6
TR49	11.8	13.2	12.5 ± 0.7	17	18	18 ± 0.3
TR36	10.4	14.6	12.5 ± 2.1	25	25	25 ± 0.1
TR51	12.0	11.1	11.5 ± 0.4	24	18	21 ± 2.9
TR101	8.9	16.5	12.7 ± 3.8	17	25	21 ± 4.2
TR2	11.5	13.0	12.3 ± 0.7	18	19	18 ± 0.7
TR16	8.7	12.9	10.8 ± 2.1	16	21	19 ± 2.3
TR87	11.0	13.3	12.1 ± 1.2	18	20	19 ± 0.9
TR54	9.8	10.9	10.4 ± 0.5	19	18	18 ± 0.3
Min	8.7	10.2	10.4	15.5	14.0	15.6
Max	15.1	17.0	15.7	33.1	34.0	30.6
Mean	12.1	13.7	12.9	19.4	20.8	20.1

TR, *Triticum araraticum,* Min, minimum; Max, maximum

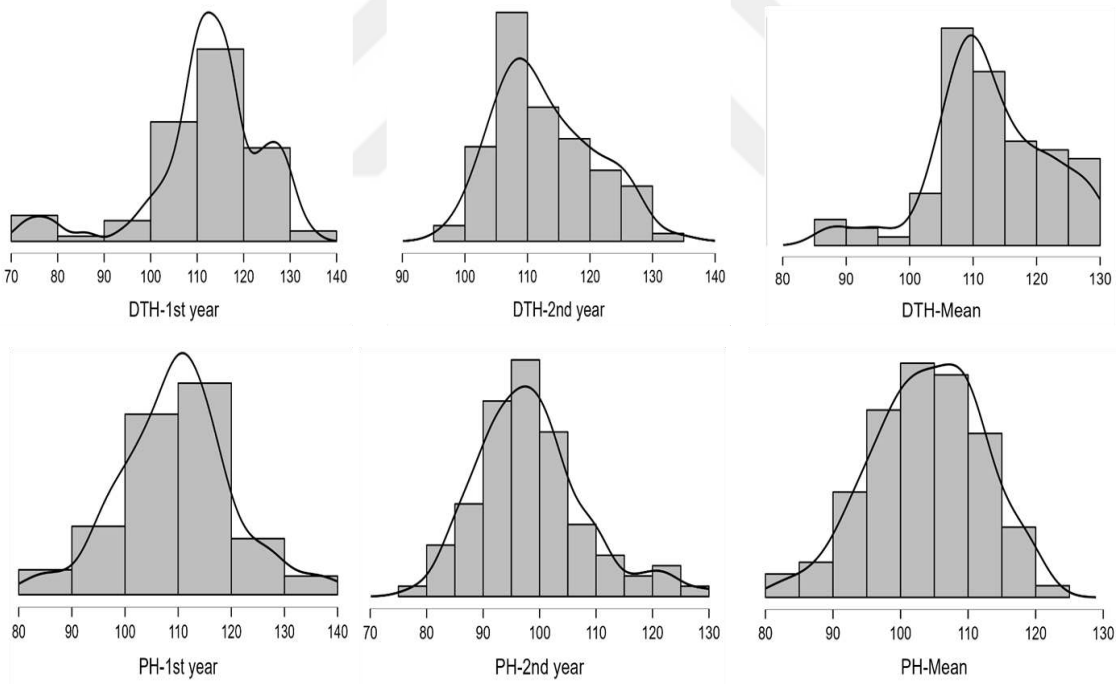

Figure 4.11. Graphical distribution of days to heading and plant height (cm) across two growing seasons along with the overall mean.

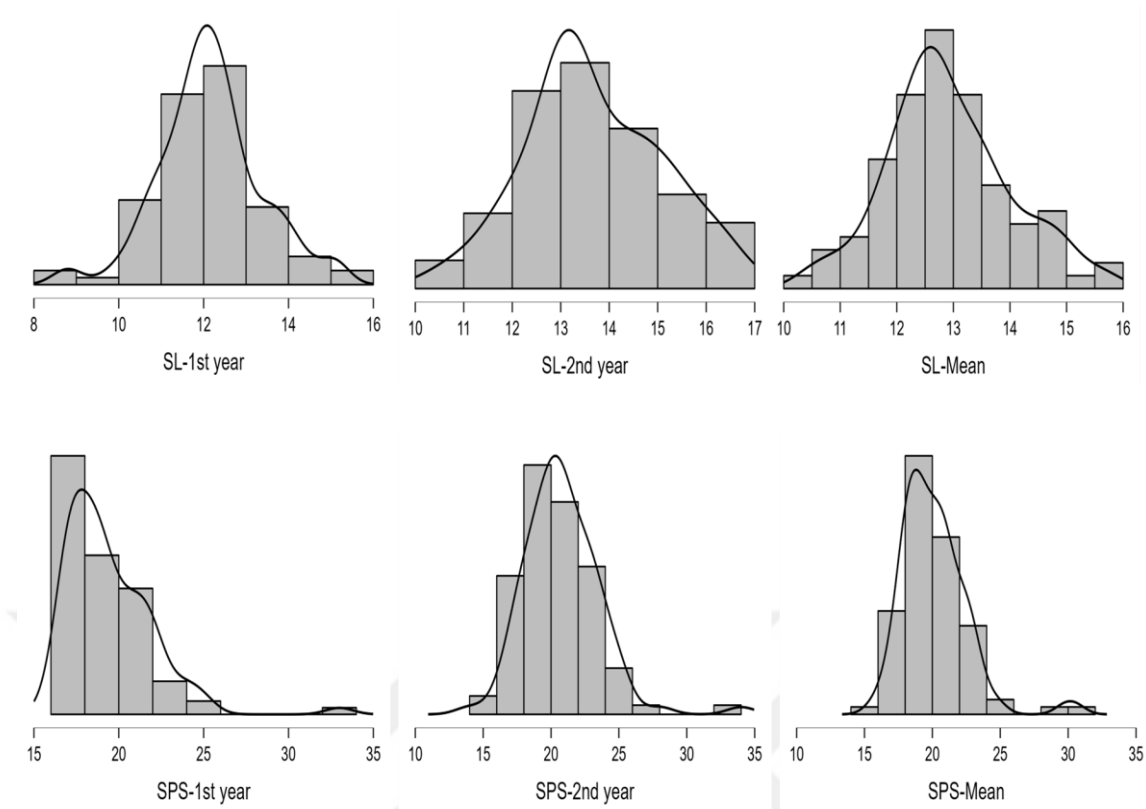

Figure 4.12. Graphical distribution of spikelet length (cm) and spikelets per spike across two growing seasons and their overall mean.

4.4.2. Post-harvest parameters

Analysis of variance showed statistically significant variations among genotypes for spikelet yield per plant (SY), grain yield per plant (GY), and thousand kernel weight (TKW) at probability level of P <.001 (Table 4.22). Moreover, environment had significant effect on the post-harvest parameters and interaction between genotype and environment was also significant indicating the variation in genotypic response to the change in environment. Among post-harvest parameters, SY varied between 5.1 and 79.9 g with average yield of 41.9 g in the firs growing season, while in the second growing season ranged from 10.1 and 68.1 g with average yield of 33.6 g, indicating a decrease in the average spikelet yield across second growing season (Table 4.23). On the other hand, GY varied significantly across two growing seasons. In the first growing season SY ranged from 1.1 to 30.1 g in the first growing season and from 1.1 to 22.9 g in the second growing season, with average values 12.5 g and 7.7 g, respectively. Moreover, TKW varied from 5.4 to 27.9 g in the first growing season with an average weight of 15.7 g, while in the second growing season it varied between 4.1 to 22.2 g with an average of 13.0 g.

The findings indicate significant variations among genotypes across two growing seasons under rainfed conditions. Graphical distribution of parameters measured after harvest across two growing seasons along with their mean is shown in the Figure 4.12. Wheat wild relatives are characterize by brittleness of spike that results in disarticulation of spikelets at maturity. Therefore,

spikelet yield per plant or hulled grain yield was measured to estimate the plant yield. Grain yield and thousand kernel weight is considerably low in wheat wild relatives as compared to bread and durum wheat. A study conducted by Frederike et al. (2023) to phenotype various wheat wild relatives including *T. araraticum,* for agro-morphological parameters reported spikelet yield in *T. araraticum* ranging from 8.5 to 68.4 g with average yield of 38.4 g. In contrast, hulless grain yield was recorded between 4.3 and 39.2 g, with average yield of 17.7 g, while thousand kernel weight ranged from 10.4 to 34.4 g with an average of 26.3g. The findings of these studies are in great agreement with our results and supports the lower grain yield and thousand kernel weight in wheat wild relatives than the modern bread wheat, where it ranges from 37-60 g depending on the cultivar (Groos et al. 2003). Thousand kernel weight is an important determinant of plant grain yield and should be targeted during de novo domestication of wheat wild relatives.

Table 4.23. Analysis of variance (ANOVA) of genotypes under study for post-harvest parameters.

	Post-harvest Parameters			
Source of variation	**df**	**SY (g)**	**GY (g)**	**TKW (g)**
Genotype (G)	89	1212***	132***	60.7***
Environment (E)	1	14041***	3817***	1374.8***
Replication	6	435*	42	6.0
G X E	89	591***	59***	40.6***
Residuals	534	181	27	3.2

* P <0.05, ** P <0.01, *** P <0.001, level of significance; df, degrees of freedom; SY, spikelet yield per plant; GY, grain yield per plant; TKW, thousand kernel weight.

Table 4.24. Mean data of post-harvest parameters across two growing seasons and the overall mean.

