Data Article

Datasets for grain protein content, yield-related traits, and candidate genes in a durum wheat RIL population derived from a "hexaploid × tetraploid" interspecific cross

Angelica Giancaspro, Stefania Lucia Giove, Ilaria Marcotuli, Agata Gadaleta[*]

Department of Agricultural and Environmental Science (DiSAAT), University of Bari "Aldo Moro", Via G. Amendola 165/A, 70126 Bari, Italy

ARTICLE INFO

ABSTRACT

Data described in this article refer to the evaluation of genetic variability for quantity (grain protein content, GPC) and composition (HMW-glutenin subunits and gliadins) of seed storage proteins, and two yield components (grain yield per spike, GYS, and thousand-kernel weight, TKW) in a durum wheat recombinant inbred line (RIL) population derived by an interspecific cross between the common wheat accession 02-5B-318 and the durum cv. Saragolla. This article provides datasets relative to GPC, GYS and TKW collected in the two parents and in 135 durum RIL progenies from plants grown in field trials conducted in Valenzano (Metropolitan City of Bari, BA, Italy) by a randomized complete block design with three replicates. Data on GPC were acquired from Near-Infrared Reflectance on whole-meal flour and are expressed as percentage of proteins on a dry weight basis. Data relative to composition of seed storage proteins refer to high molecular weight glutenin subunits (encoded by *Glu-A1* and *Glu-B1* loci) and gliadins (encoded by *Gli-B1* locus) extracted from whole-grain samples and identified based on their electrophoretic relative mobility on SDS-PAGE. This paper also provides datasets for the detection of quantitative trait loci

---

[*] Corresponding author.
    E-mail address: agata.gadaleta@uniba.it (A. Gadaleta).

(QTLs) for GPC, GYS, TKW on a durum wheat genetic linkage map previously developed in the same durum population genotyped with the Illumina 90 K iSelect SNP array. The present article finally supports information for the identification of candidate genes related to wheat grain quantity, composition, and yield by providing data relative to all the SNP markers mapped in the QTL confidence intervals for each trait of interest (GPC, GYS, TKW). Data described in this paper support the published original research article titled "Genetic variation for protein content and yield-related traits in a durum population derived from an inter-specific cross between hexaploid and tetraploid wheat cultivars" (Giancaspro et al., 2019).

Specifications Table

Subject	Agricultural Sciences - Agronomy and Crop Science
Specific subject area	The subject area deals with the evaluation of agronomic traits of crop species (durum wheat) including quality, quantity, and productivity. The specific area also includes molecular studies, as investigating genetic loci (QTLs and candidate genes) controlling the traits of interest.
Type of data	Table
	Figure
How the data were acquired	Data on wheat quality and productivity described in this article refer to 135 durum wheat RI lines obtained by the interspecific cross "02-5B-318 × Saragolla", grown in replicated field trials at the location of Valenzano (Metropolitan City of Bari, BA, Italy) for three years (2015, 2016, 2017) [2].
	Data on grain protein content (GPC) were acquired by Near-Infrared Reflectance (NIR) spectroscopy on a 2-g sample of whole-meal flour using a SpectraAlyzer device (Basic model, Zeuton). For each wheat line, GPC was expressed as the percentage of proteins on a dry weight basis, averaged between two technical replicates. Data on grain yield per spike (GYS) were obtained by dividing the total grain yield per row on the number of spikes per row (about 70-80 spikes). Data on thousand-kernel weight (TKW) were derived from a 15-gram seed sample per each line, as the average of two technical replicates.
	Data on grain storage proteins composition were acquired from SDS-PAGE electrophoresis of wheat seed extracts. Gliadins and HMW-glutenin subunits were extracted from whole-grain samples according to the protocols by Payne et al. [3] and Bushuk and Zillman [4], respectively. Protein identification was based on relative mobility in SDS-electrophoresis run in Protean II Xi vertical cells (Bio-Rad Laboratories); gel imaging acquisition and software analysis were performed by DigiDoc (Bio-Rad Laboratories).
	QTL detection was performed using the Inclusive Composite Interval Mapping (ICIM) method [5] implemented in QGene 4.0 software [6]. Genotypic data for QTL mapping were acquired from the 4,366 SNP-based durum wheat genetic linkage map developed by Giancaspro et al. [2].
	Putative functions of SNP markers located in the QTLs confidence intervals for GPC, GYS and TKW were acquired by a bioinformatic survey: SNP sequences were blasted against draft genomes of tetraploid and hexaploid wheat cultivars by using the TBLASTX algorithm at: http://ncbi.nlm.nih.gov/BLAST. Only matches scoring $\geq 80\%$ identity and $>10^{-7}$ E-value were considered for the identification of candidate genes.
Data format	Analysed
	Filtered

