# REVIEW



# **Comparison of durum with ancient tetraploid wheats from an agronomical, chemical, nutritional, and genetic standpoints: a review**

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**Abstract** Under intense breeding, modern wheats, such as durum (*Triticum turgidum L*. ssp. *durum)*, are believed to have lost nutritional quality and protein content while increasing productivity. Emmer (*Triticum turgidum* ssp*. dicoccum* Thell) and wild emmer (*Triticum turgidum* ssp. *dicoccoides*) are alternative resources for breeding programs by ofering favorable alleles to be introgressed into modern materials and thus broadening their genetic diversity. Studies conducted so far have shown that durum wheat has better performance in agronomical qualities and protein quality than *T. dicoccum* and *T. dicoccoides*. However, its grain protein content (GPC) and Fe/Zn concentrations are lower. Several QTL for yield, GPC, and nutrient content in *T. dicoccoides* have been described, demonstrating its potential for transfer of important genes such as *Gpc-B1* into modern cultivars. The *Gpc-B1* gene increased the grain protein and

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Fe and Zn contents, but the agronomic performance of some of the modern recipients was reduced. Understanding the correlations and relationships between agronomic, chemical, and nutritional qualities would simplify selection through breeding for a single trait. Combining this knowledge with conventional breeding, MAS, and new breeding techniques would facilitate the QTL studies in these ancestral wheats and the development of new durum cultivars while retaining the agronomic qualities. In this review, we compare some grain parameters of *T.* durum, *T. dicoccum*, and *T. dicoccoides* wheats, including Fe and Zn content and their genetic aspects, and the existing information is analyzed and integrated for the future prospects of durum wheat improvement.

**Keywords** Durum wheat · Ancestral tetraploid wheats  $\cdot$  Grain qualities  $\cdot$  Zn and Fe content  $\cdot$  QTL

# **Introduction**

Wheat is a staple food for nearly one-third of the world's population, making it relevant for global food security (Sing et al. [2022\)](#page-19-0). In fact, most of the products found in the market derive from bread wheat (*Triticum aestivum* L.–a hexaploid species; 2*n*=6*x*=42 chromosomes) and durum wheat (*Triticum turgidum* L. ssp. *durum*–a tetraploid species;  $2n=4x=28$  chromosomes). Even though the area cultivated with durum wheat constitutes only about 5% of the total wheat growing area, durum is important for human nutrition, and it is mainly used for pasta, couscous, and other semolina-based products widely consumed in many areas of the world (Sharma et al. [2019\)](#page-19-1).

Durum grain contains vitamins and micronutrients, which may contribute to a healthy diet. However, their levels are insufficient; considering that a large number of people around the world rely on durum as their main staple, which is strongly related to inadequate food intake and the low nutrient content of staple foods such as wheat (Swamy et al. [2021\)](#page-20-0). Currently, there is a demand for healthy and nutritious crops that are not intensively bred and produced (Longin et al. [2016](#page-18-0)). In this context, ancient tetraploid wheats  $(2n=4x=28, AABB$  genome) such as wild emmer (*Triticum turgidum* ssp. *dicoccoides*) and its domesticated form, emmer (*Triticum turgidum* ssp. *dicoccum* Thell.) are gaining popularity, marketed as an alternative to improve the grain quality and the nutritional value. These stocks can be used to introgress favorable alleles into modern cultivars, to broaden their genetic diversity. Much of this appears to be happening in durum breeding programs (Cakmak et al. [2004;](#page-15-0) Kuznetsova et al. [2019;](#page-17-0) Biradar et al. [2022\)](#page-15-1).

Despite the popularity and usefulness of these ancient tetraploid wheats, there is limited and dispersed information on their qualities. This review aims to compile and compare the existing information about agronomic, chemical, and nutritional grain parameters between modern (*T. durum*) and ancient tetraploid wheats (*T. dicoccum* and *T. dicoccoides*). This may beneft durum wheat breeding programs, growers, the food industry, and consumers.

# *T. durum*, *T*. *dicoccum*, and *T. dicoccoides* domestication and generalities about their qualities

Durum wheat, *T*. *dicoccum*, and *T. dicoccoides* belong to the Poaceae family. They evolved naturally through hybridization of a wild diploid wheat *T. urartu*  $(2n=2x=14, AA$  genome), with goat grass *Aegilops speltoides*  $(2n=2x=14, BB)$ genome). Neither of the two was ever domesticated (Dvorák et al. [1993\)](#page-16-0), The frst hybridization event resulted in a hulled type of wheat known as *T. dicoccoides,* some 300,000–500,000 years before present (yr BP). *T. dicoccoides* naturally grows in the Fertile Crescent and it was rediscovered in 1906 by Aaron Aaronsohn in eastern Galilee. Domestication of *T. dicoccoides* appears to have occurred at multiple sites independently in the Levant region (Peng et al. [2011\)](#page-19-2). Through the process of domestication and selection made by hunter-gatherers, the cultivated form known as emmer (*T. dicoccum* or *dicoccon),* another hulled wheat, appeared about  $10,000$  years BP (Peng et al.  $2011$ ), most likely in the southeast Turkey (Özkan et al. [2005](#page-18-1)). Around 8,500 years ago, a more easily thresheable form appeared, probably as a consequence of selection and spontaneous mutations (Özkan et al. [2005](#page-18-1)). Geographic distribution of *T*. *dicoccum* and *T. dicoccoides* has changed through the domestication process; currently, *T. dicoccum* is mainly present in Ethiopia, Iran, Turkey, Central Europe, Italy, Spain, and India (Biradar et al. [2022\)](#page-15-1) while *T. dicoccoides* is narrowly distributed in Turkey, Iraq, and Iran (Özkan et al. [2011\)](#page-18-2). Due to the long history of cultivation in a wide range of environments, broad genetic diversity is evident in these ancient wheats (Biradar et al. [2022](#page-15-1)). This offers avenues for enhancing quality and nutritional value of durum wheat.

The quality traits of durum wheat meet the requirements of farmers, food industries, and consumers. It is used mainly to produce pasta products (Araya-Flores et al. [2020](#page-14-0)). Durum is expected to produce high vitreous kernels content≥90%, test weight≥80 kg hL−1, hardness, moisture content≤14%, protein content≥13%, and bright yellow color, and high semolina extraction yield (Colasuonno et al. [2019](#page-15-2)). These parameters do not directly address the nutritional value, such as the content of minerals, like zinc (Zn) and iron (Fe). Which can mitigate micronutrient defciencies, known as "hidden hunger"; a consequence of the low intake and absorption of these micronutrients (Lowe [2021\)](#page-18-3).

The quality of *T. dicoccum* and *T. dicoccoides* is related to their high protein content (Stehno [2007\)](#page-20-1) with high degree of digestibility and an appropriate amino acid profle (Kuznetsova et al. [2019\)](#page-17-0) and serving as a source of antioxidants and minerals (Cak-mak et al. [2004\)](#page-15-0) with high fiber content and resistant starch (Mohan and Malleshi [2006](#page-18-4)), and low glycemic index. These are valuable for diabetic nutrition (Buvaneshwari et al. [2003\)](#page-15-3). Making wild tetraploid species attractive resources for durum wheat breeding programs, which aim at the improvement of quality and nutritional value of the grain (Anuarbek et al. [2020;](#page-14-1) Biradar et al. [2022](#page-15-1)).

## **Agronomic quality traits**

# Yield

Increased grain yield has been one of the most important selection goals in crop breeding, including wheat. However, because yield is a multifactorial trait regulated by multiple genes, environmental factors, and their interactions, phenotypic selection has never been simple (Arriagada et al. [2020\)](#page-14-2). With a large number of genotypes and a wide range of environments in which durum, *T. dicoccum*, and *T. dicoccoides* are grown, grain yield ranges reported worldwide are wide. The largest producer of durum wheat is the European Union (EU), followed by Canada, Turkey, the United States, Algeria, Mexico, Kazakhstan, Syria, and India (EUROSTAT [2022;](#page-16-1) AAFC [2022;](#page-14-3) USDA [2022](#page-20-2)). Reported average durum grain yields range between 1.6 and 6.5 t ha<sup>-1</sup> of grains (Longin et al. [2016;](#page-18-0) Atar and Kara [2017](#page-14-4); Özberk [2018;](#page-18-5) Rachoń et al. [2020](#page-19-3); Chaieb et al. [2020;](#page-15-4) USDA [2022;](#page-20-2) AAFC [2022](#page-14-3); EC [2022;](#page-16-2) ODEPA [2022](#page-18-6)). This includes rainfed and irrigated areas; for example, during the 2021/22 season the average grain yield in the Northern Plains of the USA, under rainfed conditions, was 1.6 t ha<sup> $-1$ </sup>, while in the same year, in Chile, on irrigated area, the average grain yield was  $6.5$  t ha<sup>-1</sup> (ODEPA [2022\)](#page-18-6).The range for grain yield of *T. dicoccum* was 1.8–4.3 t ha−1 (Troccoli and Codianni [2005](#page-20-3); De Vita et al. [2006](#page-16-3); Pagnotta et al. [2009](#page-18-7); Marino et al. [2016](#page-18-8); Longin et al. [2016;](#page-18-0) Atar and Kara [2017](#page-14-4); Rachoń et al. [2020](#page-19-3); Biel et al. [2021](#page-15-5); Ehsanzadeh et al. [2021;](#page-16-4) Biradar et al. [2022](#page-15-1)). Unfortunately, no recent data for *T. dicoccoides* is available.