	SY (g)			**GY (g)**			**TKW (g)**		
G	**22-23**	**23-24**	**Mean**	**22-23**	**23-24**	**Mean**	**22-23**	**23-24**	**Mean**
TR38	34.5	34.3	34.4 ± 0.1	10.1	8.3	9.2 ± 0.9	14.3	13.8	14.1 ± 0.3
TR9	28.8	21.0	24.9 ± 3.9	8.8	6.1	7.4 ± 1.3	13.3	13.8	13.6 ± 0.3
TR74	41.7	37.0	39.4 ± 2.3	10.4	8.0	9.2 ± 1.2	13.4	12.5	13.0 ± 0.5
TR83	32.6	38.4	35.5 ± 2.9	9.1	9.8	9.5 ± 0.4	14.6	12.4	13.5 ± 1.1
TR45	76.5	67.7	72.1 ± 4.4	24.9	17.1	21.0 ± 3.9	18.0	16.2	17.1 ± 0.9
TR25	61.8	65.1	63.4 ± 1.6	18.2	17.8	18.0 ± 0.2	16.9	13.5	15.2 ± 1.7
TR7	31.2	36.0	33.6 ± 2.4	8.7	8.8	8.8 ± 0.1	20.9	12.4	16.6 ± 4.3
TR97	62.8	35.6	49.2 ± 13.6	17.1	6.3	11.7 ± 5.4	16.8	11.0	13.9 ± 2.9
TR39	37.8	23.2	30.5 ± 7.3	12.1	5.3	8.7 ± 3.4	15.7	10.7	13.2 ± 2.5
TR41	42.3	30.9	36.6 ± 5.7	11.1	4.0	7.5 ± 3.5	16.0	9.8	12.9 ± 3.1
TR67	29.8	27.5	28.7 ± 1.1	5.5	5.3	5.4 ± 0.1	8.4	9.8	9.1 ± 0.7
TR62	50.3	43.1	46.7 ± 3.6	16.7	11.3	14.0 ± 2.7	13.9	13.4	13.6 ± 0.2
TR72	55.0	53.2	54.1 ± 0.9	17.1	11.2	14.1 ± 2.9	16.7	12.6	14.6 ± 2.0
TR68	68.7	68.1	68.4 ± 0.3	22.9	22.9	22.9 ± 0.0	14.3	15.2	14.7 ± 0.4

Table 4.24 Continue

TR19	39.0	40.1	39.6 ± 0.5	12.7	12.3	12.5 ± 0.2	21.0	13.1	17.1 ± 3.9
TR86	42.8	52.5	47.6 ± 4.8	16.0	15.2	15.6 ± 0.4	14.0	16.5	15.3 ± 1.2
TR64	56.3	47.5	51.9 ± 4.4	17.5	12.7	15.1 ± 2.4	15.2	17.2	16.2 ± 1.0
TR105	49.3	36.7	43.0 ± 6.3	12.9	8.6	10.7 ± 2.1	11.1	11.4	11.3 ± 0.2
TR13	31.0	25.8	28.4 ± 2.6	10.3	8.0	9.2 ± 1.2	16.2	17.2	16.7 ± 0.5
TR58	79.9	34.6	57.3 ± 22.6	23.1	7.9	15.5 ± 7.6	8.9	11.4	10.1 ± 1.3
TR91	39.5	16.7	28.1 ± 11.4	12.0	3.9	7.9 ± 4.0	16.1	15.4	15.7 ± 0.3
TR102	60.6	33.3	46.9 ± 13.6	16.5	6.9	11.7 ± 4.8	15.2	13.5	14.4 ± 0.8
TR81	52.8	49.8	51.3 ± 1.5	14.2	10.2	12.2 ± 2.0	17.0	10.3	13.6 ± 3.4
TR65	76.6	47.7	62.2 ± 14.5	26.4	12.5	19.4 ± 7.0	15.1	14.5	14.8 ± 0.3
TR23	32.0	30.8	31.4 ± 0.6	7.5	7.4	7.4 ± 0.1	15.6	12.4	14.0 ± 1.6
TR31	25.7	31.1	28.4 ± 2.7	7.4	7.5	7.5 ± 0.1	17.2	12.4	14.8 ± 2.4
TR92	23.2	41.2	32.2 ± 9.0	7.8	11.7	9.7 ± 1.9	13.9	13.8	13.9 ± 0.0
TR17	55.0	46.8	50.9 ± 4.1	12.9	13.3	13.1 ± 0.2	19.5	22.2	20.9 ± 1.4
TR5	28.3	23.1	25.7 ± 2.6	7.1	4.8	6.0 ± 1.1	8.5	11.1	9.8 ± 1.3
TR90	41.0	53.8	47.4 ± 6.4	9.8	12.9	11.3 ± 1.5	11.3	12.6	12.0 ± 0.7
TR8	27.3	38.5	32.9 ± 5.6	7.9	6.0	6.9 ± 1.0	18.6	12.4	15.5 ± 3.1
TR14	37.5	39.5	38.5 ± 1.0	11.9	11.1	11.5 ± 0.4	13.8	10.9	12.4 ± 1.5
TR73	40.9	37.3	39.1 ± 1.8	13.1	9.6	11.4 ± 1.8	18.5	13.3	15.9 ± 2.6
TR70	71.8	47.0	59.4 ± 12.4	21.1	8.8	14.9 ± 6.1	18.9	12.3	15.6 ± 3.3
TR44	40.1	15.0	27.6 ± 12.5	9.5	1.7	5.6 ± 3.9	11.7	5.0	8.4 ± 3.4
TR28	32.4	16.2	24.3 ± 8.1	11.1	4.6	7.8 ± 3.2	17.2	16.0	16.6 ± 0.6
TR1	53.3	30.1	41.7 ± 11.6	16.1	6.0	11.1 ± 5.1	16.2	12.9	14.5 ± 1.7
TR52	43.3	26.3	34.8 ± 8.5	11.1	5.7	8.4 ± 2.7	25.9	13.7	19.8 ± 6.1
TR20	31.2	18.8	25.0 ± 6.2	9.7	5.3	7.5 ± 2.2	19.5	16.1	17.8 ± 1.7
TR35	26.1	25.4	25.8 ± 0.3	6.0	3.4	4.7 ± 1.3	13.4	10.6	12.0 ± 1.4
TR50	39.9	42.3	41.1 ± 1.2	7.0	6.6	6.8 ± 0.2	9.2	10.5	9.9 ± 0.6
TR53	69.8	42.2	56.0 ± 13.8	18.9	8.5	13.7 ± 5.2	14.1	13.6	13.9 ± 0.2
TR103	60.7	41.9	51.3 ± 9.4	17.9	8.6	13.2 ± 4.7	18.9	12.1	15.5 ± 3.4
TR42	51.9	52.0	51.9 ± 0.0	12.0	10.5	11.3 ± 0.8	11.3	10.0	10.6 ± 0.6
TR71	57.9	11.4	34.6 ± 23.3	11.6	1.1	6.3 ± 5.2	18.4	4.1	11.3 ± 7.2
TR43	54.2	30.5	42.3 ± 11.8	18.2	6.5	12.3 ± 5.9	17.1	11.3	14.2 ± 2.9
TR79	69.8	38.3	54.0 ± 15.7	24.0	10.2	17.1 ± 6.9	18.4	12.6	15.5 ± 2.9
TR59	61.3	47.0	54.1 ± 7.1	16.1	11.0	13.5 ± 2.6	14.8	10.2	12.5 ± 2.3
TR57	38.7	23.0	30.8 ± 7.9	23.5	4.0	13.8 ± 9.8	13.0	10.1	11.6 ± 1.5
TR4	61.4	19.5	40.5 ± 21.0	18.3	4.4	11.3 ± 7.0	18.3	15.0	16.6 ± 1.7
TR88	44.4	31.2	37.8 ± 6.6	12.5	5.8	9.1 ± 3.3	16.0	17.3	16.7 ± 0.6
TR18	55.8	15.8	35.8 ± 20.0	14.6	3.2	8.9 ± 5.7	12.9	10.2	11.6 ± 1.3
TR55	57.8	32.2	45.0 ± 12.8	18.6	8.2	13.4 ± 5.2	16.6	12.5	14.5 ± 2.1
TR30	38.7	29.8	34.2 ± 4.5	30.1	8.5	19.3 ± 10.8	22.8	16.1	19.4 ± 3.3
TR77	32.1	24.5	28.3 ± 3.8	8.0	5.9	6.9 ± 1.0	10.5	11.5	11.0 ± 0.5
TR12	30.3	29.2	29.8 ± 0.6	9.5	7.9	8.7 ± 0.8	25.1	15.3	20.2 ± 4.9
TR95	34.1	39.2	36.6 ± 2.5	9.3	6.8	8.0 ± 1.2	14.4	9.6	12.0 ± 2.4
TR80	40.8	12.9	26.9 ± 14.0	8.6	2.2	5.4 ± 3.2	14.4	9.3	11.9 ± 2.5
TR60	49.3	49.2	49.3 ± 0.0	13.1	9.9	11.5 ± 1.6	12.6	17.8	15.2 ± 2.6