Description of data collection	Data described in this article refer to 135 durum wheat recombinant inbred lines obtained by an interspecific cross between the bread wheat accession 02-5B-318 (derived from the Chinese cv. Sumai-3) and the élite durum wheat cv. Saragolla [2]. The two crossing parents were chosen because different for several agronomic traits related to grain quality (grain protein content, yellow index, gluten index, plant height, spike compactness), productivity (yield components), and resistance to Fusarium Head Blight (FHB-resistant 02-5B-318, FHB-susceptible Saragolla). The same population was previously employed for several aims: development of a durum wheat genetic linkage map [2], identification of cell wall traits conferring resistance to FHB [7,8], mapping of QTLs for FHB resistance, quality- and yield-related traits [1,2,9], map-based cloning of FHB resistance genes [10].
	Datasets in this paper only refer to the "02-5B-318 × Saragolla" progenies lacking D-genome chromosomes (tetraploid subset), whereas all wheat RILs carrying D-genome sequences (hexaploid subset) were excluded from the analyses.
	Data on GPC, GYS and TKW of parents and durum RILs were collected from plants grown in replicated field trials at the location of Valenzano (Metropolitan City of Bari, BA, Italy) for three years (from 2015 to 2017) by using a randomized complete block design with three replicates.
	QTL detection was performed by QGene software [6] using the ICIM method [5]: a LOD threshold ≥ 3 was set for the identification of putative QTLs. Trait-associated SNPs at LOD ≤ 2 were considered not significant. Suggestive QTLs were classified as one or more trait-associated SNP marker at the subthreshold of $2.0 < LOD < 3.0$. The following criteria were used for classification of additive effects: positive additive effects were associated with increased trait values from Saragolla alleles, whereas negative additive effects were contributed from 02-5B-318 alleles.
	Parents and durum RILs were characterized for seed storage protein subunits encoded by the HMW-GS loci *Glu-A1* and *Glu-B1*, and the gliadin locus *Gli-B1*. "02-5B-318 × Saragolla" progenies were scored for carrying the alleles coming from 02-5B-318 parent (2* HMW-GS, 7 + 9 HMW-GS, γ-42 gliadin) or Saragolla parent (null 2* HMW-GS, 6 + 8 HMW-GS, γ-45 gliadin). Data on protein composition were acquired based on their relative mobility in vertical SDS-PAGE.
	For the identification of candidate genes among SNPs mapping in the QTLs confidence intervals for GPC, GYS and TKW, only sequence alignments scoring $\geq 80\%$ identity and $>10^{-7}$ E-value were considered, and the corresponding putative genes evaluated for their actual involvement in metabolic pathways related to wheat protein quality/content and productivity. Matches with $< 80\%$ identity were not considered.
Data source location	Field data collection: • Azienda Agricola "Martucci" • Valenzano (Metropolitan City of Bari, BA) • Italy • Lat. 41.0438° N, long. 16.8842° E, elevation 85 m above sea level. Secondary data production (analyses and filtering): • University of Bari "Aldo Moro", Department of Agricultural and Environmental Science (DiSAAT) • Metropolitan City of Bari (BA) • Italy • Lat. 41.12688° N, long. 16.86596° E, elevation 5 m above sea level.
Data accessibility	Repository name: Mendeley Data Data identification number: DOI:10.17632/g6gsfn9k9j.1 Direct URL to data: https://data.mendeley.com/datasets/g6gsfn9k9j/1
Related research article	A. Giancaspro, S.L. Giove, S.A. Zacheo, A. Blanco, A. Gadaleta, Genetic variation for protein content and yield-related traits in a durum population derived from an inter-specific cross between hexaploid and tetraploid wheat cultivars, Front. Plant Sci. 10 (2019) 1509.

Value of the Data

- Datasets reported in the present article are valuable as they include original data on new genetic variability for seed storage protein quantity and quality originated by crossing the common wheat line 02-5B-318 and the durum cv Saragolla. Moreover, this paper supplies detailed protocols and references to allow experimental research reproducibility.
- Data described in this article are addressed to the scientific community working on durum wheat breeding. Scientists who can benefit from the reported datasets are especially those breeders interested in exploiting the genetic variability within the RIL population derived from the cross "02-5B-318 × Saragolla".
- Data on GPC and seed storage protein composition reported in the present article can be used for further identification of high-quality wheat lines to be employed - directly or as donor genotypes - in breeding programs for the development of novel durum varieties with increased commercial and nutritional relevance. Data relative to QTL mapping and candidate genes can be helpful for further dissecting the molecular basis of wheat quality and yield-related traits. Particularly, these data may support the development of new QTL-associated genetic markers exploitable in MAS breeding programs.

1. Data Description

Table 1 reports data relative to grain protein content (GPC) of two parents and 135 durum RILs derived by the interspecific cross "02-5B-318 × Saragolla". Data refer to wheat lines grown in replicated field trials at Valenzano (Metropolitan City of Bari, BA, Italy) in years 2015 (GPC_Val15), 2016 (GPC_Val16), and 2017 (GPC_Val17). Average of environments (GPC_Mean) is also reported. For each line, reported GPC is the mean of three field replicates, each averaged between two measurements. GPC is reported as protein percentage on dry matter calculated by the following formula: GPC% d.m. = [Tot. GPC% / (100 − H%)] × 100.

Table 2 lists data relative to grain yield per spike (GYS) of two parents and 135 durum RILs derived by the interspecific cross "02-5B-318 × Saragolla". Data refer to wheat lines grown in replicated field trials at Valenzano (Metropolitan City of Bari, BA, Italy) in years 2015 (GYS_Val15), 2016 (GYS_Val16), and 2017 (GYS_Val17). Average of environments (GYS_Mean) is also reported. For each line, reported GYS is the mean of three field replicates, each averaged between two measurements.

Table 3 supplies data relative to thousand-kernel weight (TKW) of two parents and 135 durum RILs derived by the inter-specific cross "02-5B-318 × Saragolla". Data refer to wheat lines grown in replicated field trials at Valenzano (Metropolitan City of Bari, BA, Italy) in years 2015 (TKW_Val15), 2016 (TKW_Val16), and 2017 (TKW_Val17). Average of environments (TKW_ Mean) is also reported. For each line, reported TKW is the mean of three field replicates, each averaged between two measurements.