In general, grain yields reported for durum were higher than for *T. dicoccum* (Table [1\)](#page-3-0). Rachon et al. [\(2020](#page-19-3)) lists a diference of 46% between the average yield of durum  $(6.0 \text{ t ha}^{-1})$  and *T. dicoccum*  $(3.2 \text{ t})$  $ha^{-1}$ ) in a study performed in different environments from 2015 to 2017, in Poland. Longin et al. ([2016\)](#page-18-0) observed a 41% lower yield in *T. dicoccum* (3.6 t ha<sup>-1</sup>) than durum (6.1 t ha<sup>-1</sup>) in a study at four locations in Germany. Lower *T. dicoccum* yields compared to durum could be attributed to a less intensive breeding process, resulting in "the primitiveness" of the *T. dicoccum*, as described by Ehsanzadeh et al. [\(2021](#page-16-4)). This results in smaller grain (Pagnotta et al. [2009\)](#page-18-7) with lower remobilization of assimilates into the grain, a high number of non-reproductive tillers (Ehsanzadeh et al. [2021](#page-16-4)), taller plants prone to lodging (Longin et al. [2016](#page-18-0)), and, on the other hand, high protein/nutrient content (Pagnotta et al. [2009\)](#page-18-7) relative to the cultivated materials.

Despite its lower grain yields, studies have shown that the performance of *T. dicoccum* is more stable than durum across diferent environments, even under (abiotic) stresses such as drought (Ehsanzadeh et al. [2021\)](#page-16-4). This suggests better adaptation to environmental stressors (Longin et al. [2016;](#page-18-0) Rachoń et al. [2020;](#page-19-3) Ehsanzadeh et al. [2021\)](#page-16-4) or higher plasticity. Durum wheat, and modern wheats in general, are more susceptible to abiotic and biotic stressors perhaps as a consequence of extensive breeding selection over time for good adaptation to specifc environments. For example, weather conditions such as temperature and rainfall during anthesis, and when the crop is close to harvest, are critical factors for the crop development (Villegas et al. [2016](#page-20-4); Cabas-Lühmann and Manthey [2020](#page-15-6)). Villegas et al. [\(2016](#page-20-4)) found that fnal durum grain yields were reduced when the average daily temperature during anthesis was above 6.9  $\degree$ C and below 10.8  $\degree$ C during grain filling. The optimum temperatures for high grain yields in durum should be between 18 and 24 °C during grain filling; higher temperatures at that stage, even for short periods, can result in losses of 20% or more. Temperatures  $\geq$  24 °C, and rainfall during durum harvest time had a detrimental effect on test weight because of the swollen and contraction of the endosperm and pericarp (Cabas-Lühmann and Manthey [2020\)](#page-15-6).

#### Test weight (TW)

Test weight is one of the oldest parameters used to classify grain. It is given as the grain weight per unit volume (density). A higher TW indicates large and plump kernels, which means higher starch content and less bran, therefore higher semolina extraction, indicating the milling potential (Dexter and Marchylo [2001\)](#page-16-5). Test weight is a quantitative trait; it depends on the expression of several genes, and it is infuenced by the genotype and by the genotype $\times$ environment interactions (Sissons et al. [2020](#page-19-4)). Durum TW

<span id="page-3-0"></span>**Table 1** Mean, standard deviation, and range for agronomical qualities, chemical qualities, and Fe and Zn concentration in tetraploid wheats

Trait			Mean $\pm$ SD Range	References
Durum wheat				
$G$ Y	3.7	1.9	$1.6 - 6.5$	Longin et al. 2016; Atar and Kara 2017; Özberk 2018; Rachoń et al. 2020; Chaieb et al. 2020; USDA 2022; AAFC 2022; EC 2022; ODEPA 2022
TW	79.5	2.4	77.8-83.2	De Vita et al. 2007; Bilgin et al. 2009; De Vita et al. 2010; Fu et al. 2018; Özberk 2018; Rachoń et al. 2020; US wheat commission 2022; Canadian cereals 2022
<b>TKW</b>	42.2	3.6	38.8-49.3	De Vita et al. 2007; Bilgin et al. 2009; Taneva et al. 2015; Fatiukha et al. 2020a; Rachoń et al. 2020; Wang and Fu 2020; Akman and Karaduman 2021; Canadian cereals 2022
VK	82.4	6.8	$60 - 99$	Subira et al. 2014; Fu et al. 2018; Taneva et al. 2015; Özberk 2018; Cabas-Lühmann and Manthey 2020; Vecherska et al. 2021; US wheat commission 2022; Canadian cereals 2022
GPC	14.3	1.9	$12 - 18$	Pagnotta et al. 2009; Giuliani et al. 2009; Blanco et al. 2012; Sayaslan et al. 2012; Hassan et al. 2016; Uppal and Bhise 2018; Geisslitz et al. 2018; Rachoń et al. 2020; Fatiukha et al. 2020a
$GZnC$ 33.2		10.0	21.4-49.3	Cakmak et al. 2000; Ficco et al. 2009; Zhao et al. 2009; Guzmán et al. 2014; Magallanes-López et al. 2017
GFeC 36.6		7.8	28.8-49.6	
T. dicoccum				
$G$ Y	2.9	0.8	$1.8 - 4.3$	Troccoli and Codianni 2005; De Vita et al. 2006; Pagnotta et al. 2009; Marino et al. 2016; Longin et al. 2016; Atar and Kara 2017; Rachoń et al. 2020; Biel et al. 2021; Ehsanzadeh et al. 2021; Biradar et al. 2022
TW	73.2	2.2	70.4-75.6	De Vita et al. 2006; De Vita et al. 2007; Pagnotta et al. 2009; Rachoń et al. 2020; Kalathuga et al. 2021
<b>TKW</b>	39.6	6.9	33.6-49.2	De Vita et al. 2006; De Vita et al. 2007; Marino et al. 2009; Mondini et al. 2014; Taneva et al. 2015; Desheva et al. 2016; Rachoń et al. 2020; Akman and Karaduman 2021; Kalathunga et al. 2021
VK	81.0	17.3	56-94	Desheva et al. 2016; Taneva et al. 2015; Rachon et al. 2020; Vecherska et al. 2021
<b>GPC</b>	16.5	3.0	$11 - 22$	De Vita et al. 2006; Stehno 2007; Pagnotta et al. 2009; Giuliani et al. 2009; Oak et al. 2011; Giacintucci et al. 2014; Konvalina et al. 2012; Lacko et al. 2015; Kuznetsova et al. 2019; Geisslitz et al. 2018; Rachoń et al. 2020; Biel et al. 2021; Biradar et al. 2022
$GZnC$ 36.6		15.6	$22.8 - 58.7$	Zhao et al. 2009; Velu et al. 2017; Guzmán et al. 2014; Velu et al. 2017
GFeC 37.7		5.3	32.8-43.3	
	T. dicoccoides			
GPC	20.9	3.1	$15 - 24$	Ciaffi et al. 1992; Hassan et al. 2007; Peleg et al. 2009a, b; Tonk et al. 2010; Liu et al. 2019; Fatiukha et al. 2020a
$GZnC$ 83.6		12.5	74.0-89.4	Cakmak et al. 2000; Cakmak et al. 2004; Peleg et al. 2008; Gómez-Becerra et al. 2010; Liu et al. 2021
GFeC 64.4		24.2	$41.0 - 104.1$	

*GY* Grain yield (t ha−1); *TW* Test weight (kg hL−1); *TKW* Thousand kernel weight (g); *VK* Vitreous kernels (%); *GPC* Grain protein content (%); *GZnC* Grain zinc concentration (mg g−1); *GFeC* Grain Iron concentration (mg g−1)

fluctuates between 77.8 and 83.2  $kg$  hL<sup>-1</sup> (De Vita et al. [2007,](#page-16-6) [2010;](#page-16-7) Bilgin et al. [2009](#page-15-7); Fu et al. [2018](#page-16-8); Özberk [2018;](#page-18-5) Rachoń et al. [2020;](#page-19-3) US wheat commission [2022;](#page-20-5) Canadian Cereals [2022\)](#page-15-8) while *T. dicoccum* ranges from 70.4–75.6 kg hL<sup>-1</sup> (De Vita et al. [2006,](#page-16-3) [2007;](#page-16-6) Pagnotta et al. [2009;](#page-18-7) Rachoń et al. [2020;](#page-19-3) Kalathunga et al. [2021\)](#page-17-1). In Turkey, Özberk ([2018\)](#page-18-5) reported a mean value of 77.8  $kg \text{ hL}^{-1}$  for various durum wheat cultivars. Rachoń et al. [\(2020](#page-19-3)) in Poland determined that durum wheat has the highest TW with 82.8 kg hL−1 versus 75.2 kg hL−1 of *T. dicoccum,* whereas in a study made by Pagnotta et al.  $(2009)$  $(2009)$  the mean TW of *T. dicoccum* was 72.9 kg hL<sup>-1</sup> in Italy. At a commercial level, the durum TW were 81.4 and 79.7 kg  $hL^{-1}$  during the 2021/22 season in Canada and the United States, respectively. The mean and SD for TW per species are summarized in Table [1.](#page-3-0) In general, the TWs reported for durum were higher than for T. *dicoccum*; however, the SD showed a very similar variation after analyzing the data. There is no data for *T. dicoccoides* TW in this review.