Table 4.24 Continue

TR34	50.5	46.4	48.4 ± 2.1	17.5	9.5	13.5 ± 4.0	16.3	16.5	16.4 ± 0.1
TR93	41.1	37.3	39.2 ± 1.9	10.5	10.2	10.4 ± 0.1	17.3	15.5	16.4 ± 0.9
TR22	35.3	36.2	35.7 ± 0.5	6.9	6.5	6.7 ± 0.2	15.0	12.9	14.0 ± 1.1
TR40	35.9	10.1	23.0 ± 12.9	8.8	2.4	5.6 ± 3.2	19.4	9.0	14.2 ± 5.2
TR56	55.7	41.1	48.4 ± 7.3	16.5	7.0	11.7 ± 4.8	15.5	13.2	14.4 ± 1.1
TR99	16.4	19.0	17.7 ± 1.3	3.0	3.4	3.2 ± 0.2	15.9	13.9	14.9 ± 1.0
TR89	49.4	20.8	35.1 ± 14.3	14.3	3.9	9.1 ± 5.2	21.4	13.7	17.5 ± 3.9
TR15	29.9	29.4	29.7 ± 0.2	9.5	9.8	9.7 ± 0.2	20.1	17.4	18.7 ± 1.3
TR11	40.1	37.7	38.9 ± 1.2	11.1	11.3	11.2 ± 0.1	16.6	14.4	15.5 ± 1.1
TR82	67.8	44.2	56.0 ± 11.8	24.7	11.1	17.9 ± 6.8	21.4	15.6	18.5 ± 2.9
TR69	59.7	30.0	44.8 ± 14.8	19.7	4.3	12.0 ± 7.7	24.4	8.2	16.3 ± 8.1
TR37	22.5	31.2	26.9 ± 4.3	6.5	5.7	6.1 ± 0.4	16.8	11.1	14.0 ± 2.8
TR61	26.9	28.1	27.5 ± 0.6	4.4	4.0	4.2 ± 0.2	15.6	12.1	13.8 ± 1.8
TR26	12.2	12.7	12.4 ± 0.2	1.1	2.1	1.6 ± 0.5	9.2	13.0	11.1 ± 1.9
TR47	61.9	43.6	52.8 ± 9.1	15.3	9.7	12.5 ± 2.8	27.9	11.6	19.7 ± 8.1
TR94	60.9	15.1	38.0 ± 22.9	19.4	1.8	10.6 ± 8.8	18.2	9.0	13.6 ± 4.6
TR21	34.6	19.5	27.1 ± 7.5	10.6	4.8	7.7 ± 2.9	16.2	13.6	14.9 ± 1.3
TR76	37.2	25.0	31.1 ± 6.1	8.7	4.1	6.4 ± 2.3	14.2	12.5	13.3 ± 0.9
TR100	15.6	26.4	21.0 ± 5.4	6.4	7.6	7.0 ± 0.6	11.5	13.3	12.4 ± 0.9
TR98	15.5	30.0	22.7 ± 7.2	4.5	6.2	5.3 ± 0.8	14.0	18.9	16.5 ± 2.5
TR85	18.3	50.1	34.2 ± 15.9	10.7	14.8	12.8 ± 2.0	13.8	15.2	14.5 ± 0.7
TR84	22.4	26.7	24.5 ± 2.1	8.9	5.7	7.3 ± 1.6	15.3	12.8	14.0 ± 1.3
TR96	44.5	28.3	36.4 ± 8.1	12.0	5.9	8.9 ± 3.1	18.3	13.0	15.6 ± 2.7
TR49	46.7	35.9	41.3 ± 5.4	12.9	6.8	9.9 ± 3.1	19.2	16.4	17.8 ± 1.4
TR36	5.1	28.1	16.6 ± 11.5	2.3	5.2	3.8 ± 1.5	5.6	12.1	8.8 ± 3.3
TR51	10.6	13.9	12.3 ± 1.7	1.7	1.6	1.6 ± 0.0	5.4	7.8	6.6 ± 1.2
TR101	21.3	42.8	32.1 ± 10.7	9.7	7.4	8.6 ± 1.1	12.4	10.1	11.2 ± 1.2
TR2	15.7	33.4	24.5 ± 8.8	4.8	9.6	7.2 ± 2.4	14.6	19.2	16.9 ± 2.3
TR16	23.2	13.3	18.3 ± 4.9	8.6	3.6	6.1 ± 2.5	12.3	11.8	12.0 ± 0.3
TR87	23.8	32.9	28.3 ± 4.5	7.3	9.2	8.2 ± 0.9	13.1	13.5	13.3 ± 0.2
TR54	26.6	37.8	32.2 ± 5.6	7.6	10.6	9.1 ± 1.5	11.6	14.5	13.1 ± 1.5
Min	5.1	10.1	12.3	1.1	1.1	1.6	5.4	4.1	6.6
Max	79.9	68.1	72.1	30.1	22.9	22.9	27.9	22.2	20.9
Mean	41.9	33.6	37.7	12.5	7.7	10.1	15.7	13.0	14.3

SY, spikelet yield per plant; GY, grain yield per plant; TKW, thousand kernel weight; Min, minimum; Max, maximum.

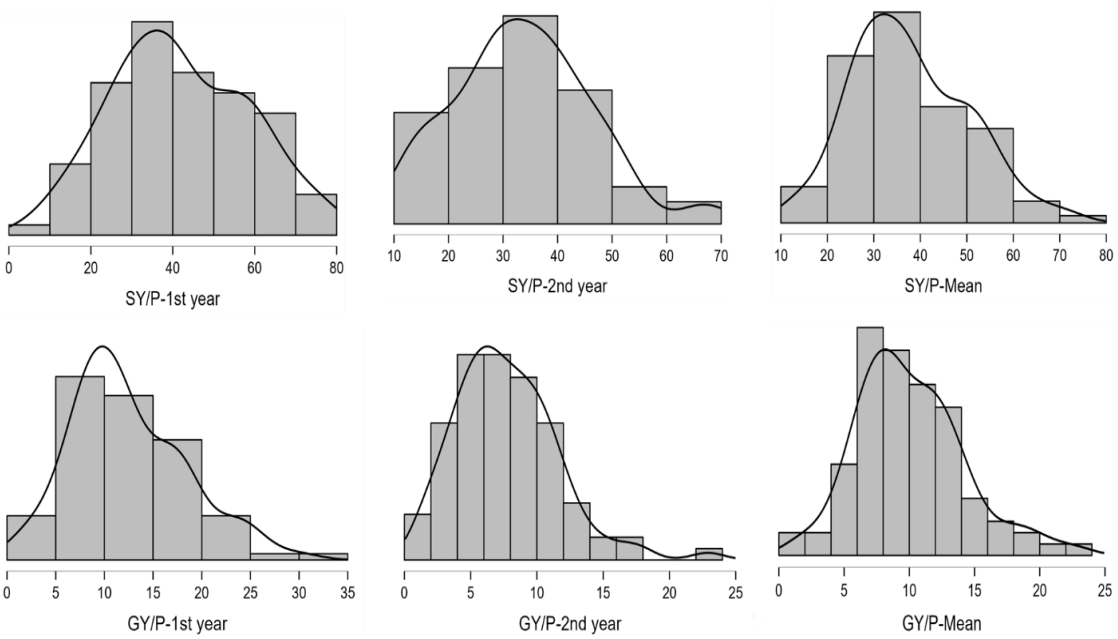

Figure 4.13. Graphical distribution of spikelet yield per plant (SY) and grain yield per plant (GY) across two growing seasons and the overall mean.

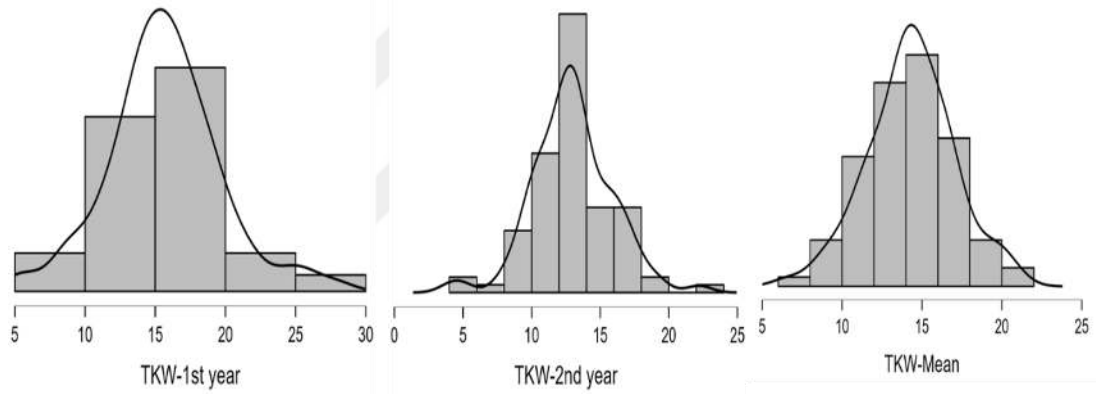

Figure 4.14. Graphical distribution of thousand kernel weight (g) across two growing seasons and the overall mean.

4.4.3. Physiological traits

Analysis of variance (ANOVA) showed statistically significant variation among genotypes for stomatal conductance measured on both third basal leaf ($gsw_{1)}$ and flag leaf (gsw_2) at probability level of P <0.01 (Table 4.23). However, the variations among genotypes for quantum yield of photosystem II measured on third basal leaf ($PhiPSII_1$) were statically significant at probability level of P <0.05 (Table 4.23), while the results were non-significant for the quantum yield measured on Flag leaf ($PhiPSII_2$). Moreover, descriptive statistics showed that gsw_1 was ranged from 64.3 to 576.6 mmol-$m^{-2}s^{-1}$ with an average of 285.8 mmol-$m^{-2}s^{-1}$, while gsw2 was recorded between 49.9 and 500.5 mmol-$m^{-2}s^{-1}$ with an average of 172.7 mmol-$m^{-2}s^{-1}$ (Table 4.24). Descriptive statistics show a significant decrease in gsw_2 in comparison to gsw_1 indicating water deficit conditions where plants tend to close their stomata to maintain the water balance. On the other hand, PhiPSII was ranged

from 0.19 to 0.61 with an average yield of 0.41, while PhiPSII was recorded between 0.24 and 0.58 with an average yield of 0.37 (Table 4.34).

Physiological parameters are crucial indicator of plants physiological health. Stomatal conductance together with chlorophyll fluorescence parameters like quantum yield of photosystem II provides clear picture of plants physiological health specifically under drought stress conditions. The studies conducted to measure stomatal conductance in wheat reported it between 145 and 351 mmol-$m^{-2}s^{-1}$ with an average of 262 mmol-$m^{-2}s^{-1}$ under control conditions, while between 211 and 546 mmol-$m^{-2}s^{-1}$ with an average of 338 mmol-$m^{-2}s^{-1}$ under heat stress (Sharma et al. 2015). However, Khamssi et al. (2012) reported stomatal conductance values ranging from 325 to 571.4 mmol-$m^{-2}s^{-1}$ and 156 to 421 mmol-$m^{-2}s^{-1}$ under irrigated and rainfed conditions respectively. These findings align with the results of the current study with some variations that may result from the differences in the environmental factors or the different wheat species under study. On the other hand, the studies conducted to get insights into the physiological health of the wheat plant by measuring the quantum yield of photosystem II (PhiPSII) on flag leaf reported it between 0.31 and 0.43 under optimum growth conditions (Slapakauskas and Ruzgas, 2005), and between 0.36 and 0.69 for the 50 cultivars grown under rainfed conditions, while between 0.50 and 0.68 for the control group planted to validate the readings (Jin et al. 2013).