Table 4 reports the composition of grain storage proteins in two parents and 135 durum RI lines obtained by the interspecific cross "02-5B-318 × Saragolla". Parents and RILs were characterized for protein subunits encoded by the HMW-GS loci *Glu-A1* and *Glu-B1*, and the gliadin locus *Gli-B1*. The common wheat parent 02-5B-318 carried the *1Ax2** allele of *Glu-A1* gene encoding the 2* HMW-GS, the *Bx7* and *By9* alleles of *Glu-B1* gene encoding 7 + 9 HMW-GS, and the allele for γ-42 gliadin at *Gli-B1* locus. The durum wheat parent Saragolla had the following allele combination: null allele at the *Glu-A1* locus*; Bx6* and *By8* alleles of *Glu-B1* gene encoding 6 + 8 HMW-GS, and the allele for γ-45 gliadin at *Gli-B1* locus.

Fig. 1 depicts SDS-PAGE analysis of seed extracts from the two parents and some durum RILs obtained by the interspecific cross "02-5B-318 × Saragolla". In the photo, wheat lines were screened for the HMW glutenin subunits encoded by *Glu-A1* and *Glu-B1* loci and were classified for carrying the allele combination of 02-5B-318 parent (2*/ 7 + 9 HMW-GS) or Saragolla

Table 1

Grain protein content (GPC) in two parents and 135 durum wheat RILs derived by the "02-5B-318 × Saragolla" inter-specific cross. Data refer to three environments (GPC_Val15; GPC_Val16; GPC_Val17) and the average of environments (GPC_Mean). Reported values represent the mean of three field replicates, each averaged between two measurements. % d.m. = percentage proteins on dry matter calculated as: [Tot. GPC% / (100 - H%)] × 100.

Genotype	Line	Line name	GPC_Val15 (% d.m.)	GPC_Val16 (% d.m.)	GPC_Val17 (% d.m.)	GPC_mean (% d.m.)
Common	Parent	02-5B-318	13.88	14.45	12.37	13.57
Durum	Parent	Saragolla	12.33	17.12	13.25	14.23
Durum	RIL (F_7:F_8)	1	16.45	15.74	13.56	15.25
Durum	RIL (F_7:F_8)	2	17.09	17.59	13.82	16.17
Durum	RIL (F_7:F_8)	3	15.25	13.82	12.99	14.02
Durum	RIL (F_7:F_8)	4	18.41	16.27	14.57	16.42
Durum	RIL (F_7:F_8)	5	–	16.79	12.41	14.60
Durum	RIL (F_7:F_8)	6	16.28	18.79	13.34	16.14
Durum	RIL (F_7:F_8)	7	16.34	18.21	13.55	16.04
Durum	RIL (F_7:F_8)	8	17.57	17.14	13.42	16.05
Durum	RIL (F_7:F_8)	9	–	–	–	–
Durum	RIL (F_7:F_8)	10	15.30	16.50	12.82	14.87
Durum	RIL (F_7:F_8)	11	14.39	13.44	13.89	13.91
Durum	RIL (F_7:F_8)	12	15.07	14.65	14.41	14.71
Durum	RIL (F_7:F_8)	13	15.57	17.87	14.22	15.89
Durum	RIL (F_7:F_8)	14	17.99	15.59	15.26	16.28
Durum	RIL (F_7:F_8)	15	14.37	14.92	14.33	14.54
Durum	RIL (F_7:F_8)	16	18.64	18.37	16.04	17.69
Durum	RIL (F_7:F_8)	17	15.45	15.72	14.80	15.32
Durum	RIL (F_7:F_8)	18	18.63	16.71	15.23	16.86
Durum	RIL (F_7:F_8)	19	15.53	17.14	13.72	15.46
Durum	RIL (F_7:F_8)	20	18.27	17.53	15.56	17.12
Durum	RIL (F_7:F_8)	21	14.38	16.41	13.73	14.84
Durum	RIL (F_7:F_8)	22	13.34	14.97	13.21	13.84
Durum	RIL (F_7:F_8)	23	13.99	16.35	14.32	14.89
Durum	RIL (F_7:F_8)	24	15.39	15.34	13.27	14.67
Durum	RIL (F_7:F_8)	25	16.74	17.59	14.32	16.22
Durum	RIL (F_7:F_8)	26	14.71	15.60	14.55	14.96
Durum	RIL (F_7:F_8)	27	13.24	16.22	13.43	14.30
Durum	RIL (F_7:F_8)	28	13.80	15.71	13.78	14.43
Durum	RIL (F_7:F_8)	29	–	–	–	–
Durum	RIL (F_7:F_8)	30	16.41	14.22	14.95	15.19
Durum	RIL (F_7:F_8)	31	17.50	15.56	16.67	16.58
Durum	RIL (F_7:F_8)	32	14.45	16.28	14.88	15.20
Durum	RIL (F_7:F_8)	33	15.15	15.77	13.94	14.95
Durum	RIL (F_7:F_8)	34	17.73	17.34	15.08	16.72
Durum	RIL (F_7:F_8)	35	17.07	16.49	15.58	16.38
Durum	RIL (F_7:F_8)	36	17.27	16.51	16.30	16.69
Durum	RIL (F_7:F_8)	37	17.99	17.64	17.65	17.76
Durum	RIL (F_7:F_8)	38	16.55	17.34	15.96	16.62
Durum	RIL (F_7:F_8)	39	18.98	16.22	17.88	17.69
Durum	RIL (F_7:F_8)	40	19.57	19.12	15.77	18.15
Durum	RIL (F_7:F_8)	41	15.78	15.57	14.88	15.41
Durum	RIL (F_7:F_8)	42	–	–	–	–
Durum	RIL (F_7:F_8)	43	17.93	14.43	16.18	16.18
Durum	RIL (F_7:F_8)	44	17.01	14.82	15.27	15.70
Durum	RIL (F_7:F_8)	45	15.00	15.35	14.65	15.00
Durum	RIL (F_7:F_8)	46	16.42	18.33	14.79	16.51
Durum	RIL (F_7:F_8)	47	18.41	19.77	16.21	18.13
Durum	RIL (F_7:F_8)	48	17.40	15.42	13.73	15.52
Durum	RIL (F_7:F_8)	49	15.47	15.15	13.88	14.83
Durum	RIL (F_7:F_8)	50	–	–	–	–
Durum	RIL (F_7:F_8)	51	14.97	15.49	14.95	15.13
Durum	RIL (F_7:F_8)	52	–	–	–	–
Durum	RIL (F_7:F_8)	53	14.47	16.54	13.80	14.94