## Thousand kernel weight (TKW)

TKW is a measure of grain size. Dexter et al. ([2001\)](#page-16-5) observed that values of TKW below 40 g were associated with reduced milling quality and four extraction rates. The average TKW for durum ranges from 38.8 to 49.3 g (De Vita et al. [2007](#page-16-6); Bilgin et al. [2009](#page-15-7); Taneva et al. [2015](#page-20-6); Fatiukha et al. [2020a](#page-16-9); Rachoń et al. [2020](#page-19-3); Wang and Fu [2020](#page-20-7); Akman and Karaduman [2021](#page-14-5); US wheat commission [2022](#page-20-5); Canadian cereals [2022](#page-15-8)). For *T. dicoccum*, the values of TKW range from 33.6 to 49.2 (De Vita et al. [2006](#page-16-3), [2007](#page-16-6); Marino et al. [2009;](#page-18-10) Mondini et al. [2014](#page-18-11); Taneva et al. [2015](#page-20-6); Desheva et al. [2016;](#page-16-12) Rachoń et al. [2020](#page-19-3); Akman and Karaduman [2021;](#page-14-5) Kalathunga et al. [2021\)](#page-17-1); for *T. dicoccoides*, Nevo et al. ([1986\)](#page-18-13) reported a value of 29.9 g. The mean and SD for TKW per species are summarized in Table [1.](#page-3-0) Some of the TKW values are higher for *T. dicoccum* than for durum; however, the SD showed a higher variability for *T. dicoccum*. The wide variability of this trait has been described by Desheva et al. [\(2016](#page-16-12)) in *T. dicoccum,* ranging from 21.8 to 50 g for a set of 38 genotypes. In parallel, Marino et al. ([2009\)](#page-18-10) reported values of 41.8 g for no nitrogen fertilization and 56.6 g for the N fertilized treatment. Rachoń et al. ([2020\)](#page-19-3) reported 33.9 g for *T. dicoccum*, which was signifcantly lower compared to the value of 40.7 g of durum wheat. Similar results were obtained by Akman and Karaduman [\(2021](#page-14-5)), who compared diferent *Triticum* species, determining lower values of~30 g for *T. dicoccum* versus~40 g for durum which means that *T. dicoccum* has lower milling yield since the ratio between endosperm and bran is smaller relative to durum.

#### Vitreous kernel content (VK)

Vitreous kernels have a translucent and shiny appearance since there are no air spaces between the starch and the protein matrix, which allows light to pass directly through the seed endosperm. Vitreousness is associated with grain hardness and high protein levels (Oury et al. [2015\)](#page-18-14). The pasta industry prefers highly vitreous grain because the fracture of the endosperm during milling results in semolina with greater granulation, extraction, and intense yellow color. The range of kernel vitreousness in durum can oscillate between 60 and 99% (Subira et al. [2014](#page-20-8); Fu et al. [2018;](#page-16-8) Taneva et al. [2015;](#page-20-6) Özberk [2018](#page-18-5); Cabas-Lühmann and Manthey [2020](#page-15-6); Vecherska et al. [2021;](#page-20-9) US Wheat Commission [2022](#page-20-5); Canadian cereals [2022\)](#page-15-8). However, at least 80% of vitreous kernels are expected for milling purposes (Petrova et al. [2009\)](#page-19-9). Nevertheless, some sub-classes of durum can have less than 60% vitreous kernels, mainly because of wet conditions when the grain is ready to be harvested with about 12% moisture content (Cabas-Lühmann and Manthey [2020](#page-15-6)). Subira et al.  $(2014)$  $(2014)$  reported that old and contemporary cultivars had above 80% of vitreousness, whereas old cultivars in Spain ranged from 90 to 92%. In *T. dicoccum*, a range of 56–94% was reported (Desheva et al. [2016](#page-16-12); Taneva et al. [2015;](#page-20-6) Rachoń et al. [2020;](#page-19-3) Vecherska et al. [2021\)](#page-20-9). The mean and SD for VK per species are summarized in Table [1](#page-3-0). Vitreous kernel content for both species is quite similar in general, with *T. dicoccum* having a higher level of variability. Interestingly, diferent studies have shown a greater VK content for *T. dicoccum* than for durum, as did Taneva et al. [\(2015](#page-20-6)), who identifed that *T. dicoccum* had a higher vitreousness than durum, which among 15 tested accessions ranged from 79 to 99% in *T. dicoccum* to 88% in durum. Rachoń et al. ([2020\)](#page-19-3) reported a 6% higher vitreousness in *T. dicoccum* than in durum, which showed a VK value of 86%. In another study, a collection of *T. dicoccum* characterized by Desheva et al. [\(2016](#page-16-12)) showed grain vitreousness in the range of 66–99%. As explained Sieber et al. ([2015\)](#page-19-10), VK depends on the protein content, therefore, as observed by Taneva et al.  $(2015)$  $(2015)$ , the *T. dicoccum* accessions with higher VK content also had the highest protein content. Research is needed to determine how the kernel water absorption afects the VK content of *T. dicoccum* and *T. dicoccoides.*

# Genetic architecture of grain yield and other agronomical traits

Ancient wheats have long been recognized as a source of favorable alleles for wheat improvement, and so the wild germplasm of tetraploid wheats remain a

valuable resource and useful discoveries can be made. Some studies have shown that wild emmer wheat can be exploited to improve some agronomic traits of present-day cultivars, by the introgression of desirable alleles (Ahmadi et al. [2007;](#page-14-6) Lu et al. [2022\)](#page-18-15). Recombinant inbred lines (RIL) or single chromosome-arm substitution lines (CASLs) have been used to locate genetic loci in wild germplasm that carry favorable QTL alleles (Klymiuk et al. [2019\)](#page-17-11). For example, Peleg et al. ([2009a](#page-19-6)) mapped several QTL associated with plant productivity and drought-adaptive traits in a RIL population derived from a cross between durum wheat ('Langdon') and *T. dicoccoides* ('G18-16'). Subsequently, some of these QTL were introgressed from 'G18-16' into elite Israeli durum (cv. 'Uzan') and bread wheat ('Bar Nir' and 'Zahir') via marker assisted selection. They were located on chromosomes 1B and 2B for durum and 7A in bread wheat. The introgressed QTL improved grain yield, biomass, photosynthetic capacity, and root development across diferent environments, particularly under drought conditions (Merchuk-Ovnat et al. [2016a](#page-18-16), [b,](#page-18-17) [2017](#page-18-18)). Collected information about selected QTL for grain yield (GY), grain weight (GW), and other agronomical quality traits is summarized in Table [2](#page-6-0).

Heading date is a fundamental agronomic trait that afects the maturation time and grain yield. In this sense, Zhou et al. ([2016\)](#page-20-14), using CASLs of *T. dicoccoides* chromosomes ('TDIC140') in the genetic background of common wheat ('Chinese Spring'), found QTL associated with late (on chromosomes 4A and 2B) and early (on chromosomes 3A and 7B) heading dates in the 'TDIC140' genome. Interestingly, the QTL detected on chromosome 2B related to the later heading explained the largest portions of phenotypic variation (57.2–76.7%) in diferent environments in Australia. In contrast, Lu et al. ([2022\)](#page-18-15) found a QTL fanked by *C268* and *C309* markers with an interval of 8.9 cM on *T. dicoccoides* chromosome 7B, explaining 9.1 and 12.4% of the phenotypic variation for the early heading date, which is useful for wheat breeding for rainfed conditions (Shavrukov et al. [2017\)](#page-19-11).

Grain weight (GW) per plant is an essential component of wheat yield; therefore, several QTL have been identifed in wild emmer wheat. For example, Golan et al. ([2015\)](#page-17-12) mapped a major QTL associated with GW increase on chromosome 2A positioned at 57.8 cM and linked to the *Xhbg494* marker on *T.*  *dicoccoides* 'FA-15-3'. This QTL is associated with the Grain Number Increase 1 (*GNI-A1*) gene, a regulator of foret fertility, and it was introgressed into durum wheat var. 'Langdon', where it increased GW without significantly affecting the grain (Golan et al. [2019\)](#page-17-13). Additionally, Avni et al. ([2018\)](#page-15-12) performed a QTL analysis for GW using a RIL population derived from a cross between *T. dicoccoides* ('Zavitan') and durum wheat ('Svevo'). A total of 22 QTL were identifed for TKW, of which eight were conferred by 'Zavitan'. A meta-QTL analysis identifed a locus on chromosome 6A associated with the Growth-Regulating Factor 4 (*GRF4-A*) gene; its introgression from 'Zavitan' into the 'Svevo' increased GW by up to 8%. In this same genomic region, Peleg et al. [\(2009b](#page-19-7)) located a QTL for TKW in *T. dicoccoides* acc. 'G18-16'. These results suggest that the alleles from 'Zavitan' and 'G18-16' on chromosome 6A have the potential to increase wheat yields in breeding programs (Avni et al. [2018\)](#page-15-12).