These findings are in accordance with our results indicating that environmental conditions like temperature, drought and light intensity can affect both stomatal conductance and quantum yield of photosystem II. Moreover, in our study $gsw_1$is higher than gsw_2 indicating the changes in the plant's response to environmental conditions such as high temperature, drought, among others to ensure the survival by maintaining its water balance. On the other hand, PhiPSII actually indicates the photosynthetic capacity of the plants and is measured on the basis of the fixed number of oxygen or carbon dioxide molecules released or absorbed by the plants through a light quantum (Zhen & Bugbee, 2020). The experiment was conducted under rainfed conditions and gsw and PhiPSII indicate the presence of some promising genotypes that can be utilized in the future breeding programmes to develop drought tolerant cultivars.

Table 4.25. Analysis of variance (ANOVA) of genotypes under study for physiological traits

		Physiological traits			
Source of variation	**df**	**gsw_1**	**gsw_2**	**$PhiPSII_1$**	**$PhiPSII_2$**
Replication	3	52862	12509	0.141	0.045
Genotype (G)	89	38208**	23704**	0.031*	0.019^{ns}
Residuals	267	24127	15200	0.023	0.017
CV (%)		34.25	46.17	34.25	46.17

* P <.05, ** P <.01, *** P <.001, level of significance; df, degrees of freedom; gsw, stomatal conductance; PhiPSII, quantum yield of photosystem II.

Table 4.26. Mean data of Physiological parameters measured on third basal leaf and flag leaf.

	Stomatal conductance (mmolm-2s-1)			Quantum yield of PSII		
Genotype	**gsw_1**	**gsw_2**	**Mean**	**$PhiPSII_1$**	**$PhiPSII_2$**	**Mean**
TR38	494.0	170.9	332.4 ± 161.5	0.41	0.30	0.36 ± 0.06
TR9	425.3	213.8	319.5 ± 105.7	0.44	0.43	0.44 ± 0.00
TR74	241.4	175.3	208.3 ± 33.0	0.39	0.35	0.37 ± 0.02
TR83	301.3	137.6	219.4 ± 81.8	0.42	0.34	0.38 ± 0.04
TR45	244.7	205.9	225.3 ± 19.4	0.47	0.33	0.40 ± 0.07
TR25	357.9	105.6	231.7 ± 126.2	0.50	0.29	0.40 ± 0.11
TR7	152.9	157.6	155.3 ± 2.3	0.42	0.49	0.45 ± 0.04
TR97	267.7	141.1	204.4 ± 63.3	0.31	0.37	0.34 ± 0.03
TR39	392.2	103.3	247.7 ± 144.4	0.30	0.44	0.37 ± 0.07
TR41	325.8	184.8	255.3 ± 70.5	0.36	0.31	0.34 ± 0.02
TR67	304.9	181.0	242.9 ± 62.0	0.38	0.30	0.34 ± 0.04
TR62	146.0	89.0	117.5 ± 28.5	0.43	0.34	0.38 ± 0.05
TR72	258.7	170.9	214.8 ± 43.9	0.41	0.24	0.32 ± 0.08
TR68	326.8	121.6	224.2 ± 102.6	0.58	0.47	0.52 ± 0.05
TR19	326.5	258.6	292.5 ± 34.0	0.54	0.46	0.50 ± 0.04
TR86	391.4	230.5	311.0 ± 80.4	0.43	0.45	0.44 ± 0.01
TR64	269.8	205.7	237.8 ± 32.0	0.40	0.32	0.36 ± 0.04
TR105	373.4	177.8	275.6 ± 97.8	0.39	0.27	0.33 ± 0.06
TR13	256.7	103.2	180.0 ± 76.7	0.45	0.40	0.43 ± 0.03
TR58	316.6	159.3	238.0 ± 78.7	0.41	0.40	0.41 ± 0.01
TR91	432.1	156.6	294.4 ± 137.7	0.30	0.35	0.32 ± 0.03
TR102	343.2	153.4	248.3 ± 94.9	0.43	0.27	0.35 ± 0.08
TR81	288.8	174.1	231.5 ± 57.4	0.36	0.40	0.38 ± 0.02
TR65	267.7	230.7	249.2 ± 18.5	0.30	0.54	0.42 ± 0.12
TR23	281.9	155.7	218.8 ± 63.1	0.32	0.41	0.36 ± 0.04
TR31	518.3	228.5	373.4 ± 144.9	0.30	0.33	0.31 ± 0.01
TR92	184.1	143.7	163.9 ± 20.2	0.32	0.34	0.33 ± 0.01
TR17	260.1	230.8	245.4 ± 14.7	0.41	0.38	0.40 ± 0.01
TR5	231.7	198.0	214.8 ± 16.8	0.37	0.31	0.34 ± 0.03
TR90	181.7	249.3	215.5 ± 33.8	0.40	0.31	0.36 ± 0.05
TR8	212.6	239.3	226.0 ± 13.4	0.42	0.36	0.39 ± 0.03
TR14	64.3	88.0	76.1 ± 11.8	0.29	0.28	0.29 ± 0.01
TR73	300.4	258.6	279.5 ± 20.9	0.34	0.41	0.38 ± 0.04
TR70	352.7	150.3	251.5 ± 101.2	0.34	0.35	0.35 ± 0.00
TR44	251.2	202.7	226.9 ± 24.2	0.44	0.48	0.46 ± 0.02
TR28	576.6	214.3	395.5 ± 181.2	0.33	0.39	0.36 ± 0.03
TR1	341.7	188.8	265.3 ± 76.4	0.19	0.24	0.21 ± 0.03
TR52	379.2	115.9	247.6 ± 131.6	0.36	0.36	0.36 ± 0.00
TR20	339.7	210.1	274.9 ± 64.8	0.31	0.47	0.39 ± 0.08
TR35	169.3	208.6	189.0 ± 19.6	0.39	0.35	0.37 ± 0.02
TR50	291.9	168.2	230.0 ± 61.8	0.41	0.41	0.41 ± 0.00
TR53	379.6	250.0	314.8 ± 64.8	0.47	0.36	0.41 ± 0.06
TR103	184.8	133.6	159.2 ± 25.6	0.43	0.36	0.39 ± 0.03

Table 4.26 Continue

TR42	300.6	148.8	224.7 ± 75.9	0.38	0.33	0.35 ± 0.02
TR71	114.1	112.8	113.4 ± 0.6	0.25	0.31	0.28 ± 0.03
TR43	203.5	200.4	202.0 ± 1.5	0.56	0.30	0.43 ± 0.13
TR79	124.3	125.7	125.0 ± 0.7	0.39	0.28	0.33 ± 0.06
TR59	418.3	107.6	262.9 ± 155.3	0.46	0.32	0.39 ± 0.07
TR57	230.8	123.4	177.1 ± 53.7	0.46	0.38	0.42 ± 0.04
TR4	337.7	191.8	264.8 ± 73.0	0.50	0.31	0.41 ± 0.10
TR88	341.5	239.9	290.7 ± 50.8	0.30	0.36	0.33 ± 0.03
TR18	212.1	90.4	151.3 ± 60.9	0.53	0.43	0.48 ± 0.05
TR55	215.4	153.2	184.3 ± 31.1	0.60	0.39	0.50 ± 0.11
TR30	186.8	136.8	161.8 ± 25.0	0.43	0.40	0.41 ± 0.01
TR77	151.0	124.9	137.9 ± 13.0	0.61	0.42	0.52 ± 0.09
TR12	156.8	266.5	211.7 ± 54.9	0.47	0.37	0.42 ± 0.05
TR95	218.3	150.0	184.2 ± 34.2	0.57	0.31	0.44 ± 0.13
TR80	427.9	113.4	270.6 ± 157.3	0.40	0.39	0.39 ± 0.00
TR60	338.7	83.7	211.2 ± 127.5	0.61	0.29	0.45 ± 0.16
TR34	233.6	191.0	212.3 ± 21.3	0.51	0.43	0.47 ± 0.04
TR93	263.0	120.2	191.6 ± 71.4	0.29	0.40	0.35 ± 0.05
TR22	318.9	278.7	298.8 ± 20.1	0.53	0.39	0.46 ± 0.07
TR40	102.8	93.6	98.2 ± 4.6	0.55	0.40	0.47 ± 0.07
TR56	287.4	150.1	218.7 ± 68.7	0.24	0.30	0.27 ± 0.03
TR99	313.8	390.1	352.0 ± 38.2	0.37	0.40	0.38 ± 0.01
TR89	256.9	156.4	206.7 ± 50.2	0.54	0.36	0.45 ± 0.09
TR15	240.1	203.7	221.9 ± 18.2	0.26	0.44	0.35 ± 0.09
TR11	332.0	157.5	244.8 ± 87.2	0.47	0.36	0.41 ± 0.05
TR82	365.5	181.9	273.7 ± 91.8	0.42	0.43	0.42 ± 0.00
TR69	273.4	109.5	191.4 ± 81.9	0.43	0.57	0.50 ± 0.07
TR37	81.0	73.1	77.1 ± 4.0	0.40	0.30	0.35 ± 0.05
TR61	386.8	155.4	271.1 ± 115.7	0.44	0.29	0.36 ± 0.07
TR26	369.4	347.7	358.6 ± 10.8	0.23	0.27	0.25 ± 0.02
TR47	240.7	80.6	160.7 ± 80.0	0.45	0.41	0.43 ± 0.02
TR94	229.3	49.9	139.6 ± 89.7	0.44	0.26	0.35 ± 0.09
TR21	280.9	146.6	213.7 ± 67.1	0.42	0.50	0.46 ± 0.04
TR76	182.8	56.7	119.8 ± 63.1	0.32	0.40	0.36 ± 0.04
TR100	324.7	187.0	255.9 ± 68.8	0.45	0.49	0.47 ± 0.02
TR98	316.6	154.7	235.6 ± 80.9	0.32	0.36	0.34 ± 0.02
TR85	244.0	88.0	166.0 ± 78.0	0.40	0.35	0.38 ± 0.02
TR84	404.1	185.0	294.5 ± 109.5	0.39	0.39	0.39 ± 0.00
TR96	201.4	169.3	185.4 ± 16.1	0.46	0.44	0.45 ± 0.01
TR49	394.6	500.5	447.5 ± 53.0	0.27	0.35	0.31 ± 0.04
TR36	361.2	80.2	220.7 ± 140.5	0.35	0.39	0.37 ± 0.02
TR51	251.8	126.6	189.2 ± 62.6	0.32	0.37	0.35 ± 0.02
TR101	296.2	377.0	336.6 ± 40.4	0.31	0.37	0.34 ± 0.03
TR2	180.2	93.8	137.0 ± 43.2	0.43	0.48	0.45 ± 0.02
TR16	508.3	177.9	343.1 ± 165.2	0.49	0.45	0.47 ± 0.02

Table 4.26 Continue

TR87	236.8	238.9	237.8 ± 1.1	0.34	0.37	0.36 ± 0.01
TR54	261.8	207.3	234.6 ± 27.3	0.47	0.58	0.52 ± 0.06
Min	64.3	49.9	56.4	0.19	0.24	0.21
Max	576.6	500.5	538.6	0.61	0.58	0.59
Mean	285.8	172.7	225.2	0.41	0.37	0.39

Min, minimum; Max, maximum.