Table 1 (_continued_)

Genotype	Line	Line name	GPC_Val15 (% d.m.)	GPC_Val16 (% d.m.)	GPC_Val17 (% d.m.)	GPC_mean (% d.m.)
Durum	RIL (F_7:F_8)	54	–	–	–	–
Durum	RIL (F_7:F_8)	55	17.74	16.80	15.23	16.59
Durum	RIL (F_7:F_8)	56	19.31	17.21	15.90	17.47
Durum	RIL (F_7:F_8)	57	–	18.20	18.12	18.16
Durum	RIL (F_7:F_8)	58	15.47	17.25	15.24	15.98
Durum	RIL (F_7:F_8)	59	16.32	14.72	14.87	15.30
Durum	RIL (F_7:F_8)	60	14.16	13.84	14.68	14.22
Durum	RIL (F_7:F_8)	61	15.65	15.75	14.85	15.42
Durum	RIL (F_7:F_8)	62	18.40	18.80	15.71	17.64
Durum	RIL (F_7:F_8)	63	–	–	–	–
Durum	RIL (F_7:F_8)	64	–	–	–	–
Durum	RIL (F_7:F_8)	65	17.22	15.41	15.53	16.05
Durum	RIL (F_7:F_8)	66	13.94	14.48	14.63	14.35
Durum	RIL (F_7:F_8)	67	15.92	18.67	14.88	16.49
Durum	RIL (F_7:F_8)	68	18.60	18.92	15.33	17.62
Durum	RIL (F_7:F_8)	69	14.74	16.71	14.82	15.42
Durum	RIL (F_7:F_8)	70	16.73	14.76	15.18	15.56
Durum	RIL (F_7:F_8)	71	16.04	16.46	14.29	15.60
Durum	RIL (F_7:F_8)	72	17.19	16.51	16.33	16.68
Durum	RIL (F_7:F_8)	73	16.36	19.00	14.73	16.70
Durum	RIL (F_7:F_8)	74	14.76	16.38	14.23	15.12
Durum	RIL (F_7:F_8)	75	17.29	19.05	14.73	17.03
Durum	RIL (F_7:F_8)	76	15.08	16.63	14.54	15.42
Durum	RIL (F_7:F_8)	77	16.72	16.06	15.62	16.13
Durum	RIL (F_7:F_8)	78	14.48	15.04	14.72	14.75
Durum	RIL (F_7:F_8)	79	17.45	17.04	15.61	16.70
Durum	RIL (F_7:F_8)	80	18.36	18.68	16.25	17.76
Durum	RIL (F_7:F_8)	81	16.56	16.50	16.14	16.40
Durum	RIL (F_7:F_8)	82	17.10	18.34	15.37	16.94
Durum	RIL (F_7:F_8)	83	17.04	15.91	16.02	16.32
Durum	RIL (F_7:F_8)	84	18.31	16.44	15.64	16.80
Durum	RIL (F_7:F_8)	85	–	–	14.05	14.05
Durum	RIL (F_7:F_8)	86	15.40	15.84	16.03	15.76
Durum	RIL (F_7:F_8)	87	16.38	16.12	15.08	15.86
Durum	RIL (F_7:F_8)	88	17.18	16.98	15.55	16.57
Durum	RIL (F_7:F_8)	89	18.81	15.45	13.70	15.99
Durum	RIL (F_7:F_8)	90	–	–	–	–
Durum	RIL (F_7:F_8)	91	–	16.98	13.35	15.17
Durum	RIL (F_7:F_8)	92	19.53	16.73	16.93	17.73
Durum	RIL (F_7:F_8)	93	17.44	16.10	17.70	17.08
Durum	RIL (F_7:F_8)	94	17.10	15.61	17.07	16.59
Durum	RIL (F_7:F_8)	95	16.99	18.71	14.94	16.88
Durum	RIL (F_7:F_8)	96	13.60	13.62	12.96	13.39
Durum	RIL (F_7:F_8)	97	22.10	20.18	15.98	19.42
Durum	RIL (F_7:F_8)	98	15.95	17.03	15.26	16.08
Durum	RIL (F_7:F_8)	99	14.63	15.96	15.43	15.34
Durum	RIL (F_7:F_8)	100	16.90	16.64	14.95	16.16
Durum	RIL (F_7:F_8)	101	15.29	16.28	14.63	15.40
Durum	RIL (F_7:F_8)	102	16.94	16.12	13.57	15.54
Durum	RIL (F_7:F_8)	103	–	–	–	–
Durum	RIL (F_7:F_8)	104	16.60	15.79	15.16	15.85
Durum	RIL (F_7:F_8)	105	–	–	–	–
Durum	RIL (F_7:F_8)	106	17.94	17.75	14.87	16.85
Durum	RIL (F_7:F_8)	107	15.79	17.94	14.21	15.98
Durum	RIL (F_7:F_8)	108	–	–	–	–
Durum	RIL (F_7:F_8)	109	–	17.01	16.60	16.81
Durum	RIL (F_7:F_8)	110	14.75	14.07	15.37	14.73
Durum	RIL (F_7:F_8)	111	17.92	19.12	15.94	17.66
Durum	RIL (F_7:F_8)	112	18.44	14.96	16.60	16.67