## **Chemical quality traits**

## Grain protein content

The grain protein content (GPC) and gluten quality are important quality traits for pasta manufacturing due to their efect on the frmness of cooked pasta and tolerance of overcooking. The average GPC in durum wheat ranges from 11.8 to 18.0% (Pagnotta et al. [2009](#page-18-7); Blanco et al. [2012;](#page-15-9) Sayaslan et al. [2012;](#page-19-5) Hassan et al. [2016;](#page-17-3) Uppal and Bhise [2018](#page-20-10); Geisslitz et al. [2018](#page-16-10); Fatiukha et al. [2020a;](#page-16-9) Rachoń et al. [2020](#page-19-3)), in *T. dicoccum* from 11.1 to 21.6% (De Vita et al. [2006;](#page-16-3) Stehno [2007](#page-20-1); Pagnotta et al. [2009;](#page-18-7) Giuliani et al. [2009](#page-17-2); Oak et al. [2011](#page-18-12); Giacintucci et al. [2014;](#page-17-5) Konvalina et al. [2012;](#page-17-6) Lacko et al. [2015;](#page-17-7) Kuznetsova et al. [2019;](#page-17-0) Geisslitz et al. [2018](#page-16-10); Rachoń et al. [2020;](#page-19-3) Biel et al. [2021;](#page-15-5) Biradar et al. [2022](#page-15-1)) while for *T. dicoccoides* it ranges from 14.8 to 23.6% (Ciaffi et al. [1992;](#page-15-11) Hassan et al. [2007;](#page-17-8) Peleg et al. [2009a;](#page-19-6) Tonk et al. [2010;](#page-20-13) Liu et al. [2019;](#page-17-9) Fatiukha et al. [2020a](#page-16-9)). For high-quality pasta the GPC is expected at  $\geq$  13%; GPC at or below 11% results in poor-quality pasta regardless of the drying conditions in processing (Delcour and Hoseney [2010](#page-16-13)). The protein content is a quantitative trait with low heritability, largely infuenced by

Trait	Chr	Pos $(cM)$	Interval $(cM)$	Marker name	<b>LOD</b>	PEV $(\%)$	Acc	References
GW	1B	$\overline{\phantom{0}}$		Xgm413	2.8	8.1	H <sub>52</sub>	Peng et al. 2011
	2A	$\qquad \qquad -$			3.7	15.8	H <sub>52</sub>	
	4A	$\qquad \qquad -$		Xgwm4a	4.9	14	H <sub>52</sub>	
	5A	$\overline{\phantom{0}}$		P5oM50m	2.7	9.0	H <sub>52</sub>	
	5B	$\equiv$		Xgm499	4.0	15.2	H <sub>52</sub>	
	7Α	$\overline{\phantom{0}}$		Xgwm276	$2.5\,$	7.8	H52	
	7B	$\qquad \qquad -$	$\overline{\phantom{0}}$	P55M53gu	$2.2\,$	6.6	H <sub>52</sub>	
GY	2A	$\overline{\phantom{0}}$	$\overline{\phantom{0}}$		6.3	23.9	H <sub>52</sub>	
	3A	$\qquad \qquad -$	$\overline{\phantom{0}}$	Xgm32	3.1	10.1	H <sub>52</sub>	
	5A	$\qquad \qquad -$	$\overline{\phantom{0}}$		6.3	35.6	H <sub>52</sub>	
	2B	69.4	21.0	gwm37	11.9	$13.1 - 15.5$	G18-16	Peleg et al. 2009b
	7B	17.8	17.0	wm263	8.6	$7.6 - 12.7$	G18-16	
HI	1B	58.0	18.4	gwm75	5.5	$3.5 - 4.8$	G18-16	
	2A	58.4	6.4	gwm372	5.5	4.7	G18-16	
	2B	48.8	9.2	$wPt$ -7757	19.4	$12.8 - 18.2$	G18-16	
	5B	117.3	21.1	wPt-1733	4.7	8.4	G18-16	
	6A	104.2	26.5	wPt-0139	5.6	$3.0 - 4.7$	G18-16	
	6B	69.2	21.4	wPt-11560	6.7	$4.0 - 4.8$	G18-16	
	$7\mathrm{B}$	14.1	2.6	gwm263	14.1	$13.2 - 22.4$	G18-16	
<b>KNPS</b>	1B	44.0	7.8	gwm1028	7.9	$6.4 - 6.6$	G18-16	Peleg et al. 2011
<b>TKW</b>	2A	137.2	15.2	XtPt-3136	3.5	6.7	G18-16	
	2B	134.4	11.0	XwPt-0694	5.3	6.8	G18-16	
	5A	88.9	14.4	Xwmc415a	3.3	7.0	G18-16	
	5B	55.0	10.5	Xgwm371	$7.0\,$	9.3	G18-16	
	6A	92.3	15.8	Xgwm786	4.6	$1.8 - 8$	G18-16	
	6B	126.9	17.5	XwPt-8554	9.5	$10.9 - 16.8$	G18-16	
	7A	69.7	17.9	XwPt-9555	4.9	$4.5 - 5.1$	G18-16	
	$7\mathrm{B}$	19.8	$8.8\,$	Xgwm263	5.8	11.8	G18-16	
HI	2B	116.2	17.6	XwPt-1294	5.5	$1.8 - 10.5$	G18-16	
	7В	36.6	18.3	Xgwm537	6.2	$3.2 - 11.1$	G18-16	
GW	2A	57.8	3.2	Xhbg494	12.8	0.5	$FA-15-3$	Golan et al. 2015
<b>TKW</b>	1B	$\equiv$	$\overline{\phantom{0}}$	<b>IWB20542</b>	10.9	0.2	Zavitan	Avni et al. 2018
	2A	$\overline{\phantom{a}}$		IWB50818- IWB2683/IWB44472	3.7	$0.05 - 0.07$	Zavitan	
	6A	$\overline{\phantom{m}}$	$\overline{\phantom{0}}$	<b>IWB31050</b>	$3.5 - 4.4$	$0.05 - 0.08$	Zavitan	
	7A	$\overline{\phantom{m}}$		IWA7741- IWA6562	$3.5 - 4.0$	$0.05 - 0.08$	Zavitan	
	1A	113.2	$102.1 - 114.2$	RAC875_c51346_99	5.4	$1.7 - 5.7$	$Y12-3$	Fatiukha et al. 2020a
	3A	53.8	$52.2 - 60.2$	BS00047836_51	6.3	$1.1 - 4.7$	$Y12-3$	
	7B	71.6	69.4-76.9	RAC875_c47003_445	8.4	$0.7 - 6.9$	$Y12-3$	

<span id="page-6-0"></span>**Table 2** Collected QTL's data for agronomical traits in *T. diccoccoides* accessions

*Pos* Marker position; *GW* Grain weight; *GY* Grain yield; *KNPS* Kernel number per spike; *HI* Harvest index; *TKW* Thousand kernel weight; *Chr* Chromosome; *Acc* Accession name

the environment, and it is often negatively correlated with the wheat grain yield (Blanco et al. [2012\)](#page-15-9).

The means and SD for GPC per species were sum-marized in Table [1.](#page-3-0) In general, durum data cluster at the lowest level, followed by *T. dicoccum*, and *T. dicoccoides* with the highest. However, durum had the most stable data compared to the ancestral wheats. The SD for durum was  $\pm 1.9\%$  vs  $\pm 3.0\%$  for

*T. dicoccum* and±3.1% for *T. dicoccoides*. When *T. dicoccum* and *T. dicoccoides* are compared to modern wheats, these ancestral crops list among those with the highest grain protein content (Joppa et al. [1991](#page-17-14); Stehno [2007;](#page-20-1) Pagnotta et al. [2009;](#page-18-7) Tonk et al. [2010](#page-20-13); Konvalina et al. [2012](#page-17-6); Kuznetsova et al. [2019;](#page-17-0) Rachoń et al. [2020](#page-19-3); Biradar et al. [2022\)](#page-15-1). Kuznetsova et al. [\(2019](#page-17-0)) found that the GPC of *T. dicoccum* was 3.9% higher than the common wheat, while Rachoń et al. [\(2020](#page-19-3)) found that the GPC of *T. dicoccum* was 4.7% higher than the durum wheat (19.2 vs. 14.5%, respectively). Conversely, Akman and Karaduman ([2021\)](#page-14-5) found that *T. dicoccum* and durum had almost equal grain protein contents  $(-15\%)$ . Hassan et al.  $(2007)$  $(2007)$ determined a protein content of 15% in *T. dicoccoides* vs. 9.5% in durum wheat. Tonk et al. [\(2010](#page-20-13)) reported a GPC in *T. dicoccoides* of 21.4%, which was 6% higher than the values in bread wheat (15.7%) in Turkey. Newer cultivars have lower GPC than the old ones, mainly because the breeding techniques have prioritized the increase in yields, which is negatively correlated to GPC. According to Subira et al. [\(2014](#page-20-8)), this reduced GPC from 16% to 14.2–14.7% in newer wheat cultivars during the twentieth century.