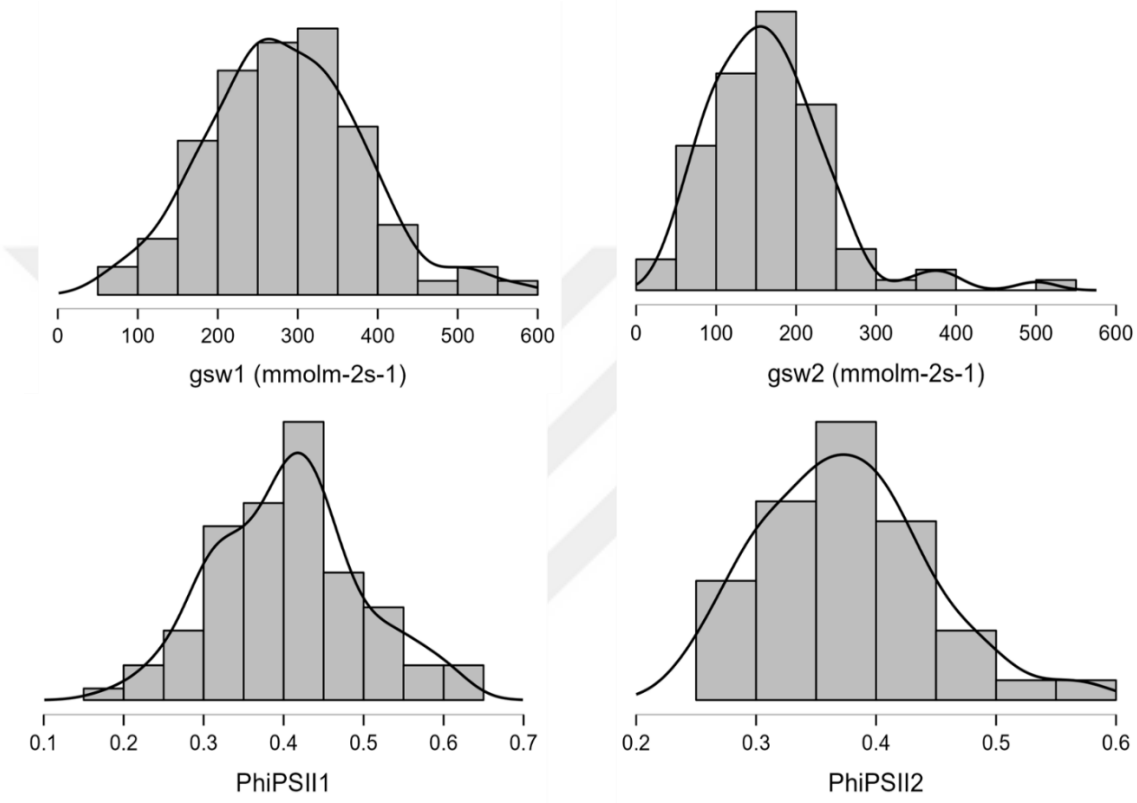

Figure 4.15. Graphical distribution of stomatal conductance and quantum yield of photosystem II measured on third basal leaf (gsw1&PhiPSII1) and flag leaf (gsw2&PhiPSII2), respectively.

4.4.4. Correlation analysis for two growing seasons

Correlation analysis was performed to determine the relationship between all the studied traits for each growing season separately to examine the trend of relationship across two growing seasons. The results revealed that days to heading (DTH) had significant and positive correlation with plant height (PH), spike length (SL), spikelets per spike (SPS) in the first growing season (2022-230, while the correlation with plant height was negative across second growing season (2023-24). Moreover, PH had significant positive correlation with SL, SPS, spikelet yield (SY) and grain yield (GY) in the first growing season, while the correlation with SL and SPS was non-significant in the second growing season. SL had significant positive correlation with SPS across both growing seasons, but the correlation with TKW was significant and negative in the second growing season. On the other hand, SPS was negatively correlated with SY and GY across both growing seasons. SY had

significant positive correlation with GY and TKW across both growing seasons. In addition to TKW, GY was also positively correlated with stomatal conductance (gsw). The relationship among all the studied traits across two years is given in the Figure 4.15.

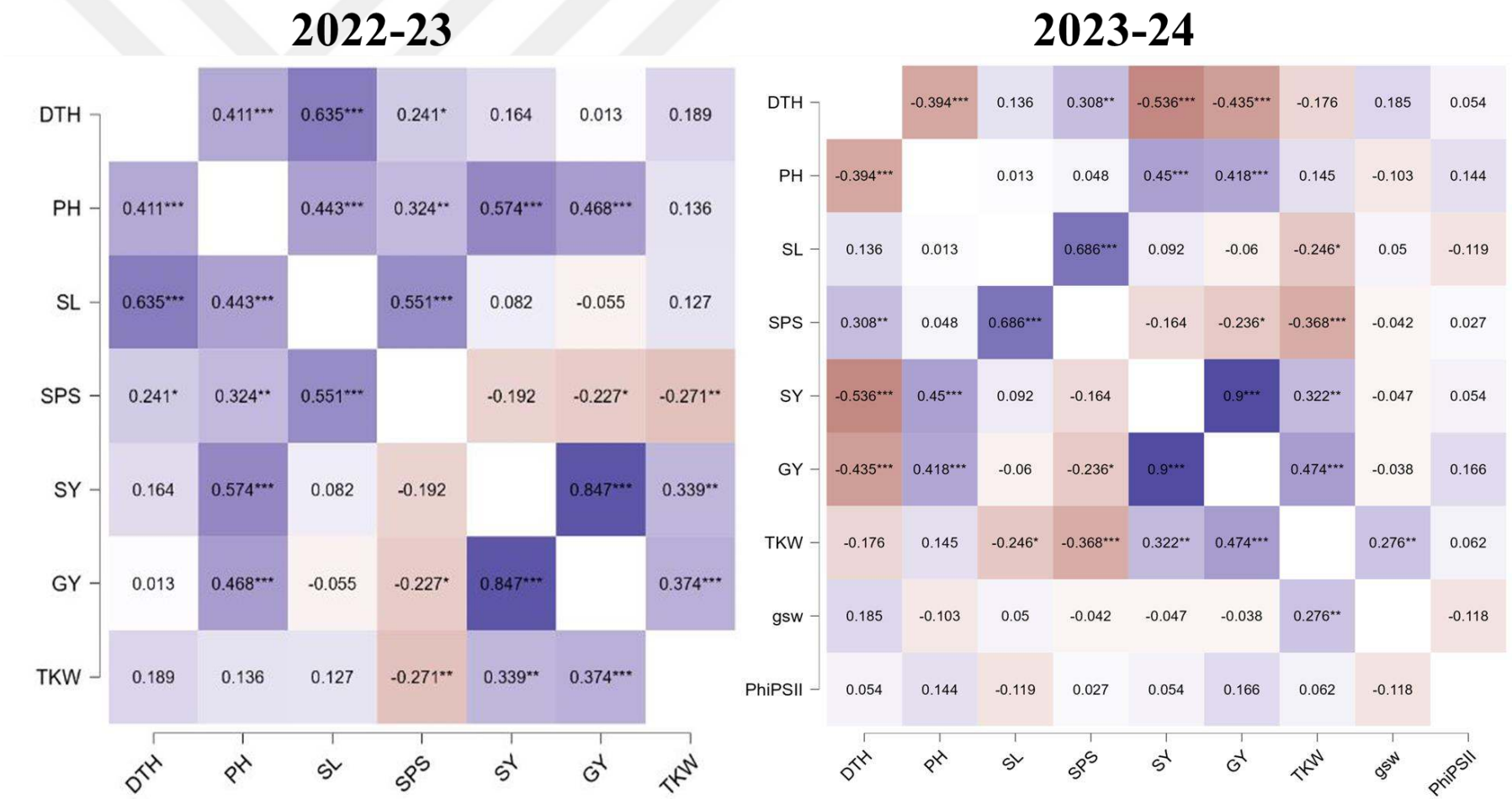

Figure 4.16. Correlation among the studied traits across two growing seasons (2022-23&2023-24).

4.4.5. Prinicpal component analysis for morpho-pysiological traits under study

Principle component analsis was also carried out for the traits measured in the field across two growing seasons (2022-23 and 2023-24) to identify the key components contributing to the total variations observed among the genotypes. As a result of PCA analysis, the first two pricipal components were the key compoents and explained 68.34 and 52.37 % in the first and second growing season, respectively (Table 4.26). Briefly, PC1 expalined 38.14 % and 32.09 % of the total variations, while PC2 explained 30.21 and 19.47 % of the total variations in the first and second growing season, respectively. The positive and negative loading of the variables show the direction, while the magnitude of the loadings show the strength of the relationship among the varables and the principal components. Moreover, the variables like plant height (PH), spikelet yield (SY), grain yield (GY) and days to heading were positvely correlated with the PC1 and were the major contributors of PC1 in the first growing season, while number of spikelets per spike (SPS) spike length (SL) and days to heaing (DTH) had the major contribtuin towards PC2 and were positively correlated with the PC2 in the first growing season. On the other hand, in the second growing season (2023-24), GY, SY and thouand kernel weight (TKW) had major contribution toward the variation explained by PC1, while SL, SPS and PH had positive correlation with PC2 and identified as major contributiors of the total variations explained by PC2 (Table 4.26). The relationship of the variables and their contributions to the principle components is furhther elaborated through biplots (Figure 4.16).