Table 1 (*continued*)

Genotype	Line	Line name	GPC_Val15 (% d.m.)	GPC_Val16 (% d.m.)	GPC_Val17 (% d.m.)	GPC_mean (% d.m.)
Durum	RIL (F$_7$:F$_8$)	113	18.83	18.67	16.57	18.02
Durum	RIL (F$_7$:F$_8$)	114	18.63	17.46	16.83	17.64
Durum	RIL (F$_7$:F$_8$)	115	–	–	16.34	16.34
Durum	RIL (F$_7$:F$_8$)	116	16.89	16.76	15.27	16.31
Durum	RIL (F$_7$:F$_8$)	117	18.65	21.14	17.22	19.00
Durum	RIL (F$_7$:F$_8$)	118	14.94	16.80	14.58	15.44
Durum	RIL (F$_7$:F$_8$)	119	16.05	16.90	14.88	15.95
Durum	RIL (F$_7$:F$_8$)	120	14.34	15.72	15.48	15.18
Durum	RIL (F$_7$:F$_8$)	121	17.55	16.20	15.49	16.41
Durum	RIL (F$_7$:F$_8$)	122	17.28	17.47	15.64	16.80
Durum	RIL (F$_7$:F$_8$)	123	20.05	20.25	16.24	18.84
Durum	RIL (F$_7$:F$_8$)	124	–	17.69	16.89	17.29
Durum	RIL (F$_7$:F$_8$)	125	16.65	16.61	14.07	15.78
Durum	RIL (F$_7$:F$_8$)	126	–	19.48	15.25	17.36
Durum	RIL (F$_7$:F$_8$)	127	14.56	15.28	14.41	14.75
Durum	RIL (F$_7$:F$_8$)	128	18.49	16.77	16.92	17.39
Durum	RIL (F$_7$:F$_8$)	129	12.18	14.69	13.92	13.60
Durum	RIL (F$_7$:F$_8$)	130	14.74	14.50	14.53	14.59
Durum	RIL (F$_7$:F$_8$)	131	19.66	19.28	16.21	18.38
Durum	RIL (F$_7$:F$_8$)	132	16.28	16.77	15.35	16.13
Durum	RIL (F$_7$:F$_8$)	133	14.10	14.58	15.42	14.70
Durum	RIL (F$_7$:F$_8$)	134	14.74	16.22	14.96	15.30
Durum	RIL (F$_7$:F$_8$)	135	–	–	–	–

Table 2

Grain yield per spike (GYS) in two parents and 135 durum wheat RILs derived by the "02-5B-318 × Saragolla" inter-specific cross. Data refer to three environments (GYS_Val15; GYS_Val16; GYS_Val17) and the average of environments (GYS_Mean). Reported values represent the mean of three field replicates, each averaged between two measurements.

Genotype	Line	Line name	GYS_Val15 (g)	GYS_Val16 (g)	GYS_Val17 (g)	GYS_mean (g)
Common	Parent	02-5B-318	1.30	1.47	0.99	1.25
Durum	Parent	Saragolla	2.26	2.78	1.68	2.24
Durum	RIL (F$_7$:F$_8$)	1	1.17	1.19	1.07	1.14
Durum	RIL (F$_7$:F$_8$)	2	1.07	0.74	1.21	1.01
Durum	RIL (F$_7$:F$_8$)	3	1.26	1.58	1.03	1.29
Durum	RIL (F$_7$:F$_8$)	4	0.99	1.24	0.81	1.01
Durum	RIL (F$_7$:F$_8$)	5	0.91	1.85	1.88	1.55
Durum	RIL (F$_7$:F$_8$)	6	1.18	1.63	1.00	1.27
Durum	RIL (F$_7$:F$_8$)	7	1.61	1.46	1.59	1.55
Durum	RIL (F$_7$:F$_8$)	8	1.11	0.93	1.25	1.10
Durum	RIL (F$_7$:F$_8$)	9	–	–	–	–
Durum	RIL (F$_7$:F$_8$)	10	1.15	1.14	1.22	1.17
Durum	RIL (F$_7$:F$_8$)	11	2.40	–	1.41	1.91
Durum	RIL (F$_7$:F$_8$)	12	1.44	1.57	1.34	1.45
Durum	RIL (F$_7$:F$_8$)	13	1.31	1.10	1.33	1.25
Durum	RIL (F$_7$:F$_8$)	14	0.73	1.06	0.63	0.81
Durum	RIL (F$_7$:F$_8$)	15	1.19	1.40	1.24	1.28
Durum	RIL (F$_7$:F$_8$)	16	0.46	0.71	0.64	0.60
Durum	RIL (F$_7$:F$_8$)	17	1.63	1.68	1.30	1.54
Durum	RIL (F$_7$:F$_8$)	18	1.05	0.93	0.99	0.99
Durum	RIL (F$_7$:F$_8$)	19	1.13	1.47	1.22	1.27
Durum	RIL (F$_7$:F$_8$)	20	0.79	1.21	1.19	1.06
Durum	RIL (F$_7$:F$_8$)	21	1.50	1.60	1.49	1.53
Durum	RIL (F$_7$:F$_8$)	22	1.51	2.18	1.59	1.76
Durum	RIL (F$_7$:F$_8$)	23	1.91	2.45	1.50	1.95

Table 2 (*continued*)