## Protein quality

Protein quality is related to gluten strength and cooked pasta quality. In wheat, there are two major protein fractions of prolamins: glutenins and gliadins. Glutenins and gliadins represent about 80% of the total protein in the endosperm of wheat. The ratio of glutenins: gliadins which upon hydration and mixing form gluten, is responsible for the gluten strength (Edwards et al. [2003](#page-16-14)). The glutenins confer the elasticity of the dough, while extensibility is mainly conferred by the gliadins (Shewry et al. [1995](#page-19-13)). In wheat breeding, the evaluation of gluten strength is based mainly on the sodium dodecyl sulfate (SDS)-sedimentation volume (Axford et al. [1978](#page-15-13)). It requires less material and is considerably faster than the gluten index, alveograph, and mixograph tests (Zhang et al. [2008](#page-20-15)). The SDS-sedimentation volume estimates the glutenin quality and, indirectly, the gluten strength (Peña et al. [2003](#page-19-14)). In tests by Oak et al. ([2011](#page-18-12)) in India, the micro-sedimentation values for all 10 T*. diccoccum* accessions were lower than those of durum, with the mean of 28.5 mm vs. 32 mm, respectively. Stehno ([2007](#page-20-1)),

reported 29 mL for *T. dicoccum* vs. 61 mL for *T. aestivum*. On the other hand, Akman and Karaduman ([2021\)](#page-14-5) identifed *T. dicoccum* 'kavilca' as having a higher macro-SDS than the durum 'Meram 2002' and 'Kunduru 1149', with values of about 35 mL and 15 mL, respectively. On the other hand, Ciaffi et al.  $(1992)$  $(1992)$  reported that about 10% of the 315 accessions of *T. dicoccoides* had considerably higher SDS-sedimentation values compared to the best-performing durum wheat tested.

Glutenins are divided into two subunits: low molecular weight subunits (LMW-GS) and high molecular weight subunits (HMW-GS) (Dick and Quick [1983](#page-16-15); Shewry et al. [1986](#page-19-15)). A signifcant association between the SDS-sedimentation values and HMW-GS and LMW-GS was reported by Dick and Quick [\(1983](#page-16-15)). Recent studies have shown that the LMW-GS may have a higher effect on the final protein quality and gluten strength than the HMW-GS (Zhen et al. [2014;](#page-20-16) Araya-Flores et al. [2020](#page-14-0)). However, because of their high heterogeneity and the abundance of allelic variants, characterization of LMW-GS is still incomplete and requires further investigation (Roncallo et al. [2021\)](#page-19-16). Interestingly, durum wheats with strong gluten showed higher expression levels of the LMW glutenin-related genes between 21 and 35 days post anthesis (DPA) and had up to 43.5% more alanine than the weak gluten lines at 42 DPA, suggesting that alanine may have a positive impact gluten strength at a particular developmental stage (Araya-Flores et al. [2020](#page-14-0)). The most used criteria to classify LMW-GS are based on their mobility in the sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE), and that is a consequence of diferences in the molecular weight. There are three types of LMW-GS: type  $B$  (42–51 kD), type *C* (20–40 kD), and type *D* (50–70 kD). The B-type is a sulfur-rich prolamin known also as the "*m*" and "*s*" subunits; the *C*-type and *D*-type are forms of *α*-/*γ*-gliadins and *ω*-gliadins, respectively; they have cysteine residues with sulfur bonds (Rutsgi et al. [2019\)](#page-19-17). Studies on durum wheat have shown that the *γ*-gliadins 45 (genetically associated with LMW-2GS) were positively correlated to *al dente* pasta and good cooking characteristics, while *γ* -gliadins 42 (genetically associated with LMW-1GS) had poor cooking properties (D'Ovidio and Masci [2004;](#page-16-16) Edwards et al. [2007\)](#page-16-17). However, the *B*-type LMW-GS has been pointed out as ultimately responsible for the gluten strength in durum wheat (Ruiz et al. [2018;](#page-19-18) Chacón et al. [2020\)](#page-15-14).

*T. dicoccum* gluten quality and technological performance is generally inferior to modern wheats, with low elasticity, high extensibility, and softer dough (De Vita et al. [2006](#page-16-3); Kuznetsova et al. [2019](#page-17-0)). However, some studies have shown that some accessions of this species have promising characteristics with similar gluten performance when compared to durum (Oak et al. [2002;](#page-18-19) [2011\)](#page-18-12). Oak et al. [\(2011](#page-18-12)) reported that among all accessions of *T. dicoccum* tested only 'DDK 1025' showed the presence of *γ* -gliadins 45 linked to *Glu-B3* LMW-GS, resulting in dough properties similar to durum wheat. On the other hand, the electrophoretic profles of Giacintucci et al. [\(2014](#page-17-5)) on non-vitreous of *T. dicoccum* did not identify LMW-GS between 16–23 kDa. The diference among the studies points to a need for additional studies in this area, which could lead to the improvement of the crop and its future uses. Further experiments could focus on the development of new *T. dicoccum* cultivars with LMW-GS (LMW-2) like durum wheat, for better dough properties.

Genetic architecture of grain protein content and quality

As noted above, modern wheat cultivars contain relatively low to moderate GPC. In this sense, wild and domesticated emmer species are a valuable genetic resource, rich in allelic variants, to improve grain quality through introgression of favorable alleles from the wild accessions (Marcotuli et al. [2020](#page-18-20); Colasuonno et al. [2021;](#page-16-18) Biradar et al. [2022\)](#page-15-1). Ruiz et al. [\(2018](#page-19-18)) and Chacón et al. [\(2020](#page-15-14)) identifed new alleles at the *Glu-B3* locus with a positive efect on gluten strength. The *B* type LMW-GS is controlled by loci *Glu-B2*, *Glu-A3*, and *Glu-B3* on the short arms of homoeologous group-1 chromosomes (Bellil et al. [2014\)](#page-15-15). Looking only the B-type LMW-GS at the *Glu-3* loci, *T. dicoccum* shows fve diferent binding patterns in Indian genotypes (Oak et al. [2002](#page-18-19)) while in a similar study, Degaonkar et al. [\(2005](#page-16-19) observed eight diferent binding patterns. Liu and Shepherd ([1996\)](#page-17-15) identifed large variation in the LMW-GS of two *T. dicoccum* accessions, with four to six *B* subunits with variations in band mobility and staining intensity.

*T. dicoccoides* has not only been identifed as an appropriate source for the transfer of genes to improve the GPC, but some genotypes within this species appear as a promising source for the improvement of gluten and rheological properties of modern wheats (Ciaffi et al. [1992](#page-15-11); Liu and Shepherd [1996](#page-17-15)). Liu and Shepherd ([1996\)](#page-17-15) showed that the *T. dicoccoides* lines from diferent countries had two to fve B subunit bands. Compared to durum wheat, there were similar bands with only minor diferences in the intensity and mobility that resembled the−43.2 gliadin in durum wheat.

Another classifcation for the LMW-GS is based on their frst amino acid residue (D'Ovidio and Masci [2004\)](#page-16-16), with three types: LMW-GS serine (s), LMW-GS methionine (m), and LMW-GS isoleucine (i) (*Glu 3* loci), and a new class reported by Huang et al. [\(2018](#page-17-16)) from *Aegilops comosa*, called LMW-leucine (l). The high variability of LMW-GS at the *Glu 3* loci in *T. dicoccoides* has also been described (Ciaffi et al. [1993\)](#page-15-16), making it an important source to identify new alleles or genes to improve modern wheat quality. Qin et al. [\(2015](#page-19-19)) amplifed DNA sequence of the LMW-GS genes usingthe know *Glu 3* alleles of wheat and related grasses and identifed fve novel LMW-GS (i) genes from *T. dicoccoides* named *emmer-1* to *emmer-5.* Among them, the coding region of *emmer-1* had 1128 bp and was the longest and may have some potential to improve the breadmaking quality of bread wheat. Masci et al. [\(2000](#page-18-21)) showed that the larger the coding region the better the wheat dough quality because of the improvement of the viscoelastic properties. In a more recent study, Xiang et al. [\(2019](#page-20-17)) evaluated the LMW-GS of two advanced lines obtained from the cross of bread wheat 'CN19' with *T. dicoccum* 'D97'. The advanced lines 'BAd7-209' and 'BAd7-213' had the LMW-GS C and D types at the *Glu-A3* locus from the wild emmer 'D97' parent. Both had a higher protein content, higher SDSsedimentation value, wet gluten content, better dough development time and stability time than the parent 'CN19'. Of the two lines, 'Bad7-209' had better dough stability time and development time than 'BAd7-213' which was attributed to the presence of the novel D-type LMW-GS at *Glu-A3* present in 'Bad7-209'.