Table 4.27. Eigenvalues of PC1 and PC2 with contribution of each variable to PC1 and PC2 under control and drought stress.

	2022-23		2023-24	
Traits	**PC1**	**PC2**	**PC1**	**PC2**
DTH	0.35	0.35	-0.40	-0.07
PH	0.50	0.12	0.33	0.31
SL	0.33	0.49	-0.16	0.61
SPS	0.09	0.55	-0.28	0.58
SY	0.49	-0.32	0.49	0.26
GY	0.43	-0.40	0.51	0.15
TKW	0.29	-0.23	0.34	-0.26
gsw	-	-	-0.03	-0.18
PhiPSII	-	-	0.09	0.04
Eigenvalue	2.66	2.11	2.96	1.75
Percentage of variance (%)	38.14	30.21	32.09	19.47
Cumulative (%)	38.14	68.34	32.09	52.37

PC1, Principal component 1; PC2, Principal component 2.

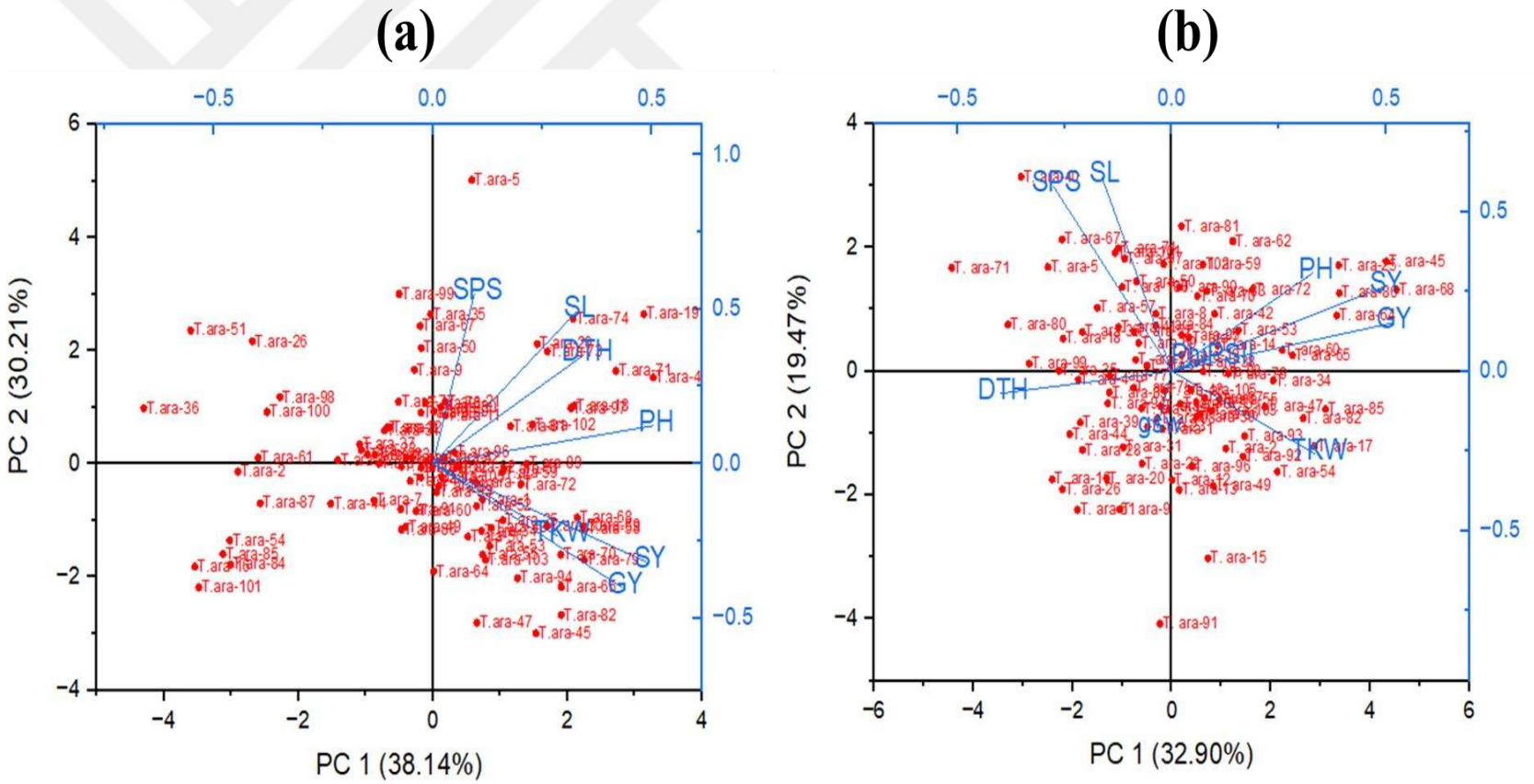

Figure 4.17. Biplot of morpho-physiological traits under study during two growing seasons (a) 2022-23 and (b) 2023-24.

5. CONCLUSIONS AND RECOMMENDATIONS

This study utilizes both controlled and field experimental settings to examine the drought tolerance and phenotypic diversity of *Triticum araraticum*. Specifically, two different experiments were carried out: one PEG-induced drought stress experiment to evaluate the potential of *T. araraticum* genotypes for drought tolerance at seedling stage and a two-year field experiment (2022-2023 and 2023-2024 growing seasons) under rainfed conditions to decipher the phenotypic diversity and drought tolerance of GGA^tA^t genome. The results of analysis of variance for drought stress experiment showed significant variations among genotypes and drought stress also significantly affected all the studied traits. Based on several seedling traits like shoot length, total root length and seedling vigour index 15 promising *T. araraticum* genotypes (TR60, TR14, TR41, TR1, TR45, TR62, TR103, TR96, TR38, TR97, TR55, TR30, TR7) were identified that can be used in the future breeding programmes to develop drought tolerant wheat cultivars. However, among other tetraploid species used for comparison, *T. dicoccoides* genotypes like DIC-232, DIC-73, DIC-107, DIC-126 performed well under drought stress and DIC-126 and DIC-232 were superior to most of the above-mentioned *T. araraticum* genotypes in terms of seedling vigour index.

On the other hand, field experiment was conducted to assess phenotypic diversity among *T. araraticum* genotypes for several morpho-physiological traits under rainfed conditions across two growing seasons. Analysis of variance revealed significant variations among genotypes, with the environment having a substantial effect on all the measured traits across both growing seasons. However, the interaction between genotype and environment was non-significant for most of the traits indicating the constant genotypic response to the change in environment in terms of the respective traits. Based on some agro-morphological traits like days to heading and grain yield, some promising *T. araraticum* genotypes (TR98, TR87, TR85, TR49, TR16, TR51, TR83, TR55, TR45, TR81, TR76, TR96, TR49) were identified, that can be used in the future wheat breeding programmes to develop early maturing cultivars. Some of these genotypes like TR96 and TR55 were also found promising for drought tolerance and indicate that they can be used to develop early maturing and drought tolerant cultivars.

Genetic diversity is a pre-requisite for all the wheat breeding programmes because it provides wheat breeders with diverse gene pool to develop crop cultivars with desired traits. Our results showed great variation among genotypes for both drought stress and morpho-physiological traits and identified some promising genotypes. Based on the results, it can be concluded that

1. Genotypes such as TR60, TR14, TR41, TR1, TR45, TR62, TR103, TR96, TR38, TR97, TR55, TR30, TR7 performed well and showed no or little reduction in seedling traits like shoot length, total root length and seedling vigour index under drought stress.

2. In comparison with *T. dicoccoides*, all the above-mentioned *T. araraticum* genotypes performed better in terms of shoot length, while for total root length and seedling vigour index the performance of both the wild relatives was comparable.
3. Based on the findings, *T. araraticum* also serve as a potential source of drought tolerance along with *T. dicoccoides*
4. The results of the field experiment also showed some promising genotypes that can be utilized in the wheat breeding programs to develop drought tolerant cultivars.

The findings revealed that the often-neglected genome of *Triticum araraticum* harbors significant potential for drought tolerance, making it a promising resource for developing drought tolerant wheat cultivars. However, the field experiment showed that grain yield of *T. araraticum* like other wheat wild relatives is very low. To fully harness the potential of *T. araraticum* in agriculture, de novo domestication strategies should be prioritized. By addressing yield limitations while preserving drought tolerance, breeders can unlock the genetic potential of this species and contribute to sustainable crop production in water-limited environments.

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APPENDICES

Supplementary Table 1. Mean data of seedling traits under control conditions.