Genotype	Line	Line name	GYS_Val15 (g)	GYS_Val16 (g)	GYS_Val17 (g)	GYS_mean (g)
Durum	RIL (F_7:F_8)	24	1.67	1.86	1.53	1.69
Durum	RIL (F_7:F_8)	25	1.44	1.40	1.21	1.35
Durum	RIL (F_7:F_8)	26	1.71	1.92	0.99	1.54
Durum	RIL (F_7:F_8)	27	1.30	1.72	1.08	1.37
Durum	RIL (F_7:F_8)	28	1.48	1.82	1.45	1.58
Durum	RIL (F_7:F_8)	29	–	–	–	–
Durum	RIL (F_7:F_8)	30	1.30	1.22	0.71	1.08
Durum	RIL (F_7:F_8)	31	0.72	0.85	0.53	0.70
Durum	RIL (F_7:F_8)	32	1.64	1.45	1.36	1.48
Durum	RIL (F_7:F_8)	33	1.48	1.31	1.07	1.29
Durum	RIL (F_7:F_8)	34	1.40	1.56	1.11	1.36
Durum	RIL (F_7:F_8)	35	1.35	2.09	1.10	1.51
Durum	RIL (F_7:F_8)	36	0.93	1.15	0.91	1.00
Durum	RIL (F_7:F_8)	37	1.29	1.40	0.68	1.12
Durum	RIL (F_7:F_8)	38	1.60	–	1.10	1.35
Durum	RIL (F_7:F_8)	39	0.72	–	0.47	0.60
Durum	RIL (F_7:F_8)	40	0.43	–	0.79	0.61
Durum	RIL (F_7:F_8)	41	1.00	1.32	0.71	1.01
Durum	RIL (F_7:F_8)	42	–	–	–	–
Durum	RIL (F_7:F_8)	43	0.88	0.97	0.52	0.79
Durum	RIL (F_7:F_8)	44	0.64	0.93	0.65	0.74
Durum	RIL (F_7:F_8)	45	1.15	1.15	0.89	1.06
Durum	RIL (F_7:F_8)	46	1.30	0.98	1.22	1.17
Durum	RIL (F_7:F_8)	47	1.29	1.29	0.98	1.19
Durum	RIL (F_7:F_8)	48	1.46	2.22	1.54	1.74
Durum	RIL (F_7:F_8)	49	2.06	1.81	1.34	1.74
Durum	RIL (F_7:F_8)	50	–	–	–	–
Durum	RIL (F_7:F_8)	51	1.38	1.49	0.99	1.29
Durum	RIL (F_7:F_8)	52	–	–	–	–
Durum	RIL (F_7:F_8)	53	1.63	1.13	1.29	1.35
Durum	RIL (F_7:F_8)	54	–	–	–	–
Durum	RIL (F_7:F_8)	55	1.05	1.18	1.38	1.20
Durum	RIL (F_7:F_8)	56	0.70	0.99	0.87	0.85
Durum	RIL (F_7:F_8)	57	0.26	1.11	0.59	0.65
Durum	RIL (F_7:F_8)	58	1.23	1.20	1.15	1.19
Durum	RIL (F_7:F_8)	59	1.69	1.80	1.13	1.54
Durum	RIL (F_7:F_8)	60	0.85	1.22	0.89	0.99
Durum	RIL (F_7:F_8)	61	1.39	1.85	1.22	1.49
Durum	RIL (F_7:F_8)	62	0.30	0.49	0.50	0.43
Durum	RIL (F_7:F_8)	63	–	–	–	–
Durum	RIL (F_7:F_8)	64	0.87	1.16	0.89	0.97
Durum	RIL (F_7:F_8)	65	-	–	–	–
Durum	RIL (F_7:F_8)	66	1.35	1.70	1.01	1.35
Durum	RIL (F_7:F_8)	67	1.31	0.75	1.10	1.05
Durum	RIL (F_7:F_8)	68	0.81	0.99	1.04	0.95
Durum	RIL (F_7:F_8)	69	1.29	0.99	1.20	1.16
Durum	RIL (F_7:F_8)	70	1.35	1.48	1.08	1.30
Durum	RIL (F_7:F_8)	71	1.44	1.46	1.18	1.36
Durum	RIL (F_7:F_8)	72	1.34	1.44	0.95	1.24
Durum	RIL (F_7:F_8)	73	1.31	1.17	1.37	1.28
Durum	RIL (F_7:F_8)	74	1.31	1.52	1.11	1.31
Durum	RIL (F_7:F_8)	75	0.91	0.65	1.33	0.96
Durum	RIL (F_7:F_8)	76	1.09	1.19	1.00	1.09
Durum	RIL (F_7:F_8)	77	1.32	2.05	0.90	1.42
Durum	RIL (F_7:F_8)	78	1.15	1.02	0.94	1.04
Durum	RIL (F_7:F_8)	79	1.19	1.55	0.95	1.23
Durum	RIL (F_7:F_8)	80	0.80	0.89	0.60	0.76
Durum	RIL (F_7:F_8)	81	1.42	1.52	0.94	1.29
Durum	RIL (F_7:F_8)	82	0.85	0.76	0.92	0.84
Durum	RIL (F_7:F_8)	83	0.84	1.01	0.71	0.85

Table 2 (*continued*)