Many QTL associated with the GPC have been located on chromosomes of tetraploid wheats (Table [3\)](#page-9-0), and some have been successfully introgressed into modern wheat cultivars using the marker-assisted selection (Kumar et al. [2018\)](#page-17-17). For

Trait	Chr	Pos $(cM)$	Interval (cM)	Markers name	<b>LOD</b>	PEV $(\%)$	Acc	References
<b>GPC</b>	6 <sub>B</sub>	$\overline{\phantom{0}}$		Xabg387-Xmwg79	18.9		$LDN(DIC-6B)$	Joppa et al. 1997
	6B	7.0		Xcdo365-Xucw67	-		$FA-15-3$	Olmos et al. 2003
	6B	$\overline{\phantom{0}}$	$0.7 - 3.1$	Xcdo365-Xucw79	-	1.5	$LDN(DIC-6B)$	Chee et al. 2001
	6B			Xuhw89	-		$FA-15-3$	Distelfeld et al. 2006
	2A	$\overline{\phantom{0}}$	-	Xcfa2164	6.8		MG29896	Blanco et al. 2012
	6A			XP39M37	6.8		MG29896	
	7B			Xgwm577	6.8		MG29896	
	2A	111.3	21.4	gwm445	7.9	$0.9 - 13.7$	G18-16	Peleg et al. 2009a
	4A	77.2	12.9	$wPt - 7558$	5.9	$1.2 - 9.7$	G18-16	
	5A	11.8	15.1	gwm154	6.4	$3.6 - 7.1$	G18-16	
	5B	149.3	21.5	wPt-11579	6.0	$1.9 - 8.5$	G18-16	
	6B	95.7	11.9	gwm771	10.4	$3.8 - 12$	G18-16	
	7A	101.2	10.9	gwm332	6.9	$3.0 - 9.6$	G18-16	
	1A	76.0	72.4-78.4	TA002402-1350	6.3	$0.6 - 4.1$	$Y12-3$	Fatiukha et al. 2020a
	2A	95.1	93.8-96.2	RAC875_c39665_175	6.7	$1.2 - 5.3$	$Y12-3$	
	3A	63.8	59.7-65.6	Excalibur_c6501_477	7.8	$1.3 - 6.5$	$Y12-3$	
	4A	35.3	33.4 - 37.9	BS00022125 51	8.1	$0.8 - 6.1$	$Y12-3$	
	4B	30.8	$30.4 - 31.4$	<b>TG0010b</b>	26.9	$1.2 - 15.3$	$Y12-3$	
	5A	33.3	$30.0 - 42.5$	RAC875 rep c106118 339	14.2	$2.3 - 12.2$	$Y12-3$	
	5A	122.1	$118.5 - 131.0$	Tdurum_contig55097_601	3.8	$1.8 - 7.2$	$Y12-3$	
	6A	71.0	$67.6 - 89.6$	wsnp_Ex_c15268_23489498	3.8	$1.8 - 7.1$	$Y12-3$	
	6B	47.1	$46.1 - 48.6$	Tdurum contig9860 281	27.8	$3.7 - 24.4$	$Y12-3$	
	7В	8.2	$6.1 - 9.5$	Tdurum_contig10861_942	3.6	$2.6 - 6$	$Y12-3$	
	7B	98.3	95.3-101.2	Kukri c14766 484	10.7	$0.8 - 7$	$Y12-3$	

<span id="page-9-0"></span>**Table 3** Collected QTL's data for grain protein content in *T. diccoccoides* accessions

*Pos*: marker position; *GPC*: Gluten protein content; *Chr*: Chromosome; *Acc*: Accession name

example, Fatiukha et al. ([2020a](#page-16-9)) identifed a total of 8 stable GPC-related QTL under fve diferent environments on chromosomes 1A, 2A, 3A, 4A, 4B, 5A, 6B, and 7B in *T. dicoccoides* 'Y12-3', which explained between 0.6 and 24.4% of the phenotypic variation for GPC. Among all the QTL detected for GPC, the most important one was *Gpc-B1,* originally detected by Joppa and Cantrell ([1990\)](#page-17-18) on chromosome 6B in T. *dicoccoides* lines 'FA-15-3' and 'F-28-8-3' from Israel. It signifcantly increased the the GPC relative to the recurrent durum parent 'Langdon' [LDN] (Joppa et al. [1991](#page-17-14)). Joppa et al. ([1997\)](#page-17-19) mapped a QTL for GPC on chromosome arm 6BS in a RIL population derived from LDN and CASL 'LDN (DIC6B)', which explained 66% of the phenotypic variation for GPC. Olmos et al. [\(2003](#page-18-22)) mapped this QTL as a simple Mendelian locus, *Gpc-B1*, located within a 0.3 cM interval fanked by DNA markers *Xucw71* and *Xucw79*. *Gpc-B1* encodes for a

*NO APICAL MERISTEM-B1* (*NAM-B1*), which is a NAC transcription factor that accelerates senescence and increases nutrient remobilization from leaves to developing grains, hence afecting the fnal GPC (Uauy et al. [2006;](#page-20-18) Avni et al. [2014](#page-14-7)). This transcription factor is nonfunctional in modern wheat. Uauy et al. ([2006\)](#page-20-18), through positional cloning, identifed a functional *NAM-B1*allele present mainly in wild wheats and landraces. The presence of *Gpc-B1* has been associated with reductions in yield and other agronomic parameters in diferent environments (Brevis and Dubcovsky [2010;](#page-15-17) Tabbita et al. [2013\)](#page-20-19). However, as suggested by Eagles et al. [\(2014](#page-16-20)), introgression of the functional allele into wheat cultivars with large grain size may increase GPC and the development of high-yielding cultivars carrying functional *GPC-B1* allele. Some approaches for conventional wheat breeding focused on increasing the grain protein content without losing grain yield, or such quality

parameters as the test weight. This can be done by introgression of alien genes from related species and fnding the QTL for grain protein with a less negative effect on grain yield and other related traits (Liu et al. [2019\)](#page-17-9). Lines without *Gpc-B1* showed an improvement in TKW and grain protein content in a study made by Liu et al.  $(2019)$  $(2019)$ , who regions on chromosome arms 2BS and 7BL with no negative effect on TKW which can be useful for grain protein content as well. Introgression of the functional *Gpc-B1* allele from wild emmer increased grain protein content in several elite and commercial cultivars of common/ durum wheat and in diferent environments (Mishra et al. [2015](#page-18-23); Vishwakarma et al. [2016](#page-20-20)), with only marginally negative impacts on yields (Tabbita et al. [2017\)](#page-20-21). Specifcally, the wild *Gpc-B1* allele had positive effects on the semolina protein content (increased 16 g kg<sup>-1</sup>), wet gluten (increased 50 g kg<sup>-1</sup>), mixing time and peak height (increased 0.65 min and 1.3 cm, respectively), cooked frmness (increased 0.9 g cm), and cooking loss (decreased 5  $g \text{ kg}^{-1}$ ) compared to the 'UC1113' and 'Kronos' NILs (Brevis and Dubcovsky [2010](#page-15-17); Tabbita et al. [2017](#page-20-21)).

#### **Nutritional value through Zinc and Iron content**

Zinc and iron content and their bioavailability

According to the World Health Organization (WHO  $2002$ ), the iron (Fe) deficiency ranks  $6<sup>th</sup>$ , while the zinc (Zn) deficiency is 5th among the 20 most important nutritional ailments in the world. This is related to "hidden hunger," a consequence of a nutrient-poor diet because of the low intake and absorption of these micronutrients. This is of concern in both developed and developing countries (Lowe [2021](#page-18-3)). Iron defciency can cause problems such as anemia, defciencies in cognitive development, maternal mortality, premature births, and low energy; zinc defciency is related to abnormalities in growth development (stunting) and a weak immune system (Santos et al. [2017\)](#page-19-20).

Cereals not only have low levels of Fe and Zn but also contain compounds such as phytate or phytic acid (PA) (myoinositol-1,2,3,4,5,6-hexakisphosphate) and fber that limit Fe and Zn bioavailability in the human body (Cakmak et al. [2002](#page-15-19); Welch and Graham [2004\)](#page-20-23). This happens because phytate generates a strong chelation with Fe and Zn, reducing their bioavailability (Coudray et al. [2001\)](#page-16-22). Bioavailability is considered high when the molar ratios of PA:Zn are  $< 5$ , moderate 5–15, and low  $> 15$ (Magallanes-López et al. [2017](#page-18-9)); for PA:Fe, the molar ratio should be  $< 1$  for high Fe bioavailability (Magallanes-López et al. [2017](#page-18-9)). One of the strategies to mitigate this problem is through the biofortifcation of crops through plant breeding programs that target high grain mineral concentrations, which have been signaled as one of the most economical and environmentally safe approaches to solving malnutrition (Cakmak et al. [2002,](#page-15-19) [2010;](#page-15-20) Welch and Graham [2004;](#page-20-23) Bouis et al. [2011](#page-15-21)). Bioavailability is the capacity to absorb theminerals in the digestive tract (Beasley et al. [2019](#page-15-22)). Some important criteria to consider when developing a biofortifed crop are the bioavailability of the nutrients, retention of the nutrients after processing, nutrients requirements and consumption in a population (Cakmak et al. [2010](#page-15-20)). To improve the micronutrient concentration in cereals through breeding, a breeding program must consider: (1) a large variation in the content of micronutrients in the seeds refecting large genetic variation, and the phytic acid content (Cakmak et al. [2002,](#page-15-19) [2010](#page-15-20)); (2) agronomical practices such as fertilization, water supply, and soil nutrient concentrations and associations with mycorrhizal fungi (Tran et al. [2021](#page-20-24)); (3) the genotype x environment interaction for a quantitative trait (Blair et al. [2009\)](#page-15-23).