Genotype	CL (cm)	SL (cm)	PRL (cm)	SRL (cm)	MSRL (cm)	TRL (cm)	TRN (cm)	GP (%)	SVI
TR-38	3.06	12.29	25.54	23.95	22.38	70.29	3.3	80	30.15
TR-9	3.68	15.57	19.82	17.62	16.23	52.28	4.1	100	35.39
TR-74	4.07	14.24	17.03	14.77	13.40	43.82	3.9	80	23.34
TR-83	3.81	16.84	20.73	21.77	20.45	61.64	3.6	90	34.30
TR-45	3.48	14.69	29.37	25.58	25.36	80.09	3.0	80	36.01
TR-25	3.45	15.31	26.48	21.59	21.11	68.71	3.9	100	41.79
TR-7	3.49	12.67	21.65	20.27	18.54	58.72	3.3	90	30.53
TR-97	4.05	17.59	24.94	20.03	18.77	62.48	3.5	70	29.88
TR-39	3.97	17.07	21.28	19.73	18.24	57.75	3.2	100	38.34
TR-41	3.68	13.51	23.59	18.67	17.93	59.45	3.2	90	33.36
TR-67	3.93	16.60	18.83	19.13	18.28	55.40	3.4	90	32.34
TR-62	3.89	12.50	21.35	19.71	18.53	58.41	3.6	100	33.85
TR-72	3.69	16.52	23.63	24.19	21.88	67.39	3.9	100	40.93
TR-68	3.22	10.87	20.25	21.52	20.95	62.14	3.8	90	29.80
TR-19	3.64	16.55	22.65	23.05	22.45	67.56	3.8	80	31.36
TR-86	3.23	12.93	19.77	22.26	21.49	62.76	3.0	70	25.55
TR-64	3.11	11.91	21.29	18.98	17.80	56.90	3.6	100	33.20
TR-105	3.07	10.99	19.62	18.94	17.62	54.87	3.2	90	27.83
TR-13	4.40	17.74	25.32	22.62	21.51	68.34	3.1	100	43.06
TR-58	3.56	12.95	21.15	23.72	20.32	61.78	3.5	100	36.66
TR-91	3.65	14.04	22.54	21.86	21.12	64.78	3.2	100	37.80
TR-102	4.11	16.33	20.92	21.90	21.40	63.72	3.4	90	35.83
TR-81	4.11	15.42	20.91	21.96	20.17	61.24	3.4	70	26.56
TR-65	3.82	14.37	23.90	23.11	20.30	64.49	3.8	90	34.35
TR-23	3.67	15.81	19.65	22.05	19.66	58.97	3.0	70	27.06
TR-31	3.41	15.42	22.32	21.41	19.88	62.07	3.6	80	29.64
TR-92	3.50	13.80	22.30	20.74	17.36	57.02	3.0	90	32.91
TR-17	4.30	18.78	21.22	20.19	19.23	59.68	3.3	80	33.19
TR-5	3.69	15.92	21.45	21.93	19.83	61.11	3.1	100	39.24
TR-90	3.86	16.60	21.73	19.26	18.61	58.95	3.2	90	34.90
TR-8	4.09	17.24	21.89	20.78	20.71	63.31	2.6	90	34.74
TR-14	2.86	11.99	17.43	20.56	17.97	53.38	3.0	90	28.94
TR-73	4.65	21.02	24.37	24.38	21.74	67.85	3.6	100	46.63
TR-70	3.83	14.58	22.21	22.03	20.30	62.81	2.8	90	33.14
TR-44	3.55	13.05	19.51	17.68	16.24	51.98	3.2	90	28.74
TR-28	3.45	14.09	21.73	20.68	20.06	61.86	3.3	100	35.84
TR-1	3.45	12.66	19.95	16.58	16.20	52.35	3.5	100	32.61
TR-52	3.94	17.07	29.74	23.16	22.39	74.51	3.5	100	46.80
TR-20	4.53	18.72	25.86	22.82	21.70	69.26	3.1	80	35.03
TR-35	4.50	16.44	20.52	21.00	19.01	58.54	2.9	80	31.72
TR-50	4.03	16.80	20.69	19.84	19.11	58.90	3.8	100	38.34
TR-53	4.06	18.98	21.17	19.37	18.41	57.98	3.8	80	31.98
TR-103	3.17	13.51	20.49	18.89	17.38	55.26	3.4	80	28.21

TR-42	3.48	15.14	19.90	18.08	17.51	54.92	3.0	100	35.06
TR-71	3.58	13.10	19.77	17.17	15.39	50.56	3.0	80	26.92
TR-43	3.82	16.60	21.75	17.66	15.69	53.12	3.5	90	35.12
TR-79	3.51	12.90	21.26	19.59	19.33	59.93	3.0	80	27.33
TR-59	4.05	16.75	24.71	23.34	21.62	67.94	3.1	90	37.83
TR-57	3.77	16.45	23.93	21.84	19.80	63.53	2.8	100	40.38
TR-4	4.51	18.78	22.00	19.46	18.06	58.12	3.6	100	40.78
TR-88	4.58	18.80	20.89	22.04	18.70	58.30	3.3	100	41.24
TR-18	4.46	18.15	27.41	20.66	20.25	67.92	3.0	100	45.56
TR-55	3.90	16.29	19.73	19.44	17.73	55.19	3.4	90	34.38
TR-30	3.81	17.61	22.54	19.95	19.82	62.18	3.5	90	36.54
TR-77	4.42	19.32	25.00	23.83	20.12	65.24	3.8	100	44.32
TR-12	3.65	16.31	21.57	19.77	20.05	61.67	2.9	100	37.87
TR-95	3.06	11.38	16.67	15.67	15.53	47.74	2.6	100	28.05
TR-80	3.25	16.62	18.10	16.57	16.55	51.21	2.7	100	34.72
TR-60	3.66	14.50	17.36	15.47	14.33	46.01	3.3	100	31.96
TR-34	3.84	16.16	21.93	20.57	19.84	61.61	3.1	90	34.41
TR-93	4.02	17.56	22.68	22.05	20.28	63.24	3.4	100	40.82
TR-22	3.44	18.06	20.22	19.06	18.38	56.98	3.7	100	38.29
TR-40	2.43	10.88	16.75	15.46	14.63	39.94	2.6	70	19.75
TR-56	4.20	16.88	22.83	22.09	21.27	65.37	2.9	100	39.82
TR-99	3.24	14.82	23.95	22.09	21.76	67.46	3.3	80	30.53
TR-89	3.80	14.58	22.40	19.16	18.54	59.47	3.7	100	36.97
TR-15	4.06	18.65	25.32	24.73	23.29	71.89	3.3	90	41.25
TR-11	3.81	15.69	22.01	24.86	21.04	64.09	2.8	90	36.84
TR-82	3.11	14.23	19.13	21.01	19.03	57.20	3.1	90	32.58
TR-69	3.90	13.98	22.07	19.48	18.56	59.18	4.2	90	32.86
TR-37	3.80	15.44	22.09	20.27	19.56	61.21	3.1	100	37.53
TR-61	4.21	17.63	23.83	21.26	18.82	61.48	2.8	100	41.46
TR-26	3.22	11.53	18.50	19.03	16.94	52.38	2.6	90	28.34
TR-47	4.40	18.76	25.47	24.80	23.77	73.01	3.3	100	44.28
TR-94	3.75	12.53	22.07	19.07	17.82	57.71	3.6	80	27.68
TR-21	3.88	13.52	22.53	19.13	16.94	56.41	3.6	100	36.05
TR-76	3.96	17.56	17.03	16.33	15.09	47.20	3.2	80	28.06
TR-100	4.11	15.29	21.01	16.43	15.93	52.88	2.8	100	36.30
TR-98	3.60	14.02	22.66	20.57	19.54	61.75	3.9	100	36.68
TR-85	4.28	17.94	21.96	19.68	19.46	60.88	3.2	100	39.90
TR-84	3.47	13.07	18.04	14.84	14.11	46.26	3.0	100	31.11
TR-96	4.16	17.17	21.15	21.69	19.36	59.88	3.6	90	35.55
TR-49	4.36	18.95	28.52	24.85	24.31	77.14	3.4	100	47.47
TR-36	3.85	12.78	21.57	15.42	14.76	51.09	3.1	80	27.48
TR-51	3.51	16.03	19.44	18.08	17.27	53.99	3.0	90	33.04
TR-101	4.22	20.53	21.72	22.36	21.83	65.38	3.4	100	43.25
TR-2	3.75	17.62	24.96	23.60	23.04	71.05	3.4	100	42.58
TR-16	3.69	20.45	23.21	24.28	22.67	68.55	3.0	90	40.91
TR-87	3.96	16.96	26.47	24.30	22.87	72.21	3.2	100	43.43

TR-54	4.23	17.15	23.91	23.45	22.14	68.19	3.2	100	41.85
IRIDE	3.26	15.39	31.66	29.00	28.21	88.09	5.9	100	47.06
Inbar	3.82	18.29	29.89	29.03	27.15	84.20	5.0	100	48.19
Çeşit-1252	3.60	15.73	26.95	24.85	24.44	75.83	3.9	100	42.68
Svevo	3.71	15.86	33.11	29.07	27.81	88.72	4.8	100	48.97
Kızıltan.91	3.51	17.45	28.61	25.70	24.97	78.54	3.8	90	41.36
DIC-030	3.75	19.19	20.27	18.84	17.59	55.46	2.8	90	36.17
DIC-246	4.65	22.96	22.83	23.94	22.20	67.23	3.4	100	46.89
DIC-062	3.81	19.09	24.37	23.92	23.41	71.18	3.5	90	39.85
DIC-073	4.16	19.85	21.39	18.19	17.54	56.47	3.7	90	37.21
DIC-163	4.67	22.03	34.09	34.42	34.03	102.15	2.9	100	56.99
DIC-232	3.34	12.62	17.11	13.56	12.82	42.76	2.8	100	29.73
DIC-249	3.92	18.58	20.10	18.58	18.59	57.28	3.5	90	35.32
DIC-395	3.78	15.28	24.72	23.23	23.00	70.72	3.7	100	40.00
DIC-399	4.94	21.32	27.31	25.38	25.12	77.55	5.3	100	48.64
DIC-038	3.57	14.54	22.00	17.56	15.76	53.51	3.1	90	32.81
DIC-012	3.62	16.09	20.79	19.18	17.76	56.31	2.9	100	36.88
DIC-107	4.26	17.39	20.68	22.40	20.54	61.76	3.0	70	28.10
DIC-126	4.33	22.93	21.40	22.09	21.22	63.84	3.4	80	36.01
TD-010	3.54	16.48	22.74	19.34	16.89	56.53	2.8	90	34.91
Minimum	2.43	10.87	16.67	13.56	12.82	39.94	2.58	70.00	19.75
Maximum	4.94	22.96	34.09	34.42	34.03	102.15	5.90	100.00	56.99
Mean	3.80	16.04	22.43	21.00	19.77	61.90	3.36	92.11	36.01

Supplementary Table 2. Mean data of seedling traits under drought stress.