Genotype	Line	Line name	GYS_Val15 (g)	GYS_Val16 (g)	GYS_Val17 (g)	GYS_mean (g)
Durum	RIL (F_7:F_8)	84	0.65	0.77	0.75	0.72
Durum	RIL (F_7:F_8)	85	–	–	1.83	1.83
Durum	RIL (F_7:F_8)	86	1.11	0.83	0.76	0.90
Durum	RIL (F_7:F_8)	87	1.20	1.19	0.84	1.08
Durum	RIL (F_7:F_8)	88	1.12	0.98	1.01	1.04
Durum	RIL (F_7:F_8)	89	0.75	0.90	1.03	0.89
Durum	RIL (F_7:F_8)	90	-	–	–	–
Durum	RIL (F_7:F_8)	91	0.42	1.41	1.48	1.10
Durum	RIL (F_7:F_8)	92	0.52	1.25	0.79	0.85
Durum	RIL (F_7:F_8)	93	1.14	–	0.64	0.89
Durum	RIL (F_7:F_8)	94	0.79	1.52	0.78	1.03
Durum	RIL (F_7:F_8)	95	0.96	0.57	1.42	0.98
Durum	RIL (F_7:F_8)	96	1.39	1.49	1.21	1.36
Durum	RIL (F_7:F_8)	97	0.22	0.38	0.61	0.40
Durum	RIL (F_7:F_8)	98	1.07	1.45	1.48	1.33
Durum	RIL (F_7:F_8)	99	1.05	1.55	1.25	1.28
Durum	RIL (F_7:F_8)	100	1.17	–	0.93	1.05
Durum	RIL (F_7:F_8)	101	1.39	1.56	1.30	1.42
Durum	RIL (F_7:F_8)	102	1.14	1.70	1.51	1.45
Durum	RIL (F_7:F_8)	103	0.43	–	–	0.43
Durum	RIL (F_7:F_8)	104	0.67	0.71	0.62	0.67
Durum	RIL (F_7:F_8)	105	–	–	–	–
Durum	RIL (F_7:F_8)	106	0.62	0.94	1.03	0.86
Durum	RIL (F_7:F_8)	107	1.39	0.78	1.26	1.14
Durum	RIL (F_7:F_8)	108	–	–	–	–
Durum	RIL (F_7:F_8)	109	0.26	1.34	0.74	0.78
Durum	RIL (F_7:F_8)	110	1.51	1.52	1.39	1.47
Durum	RIL (F_7:F_8)	111	0.68	0.56	0.64	0.63
Durum	RIL (F_7:F_8)	112	1.26	1.24	0.74	1.08
Durum	RIL (F_7:F_8)	113	0.57	0.93	0.82	0.77
Durum	RIL (F_7:F_8)	114	0.70	0.58	0.61	0.63
Durum	RIL (F_7:F_8)	115	0.71	–	0.64	0.68
Durum	RIL (F_7:F_8)	116	0.68	1.21	0.94	0.94
Durum	RIL (F_7:F_8)	117	0.43	0.80	0.64	0.62
Durum	RIL (F_7:F_8)	118	1.24	0.76	1.12	1.04
Durum	RIL (F_7:F_8)	119	1.20	1.00	1.30	1.17
Durum	RIL (F_7:F_8)	120	1.24	0.91	1.04	1.06
Durum	RIL (F_7:F_8)	121	0.96	1.03	0.96	0.98
Durum	RIL (F_7:F_8)	122	0.83	1.46	0.84	1.04
Durum	RIL (F_7:F_8)	123	0.39	0.50	0.71	0.53
Durum	RIL (F_7:F_8)	124	0.34	2.01	0.67	1.01
Durum	RIL (F_7:F_8)	125	0.65	0.56	1.06	0.76
Durum	RIL (F_7:F_8)	126	–	0.87	1.00	0.94
Durum	RIL (F_7:F_8)	127	1.34	1.58	1.15	1.36
Durum	RIL (F_7:F_8)	128	0.93	1.42	0.64	1.00
Durum	RIL (F_7:F_8)	129	1.47	1.18	1.13	1.26
Durum	RIL (F_7:F_8)	130	1.34	1.44	0.92	1.23
Durum	RIL (F_7:F_8)	131	0.97	0.92	0.90	0.93
Durum	RIL (F_7:F_8)	132	0.75	–	0.89	0.82
Durum	RIL (F_7:F_8)	133	1.32	1.34	0.87	1.18
Durum	RIL (F_7:F_8)	134	1.28	1.17	1.10	1.18
Durum	RIL (F_7:F_8)	135	–	–	–	–

Table 3

Thousand-kernel weight (TKW) in two parents and 135 durum wheat RILs derived by the "02-5B-318 × Saragolla" interspecific cross. Data refer to three environments (TKW_Val15; TKW_Val16; TKW_Val17) and the average of environments (TKW_Mean). Reported values represent the mean of three field replicates, each averaged between two measurements.