Durum wheat, and all modern cultivated wheats in general, show narrow micronutrient variation, this limits their use as a genetic source to increase Fe and Zn content (Cakmak et al. [2000](#page-15-10), [2010](#page-15-20); Ficco et al. [2009](#page-16-11); Rachón et al. [2012;](#page-19-21) Hakki et al. [2014](#page-17-20)). Magallanes-López et al. [\(2017](#page-18-9)) tested 46 durum wheat cultivars from the main durum growing areas for the bioavailability of Fe and Zn. The variation ranged from 25.7 to 40.5 mg  $kg^{-1}$  for Fe and from 24.8 to 48.8 mg  $kg^{-1}$  for Zn, with the PA acid content ranging from 4.6 to 9.5 mg  $g^{-1}$ . The values reported by Ficco et al. [\(2009](#page-16-11)) for 84 durum wheat cultivars from Italy fluctuated between 33.6–65.6 mg kg<sup>-1</sup> for Fe, 28.5–46.3 mg  $kg^{-1}$  for Zn,, and 4.6–7.6 mg  $g^{-1}$ for PA Based on the existing information, it is clear that the genetic variation available in durum wheat is insufficient for the development of cultivars rich in Fe and Zn; other genetic resources must be accessed in the breeding process. The most promising resources for the improvement of grain Zn and Fe concentrations are wild relatives, ancient wheats, and landraces (Monasterio and Graham [2000](#page-18-24); Cakmak et al. [2010](#page-15-20)). *T. dicoccum* (Monasterio and Graham [2000\)](#page-18-24) and *T. dicoccoides* have been shown to have high micronutrient concentrations (Cakmak et al. [2000,](#page-15-10) [2004,](#page-15-0) [2010;](#page-15-20) Distelfeld et al. [2007;](#page-16-23) Gomez-Becerra et al. [2010\)](#page-17-21). High concentrations of Fe and Zn has been detected in *T. dicoccoides* accessions in a greenhouse experiment (Cakmak et al. [2004](#page-15-0)) with the levels of Fe reaching up to 109 mg  $kg^{-1}$  (with a minimum value of 14 mg kg<sup>-1</sup>), with up to 190 mg kg<sup>-1</sup> for Zn (minimum of 15 mg  $kg^{-1}$ ). Similarly large variation was also detected by Guzman et al. ([2014\)](#page-17-4). Peleg et al. [\(2008](#page-19-8)) identifed the 'MM 5/4' and '24/39' *T. dicoccoides* accessions as promising micronutrient sources with 139 mg kg<sup>-1</sup> of Zn and 88 mg kg<sup>-1</sup> of Fe and adequate agronomic performance. Among a wide range of wheat germplasm surveyed at CIMMYT, *T. dicoccum* had the highest Fe and Zn concentrations (Welch and Graham [2004\)](#page-20-23).

As described before, the wild wheat ancestors have the highest Fe and Zn concentrations (Table [1](#page-3-0)) and generally they have lower grain yields compared to modern wheat cultivars. In sense there is a negative correlation between grain yield and mineral accu-mulation, especially with Zn (McDonald et al. [2008;](#page-18-25) Ficco et al. [2009](#page-16-11); Liu et al. [2014](#page-17-22); Velu et al. [2017](#page-20-12)). Modern wheats with higher grain yields appear to dilute micronutrient concentrations by increasing starch and grain density (McDonald et al. [2008;](#page-18-25) Magallanez–López et al. [2017\)](#page-18-9). However, some studies did not fnd such negative correlations (Welch and Graham [2004](#page-20-23); Peleg et al. [2008](#page-19-8)) (Table [4\)](#page-11-0). This opens an important question why modern wheats have lower mineral accumulation per grain weight unit. Currently, it is difficult to breed for high mineral concentration and high grain yield, especially for Zn, and breeding programs prioritize other traits, not related to micronutrients. Another interesting fact reported by Zhao et al. [\(2009](#page-20-11)), Gomez-Becerra et al. [\(2010](#page-17-21)), and Cakmak et al. [\(2010](#page-15-20)) is a strong positive correlation between Fe and Zn concentration and protein content, which can be explained by shared transporters between both nutrients (Kobayashi and Nishizawa [2012\)](#page-17-23). Overall, the improvement of the nutritional

G	GC	$\bf n$	<b>GPC</b>		Yield				<b>TKW</b>			
					Fe		Zn		Fe		Zn	
DW	GH	192					$-0.61$	$**$			$-0.30$	$**$
	Field	84			$-0.19$		$-0.41$	***	0.16		$-0.08$	
	Field	46	$-0.38$	***	0.17		$-0.29$	**	0.47	***	0.10	
TD	GH	152	$-0.29$	***	$-0.22$	$\ast\ast$	$-0.26$	***				
	Field	22										
	Field	19							0.17		0.47	
Td	Field	$\mathbf{1}$										
G	<b>GPC</b>						Zn/Fe			Ref		
	Fe			Zn								
DW											McDonald et al. 2008	
							0.49	***		Ficco et al. 2009		
	0.29		$**$	0.67	$\ast\ast$		0.35	**			Magallanez-Lopez et al. 2017	
TD	0.59		***	0.55	***		0.79	***		Peleg et al. 2009a		
	0.60		$**$	0.47	$\ast$		0.57	$**$		Peleg et al. 2008		
							0.50	$**$			Gomez-Becerra et al. 2010	
Td							0.77	***		Suchowilska et al. 2012		

<span id="page-11-0"></span>Table 4 Correlation coefficients between grain qualities and Zn and Fe concentrations in tetraploid wheats

*G* genotype; *DW* durum wheat; *TD T. dicoccoides*; *Td T. dicoccum*; *GC* growing conditions; *n* number of genotypes; *GPC* grain protein content; *TKW* thousand kernel weight; *GH* greenhouse; *Ref* references

\* , \*\*, and \*\*\* Signifcant at the .01, .05, and .001 probability level

value of durum cultivars may lead to an indirect increase in technological and industrial quality, which can be simultaneously improved by breeding.

# Genetic architecture of Fe and Zn

The physiological and genetic bases underlying the accumulation of Zn and Fe are poorly understood. The International Maize and Wheat Improvement Center (CIMMYT) and the Consultative Group on International Agricultural Research (CGIAR) are two important entities involved in genetic screening for Fe and Zn. In 2013, CGIAR created HarvestPlus, a program to enhance nutritional quality via biofortifcation. Due to the importance of the topic, several reviews have been made on the genetics of wheat germplasm micronutrients; among the most recent are Gupta et al. [\(2020](#page-17-24)) who reviewed wheat bioavailability and biofortifcation of Zn, Fe, and Selenium (Se), including the genetics and physiology of macronutrients, Saini et al. [\(2020](#page-19-22)) who collated information from wheat studies related to QTL associated with the biofortifcation traits including MAS and genomic selection; Sharma et al. ([2021\)](#page-19-23) reviewed wheat quality changes due to domestication (green revolution), including changes in the wild wheat ancestors and the enhancement of Fe and Zn, as well as the application of genetic engineering focused on transgenic-based Fe and Zn-enriched wheat. Here we only focus on the

genetic diversity ofered by tetraploid wheat species for the Fe and Zn improvement.