Genotype	CL (cm)	SL (cm)	PRL (cm)	SRL (cm)	MSRL (cm)	TRL (cm)	TRN	GP (%)	SVI
TR-38	3.02	9.87	14.11	15.44	13.81	41.73	3.0	80	20.25
TR-9	3.77	11.84	15.13	11.70	10.03	35.18	3.4	80	21.58
TR-74	3.20	9.90	9.53	9.68	8.43	26.39	3.5	60	10.82
TR-83	3.22	10.14	16.24	13.67	12.71	41.65	3.3	70	18.87
TR-45	3.27	12.63	16.23	18.21	17.78	51.78	3.3	60	18.51
TR-25	3.25	8.89	14.15	13.22	12.39	38.93	3.5	80	17.63
TR-7	3.95	13.95	19.37	18.02	14.48	48.32	3.0	80	25.21
TR-97	4.49	13.05	19.43	23.80	19.72	58.88	2.9	80	29.13
TR-39	3.29	13.59	15.98	16.00	13.28	42.55	3.2	60	18.05
TR-41	3.68	13.37	19.29	17.64	14.35	48.00	3.0	50	15.59
TR-67	3.69	10.28	16.30	10.44	9.66	32.38	2.3	50	13.22
TR-62	3.83	10.42	17.66	16.14	15.68	49.02	2.9	70	18.59
TR-72	3.55	10.26	17.61	14.96	13.94	45.48	3.1	100	27.87
TR-68	3.06	6.15	12.87	8.49	7.35	27.57	3.1	90	17.76
TR-19	3.19	12.47	18.50	17.22	13.21	44.93	3.3	40	13.53
TR-86	3.29	9.47	15.57	12.49	11.10	37.77	3.2	70	19.83
TR-64	3.29	5.36	12.32	11.29	10.27	32.87	2.8	50	10.03
TR-105	2.65	8.67	14.37	13.36	12.95	40.27	2.7	60	15.73
TR-13	3.51	12.26	21.92	17.49	15.43	52.78	3.1	60	19.16
TR-58	3.79	9.53	15.97	14.10	13.17	42.31	3.1	80	20.42
TR-91	3.17	3.91	12.24	13.64	11.34	17.68	3.0	60	6.43
TR-102	3.20	5.74	11.52	11.19	10.50	32.51	3.3	70	11.84
TR-81	3.48	4.10	8.70	8.39	7.83	24.37	3.0	70	9.67
TR-65	2.18	4.33	10.12	7.37	6.96	24.03	2.9	50	6.15
TR-23	2.91	6.55	11.15	10.73	10.05	27.99	3.0	50	8.35
TR-31	3.44	7.28	17.18	14.50	13.52	36.46	2.3	70	16.97
TR-92	3.00	9.33	21.90	17.90	14.13	50.16	2.7	40	12.67
TR-17	3.96	10.71	15.46	11.94	11.12	37.69	2.8	80	21.29
TR-5	2.29	6.03	12.17	10.06	8.57	29.30	2.8	90	16.73
TR-90	2.82	6.58	15.10	8.37	7.34	29.78	3.0	70	15.69
TR-8	3.96	7.50	17.42	14.01	11.51	40.45	3.0	60	16.34
TR-14	3.80	12.50	17.99	19.36	17.31	52.61	2.8	80	24.34
TR-73	3.25	6.94	14.54	12.79	10.34	35.23	3.0	60	12.75
TR-70	3.65	9.58	19.13	17.34	15.82	50.77	2.7	70	19.20
TR-44	3.05	9.90	12.99	18.45	15.32	43.62	2.9	70	20.13
TR-28	2.94	10.88	15.54	14.86	11.54	38.63	3.5	70	21.80
TR-1	3.51	11.65	18.73	10.03	8.19	35.12	3.3	60	18.29
TR-52	2.94	8.25	14.64	14.53	10.71	36.06	3.3	60	13.76
TR-20	3.20	9.96	10.81	6.03	5.29	21.39	3.0	40	8.31
TR-35	2.90	8.92	19.76	8.45	8.07	31.08	2.6	60	17.20
TR-50	3.44	11.25	18.87	17.15	15.53	49.92	3.0	40	11.52
TR-53	3.65	11.59	18.22	15.63	14.52	47.26	3.0	80	23.85
TR-103	3.80	10.42	22.08	15.41	11.89	45.87	3.4	80	25.47
TR-42	3.15	8.36	15.48	11.58	8.56	18.71	3.0	100	23.84

TR-71	3.30	10.24	18.51	17.85	14.46	47.43	3.3	40	11.96
TR-43	3.44	10.67	14.29	12.00	11.50	37.29	2.8	70	17.22
TR-79	3.05	7.61	12.91	10.51	9.03	30.98	3.0	50	14.04
TR-59	3.42	11.14	18.30	16.97	15.10	48.51	3.0	80	23.74
TR-57	3.73	12.31	17.88	16.58	15.15	48.18	3.0	80	24.77
TR-4	3.72	12.35	17.51	15.72	14.94	47.38	3.8	70	20.82
TR-88	4.78	16.18	19.06	17.11	14.57	48.21	3.2	90	31.70
TR-18	3.39	12.11	16.54	15.59	15.37	47.28	2.7	70	21.25
TR-55	3.05	12.01	17.24	16.19	15.13	47.50	3.4	100	29.91
TR-30	3.94	13.80	18.25	13.29	11.76	41.78	3.5	100	32.05
TR-77	3.28	12.38	18.80	15.14	14.11	47.02	3.2	100	31.19
TR-12	2.93	9.67	14.22	15.97	15.04	44.29	2.9	80	22.24
TR-95	2.84	8.28	18.04	13.13	11.06	40.15	2.9	70	18.31
TR-80	3.17	9.39	14.71	11.44	8.13	30.97	3.0	60	13.91
TR-60	3.25	15.47	18.69	20.57	16.50	51.68	3.3	40	14.46
TR-34	2.50	8.52	16.80	11.75	11.38	34.87	2.3	70	17.31
TR-93	3.13	6.53	12.83	10.06	9.28	31.39	2.6	80	18.03
TR-22	2.33	6.13	10.12	7.26	6.58	23.27	3.1	60	13.74
TR-40	2.70	4.36	6.93	8.01	7.39	21.71	2.8	60	8.55
TR-56	2.73	7.32	10.97	9.56	8.24	27.45	3.2	70	11.67
TR-99	2.78	9.44	10.22	9.20	7.86	25.94	3.0	60	14.17
TR-89	3.27	7.29	12.06	9.76	9.00	30.07	2.9	90	18.23
TR-15	3.05	7.33	9.55	8.63	7.99	23.69	2.6	90	16.04
TR-11	2.91	5.81	9.56	6.94	6.08	21.73	2.4	90	13.60
TR-82	2.76	7.08	8.50	7.00	6.69	21.89	2.9	80	12.30
TR-69	3.06	7.17	10.30	8.95	7.85	26.00	3.7	70	12.63
TR-37	3.08	5.94	11.00	7.14	5.75	22.50	2.6	100	16.95
TR-61	3.13	9.55	13.97	10.62	8.79	31.55	2.8	60	14.11
TR-26	2.69	4.97	8.81	6.38	6.38	9.80	3.0	50	13.78
TR-47	3.44	9.78	13.53	10.35	9.15	31.83	2.9	100	23.30
TR-94	2.73	5.45	10.35	8.11	6.02	21.20	2.3	80	14.76
TR-21	2.68	6.48	9.36	8.38	6.96	23.29	2.8	90	14.03
TR-76	3.70	10.82	12.41	11.04	9.75	31.92	2.5	100	23.95
TR-100	3.17	10.51	14.23	9.61	8.95	32.13	2.6	90	21.44
TR-98	3.34	7.96	13.19	11.20	10.12	33.44	3.0	80	16.92
TR-85	3.33	11.66	15.80	13.50	13.61	33.27	3.0	90	23.89
TR-84	2.38	6.82	9.27	7.52	6.43	22.12	2.6	70	9.73
TR-96	4.60	14.77	24.67	18.84	18.55	61.77	3.3	60	23.66
TR-49	2.91	6.24	15.89	12.66	12.27	40.43	2.6	70	15.71
TR-36	2.32	3.98	6.59	7.17	7.17	9.18	2.8	80	8.92
TR-51	3.38	9.95	17.24	9.68	7.74	32.71	2.8	50	12.27
TR-101	3.96	10.48	15.72	9.93	8.73	33.18	2.8	100	26.20
TR-2	3.06	9.69	12.54	14.68	11.22	34.98	3.5	80	20.30
TR-16	3.23	11.47	17.43	12.74	11.05	39.53	2.9	80	22.77
TR-87	3.26	9.57	12.26	9.27	7.69	27.63	2.9	80	18.54
TR-54	3.21	8.48	11.79	11.34	9.80	31.40	3.0	60	14.26

IRIDE	3.39	13.11	21.97	20.30	19.64	61.26	4.7	100	36.45
Inbar	3.29	14.87	20.81	20.19	18.98	58.78	4.8	100	35.81
Çeşit-1252	3.14	13.42	18.62	15.50	13.50	45.62	3.6	100	32.04
Svevo	3.05	13.70	17.49	17.62	14.91	47.31	3.5	90	30.23
Kızıltan.91	3.46	13.02	18.91	17.96	16.60	52.11	3.3	100	32.49
DIC-030	3.33	11.27	16.66	13.57	10.96	38.58	2.7	80	23.26
DIC-246	3.75	14.58	18.48	15.15	15.16	48.79	3.0	50	17.03
DIC-062	3.20	9.03	16.20	13.54	12.26	40.73	2.6	60	14.93
DIC-073	3.56	12.28	21.28	18.91	15.98	53.25	3.1	70	23.24
DIC-163	3.44	10.04	13.65	15.25	13.88	41.42	2.9	100	27.01
DIC-232	2.32	10.40	16.59	7.14	7.14	15.24	2.6	50	26.99
DIC-249	2.53	6.37	8.96	7.67	7.08	21.38	2.5	50	10.03
DIC-395	2.81	11.40	14.47	14.91	11.29	37.05	3.1	80	22.77
DIC-399	2.97	15.74	17.32	16.01	13.12	43.55	4.0	90	29.87
DIC-038	2.88	10.37	13.78	12.26	9.64	33.06	2.5	60	13.25
DIC-012	2.67	9.10	13.21	8.63	6.78	26.77	2.8	70	15.07
DIC-107	3.29	12.12	19.82	19.21	16.77	53.35	2.7	80	25.20
DIC-126	3.91	13.86	15.38	18.63	18.38	52.14	3.0	100	33.41
TD-010	3.35	12.32	20.81	15.06	13.30	47.40	2.8	80	26.50
Minimum	2.18	3.91	6.59	6.03	5.29	9.18	2.30	40.00	6.15
Maximum	4.78	16.18	24.67	23.80	19.72	61.77	4.80	100.00	36.45
Mean	3.24	9.78	15.21	13.08	11.54	37.28	3.01	72.94	18.98