*T. dicoccoides* has a high genetic diversity for the mineral nutrient concentrations (Cakmak et al. [2004;](#page-15-0) Peleg et al. [2008](#page-19-8)). Cakmak et al. ([2004\)](#page-15-0) evaluated two sets of *T. dicoccoides* substitution lines, the frst was the bread wheat cv. 'Chinese Spring'-*T. dicoccoides* and the second was the durum cv. 'Langdon'- *T. dicoccoides* suggested that the major genes afecting the accumulation of these micronutrients are located on chromosome 6B of *T. dicoccoides,* while 5B and 6A also appeared to be involved the Chinese Spring–*T. dicoccoides*. Several QTLs have been identifed for grain Fe and Zn content in tetraploid wheats (Table [5](#page-12-0)); these could be introduced into elite genetic backgrounds to improve the micronutrient content. In fact, a total of 5 cultivars of durum wheat rich in either Fe, Zn, or both, have been developed and released in India (Wani et al. [2022](#page-20-26)). Peleg et al. [\(2009a\)](#page-19-6), using a RIL population derived from a cross between durum wheat ('Langdon') and *T. dicoccoides* ('G18-16'), identifed 38 stable QTL associated with the wild alleles from 'G18-16', which explained between 0.7 and 19.2% of the grain mineral nutrient concentration variation, including Zn and Fe. The *T. dicoccoides* gene *Gpc-B1* described by Uayu et al. [\(2006](#page-20-18)) and Distelfeld et al. ([2007\)](#page-16-23), which has been associated with GPC increases (see above), is also related to Zn and Fe grain concentration increases (Tabbita et al. [2017\)](#page-20-21). This allele was evaluated for

<span id="page-12-0"></span>**Table 5** Collected QTL's data for grain Iron and Zinc concentration in *T. diccoccoides* accessions

Trait	Chr	Pos $(cM)$	Interval $(cM)$	Marker name	<b>LOD</b>	PEV $(\%)$	Acc	References
GZnC	2A	112.4	35.0	gwm445	10.5	$10.9 - 11.6$ G18-16		Peleg et al. $2009a$
	5A	25.8	22.0	gwm293	5.2	$1.3 - 9.3$	G18-16	
	6B	133.5	48.6	gwm1076	5.3	$2.2 - 5.4$	G18-16	
	7A	65.8	4.6	$wPt - 9555$	16.4	$9 - 23.5$	G18-16	
<b>GFeC</b>	2A	95.4	32.2	gwm1054	12.2	$8.4 - 12$	G18-16	
	5A	7.5	6.2	gwm154	9.0	$0.8 - 14.6$ G18-16		
	6B	160.5	25.2	$wPt - 5270$	8.2	$2.8 - 6.8$	G18-16	
	7A	66.5	2.4	$wPt-9555$	16.7	$8.2 - 17.8$ G18-16		
GZnC	6B	278.0	$266.0 - 309.9$	wPt-743,099-wPt-5037	3.1	11.7	MM 5/4	Velu et al. 2017
GFeC	1B	212.0	210.8-215.8	wPt-741,612 wPt-729,920	2.8	10.0	MM 5/4	
	3A	284.0	279.2-284.2	wPt-0784 wPt-8875	3.5	12.1	MM 5/4	
	5B	97.0	$94.1 - 108.6$	wPt-7400 wPt-8449	4.7	16.9	MM 5/4	
GZnC	2A	112.4	139.9-145.2	1.077.698-1.234.362		7.86-7.88 D1		Liu et al. $2021$

*GZnC* Grain zinc concentration; *GFeC* Grain iron concentration; *Chr* Chromosome; *Acc* Accession name

its efects on grain micronutrient concentrations in recombinant chromosome substitution lines (RSLs) developed from the cross 'DIC-6B' x 'Langdon' (Joppa et al. [1997](#page-17-19)). RSLs carrying the wild *Gpc-B1* allele had, on average, 12%, 18%, and 29% higher concentrations of Zn, Fe, and Mn in the grain, respectively, as compared to RSLs with the allele from Langdon (Distelfeld et al. [2007](#page-16-23)). The problem was in the association of the *Gpc-B1* allele with reductions in grain weight and yield (Uauy et al. [2006](#page-20-18); Brevis and Dubcovsky [2010;](#page-15-17) Tabbita et al. [2013](#page-20-19)). However, as discussed above, it is important to note that high-yielding wheat cultivars carry the *GPC-B1* allele, therefore, more research can be done regarding this gene (Eagles et al. [2014\)](#page-16-20). Besides, new genomic regions need to be explored (Liu et al. [2021\)](#page-17-10). Liu et al. [\(2021](#page-17-10)) characterized Fe and Zn concentrations in 161 advanced lines derived from *T. dicoccoides* through GWAS. They identifed six markers associated with grain Fe concentration, on chromosomes 3B, 4A, 4B, 5A, and 7B, and three markers associated with Zn concentration on chromosomes 1A and 2A. Some lines with the markers associated with high grain Fe and Zn concentrations showed no reduction in TKW. The Zn concentration markers on chromosome 2A were in the same interval (139.9–145.2 cM) as those of Peleg et al. ([2009a](#page-19-6)), who identifed a wild emmer GZnC-QTL (77.4–147.4 cM). Fatiukha et al. [\(2020b](#page-16-24)) identifed nine QTLs related to grain Fe content (LOD: 2.2–16.4 cM; PVE: 0.6–22.3%) and 10 QTLs for grain Zn content in the 'G18-16' accession of *T. dicoccoides*.

As mentioned earlier, the bioavailability of Zn and Fe depends on several factors which need to be considered in theimprovement of the nutritional value of modern wheats. The PA is a critical component limiting bioavailability. Reducing PA is one strategy for durum breeding programs; however, there is no defned minimum value that would not have a nega-tive effect on the crop (Ram and Govindan [2020](#page-19-24)). Considering that the main form of storage for P is PA (Raboy et al. [1991](#page-19-25)), there is a negative correlation between Zn/Fe and P (Fatiukha et al. [2020b](#page-16-24)). Peleg et al. [\(2009a\)](#page-19-6) identifed a QTL on chromosome 5B of 'G18-16' (*T. dicoccoides*) for grain P that co-localized with a QTL for GPC. This is important as selection for increased GPC is associated with increased grain PA. The wild-type allele associated with high GPC and low P, making it a future alternative for

increasing grain protein content without increasing PA. Genes involved in the biosynthesis pathway of PA are known for multiple crops, such as corn and soybean, but not for durum and/or other tetraploid wheat species. The closest identifcation of these types of genes was made in common wheat by Bhati et al. [\(2014](#page-15-24)), who identifed six genes potentially involved in the ultimate phases of the PA biosynthesis with four of those six genes encoding for inositol tetraphosphate kinases (*TaITPK1*, *TaITPK2*, *TaITPK3*, and *TaITPK4*) and the remaining encoding for the inositol triphosphate kinase (*TaIPK2*) and the inositol pentakisphosphate kinase (*TaIPK1*). The study of the genes related to PA biosynthesis may help in the development of new cultivars with low grain PA content.

## **Conclusions and future prospects**

The information gathered here may offer a better understanding of the general qualities and genetics of *T. dicoccum* and *T. dicoccoides* relative to durum wheat. A comparison of ancestral wheats with durum shows diferences in the grain physical qualities, GPC, protein quality, and the Fe/Zn content. Durum wheat is superior in grain yield, TW, TKW, and VK but its GPC and Fe/Zn concentrations are lower. protein quiality is better in durum than in ancestral wheats, but some promising alleles were detected in *T. dicoccum* for the B-type LMW-GS (Oak et al. [2002](#page-18-19); Degaonkar et al. [2005\)](#page-16-19) and in *T. dicoccoides* (Qin et al. [2015;](#page-19-19) Xiang et al. [2019](#page-20-17)). These may improve viscoelastic properties of the dough made from modern wheats. Lower agronomical performance (biomass and grain yield) of ancestral wheats had been attributed to less selection over time, and hence small grain and associated proportionately higher nutrient and protein content, and cultivation issues associated with hulled, difficult-to-thresh wheats compared to durum wheat.

Better adaptation to abiotic and biotic stressors and the genetic potential of *T. dicoccum* and, especially, *T. dicoccoides* as sources of important genes/alleles for the improvement of quality parameters in modern wheats, such as protein and mineral concentrations, are important considerations for future research. The *T. dicoccoides* gene *Gpc-B1* on chromosome 6B, frst described by Joppa and Cantrell [\(1990](#page-17-18)), has been a well-studied source for the improvement of GPC and Fe and Zn contents. The functional allele from wild emmer eas successfully introgressed into several elite and commercial wheat cultivars, for various environments. However, the presence of *Gpc-B1* is also associated with a reduction in grain yield and some other agronomic parameters in diferent environments. More research is required to identify new genes for GPC and mineral concentration without afecting agronomic qualities.

The negative phenotypic and genetic correlations between grain yield and grain protein quality, besides the positive correlations among GPC, Zn, and Fe, have been reported in various studies. In the future, it is important to understand more deeply the association between agronomical parameters, protein qualities, and mineral concentrations. This would facilitate selection through breeding. Furthermore, a study of genes related to the accumulation and transport of specifc minerals and components like PA should be assessed.

Finally, all information summarized in this review points to the importance of ancestral genetic resources for further studies, as alternative ways to address the grain protein content and mineral Zn and Fe concentrations in durum wheat. Keeping in mind that the primary goal for breeding, for food-related industries, and for growers, is the grain yield increase, further studies should focus on a combination of techniques such as conventional breeding, MAS, GWAS and gene editing. Major QTLs that are expressed in several environments can be used for MAS in breeding and for positional cloning, which may lead to parallel improvement of multiple traits, such as GPC and mineral content, without the grain yield penalty, making this a promising strategy for developing new durum cultivars with improved chemical qualities while retaining agronomic qualities.

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## **Declarations**

**Confict of interest** The Authors have no competing interest to disclose.

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Euphytica (2023) 219:61

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