Genotype	Line	Line name	TKW_Val15 (g)	TKW_Val16 (g)	TKW_Val17 (g)	TKW_mean (g)
Common	Parent	02-5B-318	32.68	43.56	30.58	35.61
Durum	Parent	Saragolla	41.76	51.52	38.16	43.81
Durum	RIL (F$_7$:F$_8$)	1	36.92	34.75	38.30	36.66
Durum	RIL (F$_7$:F$_8$)	2	34.18	21.56	42.27	32.67
Durum	RIL (F$_7$:F$_8$)	3	33.66	42.96	34.97	37.20
Durum	RIL (F$_7$:F$_8$)	4	31.23	27.17	34.4	30.93
Durum	RIL (F$_7$:F$_8$)	5	31.68	40.96	46.80	39.81
Durum	RIL (F$_7$:F$_8$)	6	37.03	40.47	36.40	37.97
Durum	RIL (F$_7$:F$_8$)	7	40.47	43.84	40.37	41.56
Durum	RIL (F$_7$:F$_8$)	8	39.23	40.23	46.37	41.94
Durum	RIL (F$_7$:F$_8$)	9	–	–	–	–
Durum	RIL (F$_7$:F$_8$)	10	42.25	37.20	38.27	39.24
Durum	RIL (F$_7$:F$_8$)	11	36.01	–	31.87	33.94
Durum	RIL (F$_7$:F$_8$)	12	39.62	40.46	41.33	40.47
Durum	RIL (F$_7$:F$_8$)	13	36.14	40.26	40.37	38.92
Durum	RIL (F$_7$:F$_8$)	14	28.24	30.24	32.23	30.24
Durum	RIL (F$_7$:F$_8$)	15	32.69	30.66	33.40	32.25
Durum	RIL (F$_7$:F$_8$)	16	37.20	40.89	39.87	39.32
Durum	RIL (F$_7$:F$_8$)	17	48.13	40.81	45.03	44.66
Durum	RIL (F$_7$:F$_8$)	18	40.48	40.34	45.40	42.07
Durum	RIL (F$_7$:F$_8$)	19	37.21	42.94	41.77	40.64
Durum	RIL (F$_7$:F$_8$)	20	42.92	47.35	53.00	47.76
Durum	RIL (F$_7$:F$_8$)	21	33.03	30.75	33.03	32.27
Durum	RIL (F$_7$:F$_8$)	22	28.03	37.05	28.33	31.14
Durum	RIL (F$_7$:F$_8$)	23	35.46	40.52	32.93	36.30
Durum	RIL (F$_7$:F$_8$)	24	45.27	50.22	45.27	46.92
Durum	RIL (F$_7$:F$_8$)	25	45.88	43.89	40.97	43.58
Durum	RIL (F$_7$:F$_8$)	26	43.23	44.00	36.10	41.11
Durum	RIL (F$_7$:F$_8$)	27	33.64	40.53	33.30	35.82
Durum	RIL (F$_7$:F$_8$)	28	36.17	40.84	36.37	37.79
Durum	RIL (F$_7$:F$_8$)	29	–	–	–	–
Durum	RIL (F$_7$:F$_8$)	30	37.78	30.27	33.27	33.77
Durum	RIL (F$_7$:F$_8$)	31	35.75	33.82	35.20	34.92
Durum	RIL (F$_7$:F$_8$)	32	33.23	40.20	–	36.72
Durum	RIL (F$_7$:F$_8$)	33	38.24	40.65	35.97	38.29
Durum	RIL (F$_7$:F$_8$)	34	43.11	40.51	39.70	41.11
Durum	RIL (F$_7$:F$_8$)	35	50.22	47.05	47.67	48.31
Durum	RIL (F$_7$:F$_8$)	36	36.54	40.51	26.43	34.49
Durum	RIL (F$_7$:F$_8$)	37	37.49	37.14	34.67	36.43
Durum	RIL (F$_7$:F$_8$)	38	47.58	–	48.20	47.89
Durum	RIL (F$_7$:F$_8$)	39	30.23	30.59	36.17	32.33
Durum	RIL (F$_7$:F$_8$)	40	30.80	25.83	36.43	31.02
Durum	RIL (F$_7$:F$_8$)	41	30.17	30.48	32.37	31.01
Durum	RIL (F$_7$:F$_8$)	42	–	–	–	–
Durum	RIL (F$_7$:F$_8$)	43	33.84	30.50	33.10	32.48
Durum	RIL (F$_7$:F$_8$)	44	26.15	23.87	30.33	26.78
Durum	RIL (F$_7$:F$_8$)	45	31.86	30.63	32.07	31.52
Durum	RIL (F$_7$:F$_8$)	46	35.53	36.99	37.67	36.73
Durum	RIL (F$_7$:F$_8$)	47	35.69	33.90	40.87	36.82
Durum	RIL (F$_7$:F$_8$)	48	40.08	60.41	45.47	48.65
Durum	RIL (F$_7$:F$_8$)	49	35.85	40.87	35.57	37.43
Durum	RIL (F$_7$:F$_8$)	50	–	–	–	–
Durum	RIL (F$_7$:F$_8$)	51	31.43	33.22	33.23	32.63
Durum	RIL (F$_7$:F$_8$)	52	–	–	–	–
Durum	RIL (F$_7$:F$_8$)	53	40.40	40.32	39.57	40.10
Durum	RIL (F$_7$:F$_8$)	54	–	–	–	–
Durum	RIL (F$_7$:F$_8$)	55	31.72	35.77	44.73	37.41

Table 3 (*continued*)

Genotype	Line	Line name	TKW_Val15 (g)	TKW_Val16 (g)	TKW_Val17 (g)	TKW_mean (g)
Durum	RIL (F$_7$:F$_8$)	56	22.55	27.05	34.90	28.17
Durum	RIL (F$_7$:F$_8$)	57	44.22	40.81	36.43	40.49
Durum	RIL (F$_7$:F$_8$)	58	34.57	37.21	34.77	35.52
Durum	RIL (F$_7$:F$_8$)	59	50.35	50.37	41.90	47.54
Durum	RIL (F$_7$:F$_8$)	60	23.78	30.47	33.27	29.17
Durum	RIL (F$_7$:F$_8$)	61	29.63	30.68	31.57	30.63
Durum	RIL (F$_7$:F$_8$)	62	22.51	15.66	22.70	20.29
Durum	RIL (F$_7$:F$_8$)	63	–	–	–	–
Durum	RIL (F$_7$:F$_8$)	64	33.97	30.49	33.93	32.80
Durum	RIL (F$_7$:F$_8$)	65	–	–	–	–
Durum	RIL (F$_7$:F$_8$)	66	31.20	30.20	26.10	29.17
Durum	RIL (F$_7$:F$_8$)	67	38.67	37.16	43.10	39.64
Durum	RIL (F$_7$:F$_8$)	68	44.77	50.20	40.33	45.10
Durum	RIL (F$_7$:F$_8$)	69	67.84	50.41	48.60	55.62
Durum	RIL (F$_7$:F$_8$)	70	39.45	40.61	36.57	38.88
Durum	RIL (F$_7$:F$_8$)	71	39.51	40.58	43.27	41.12
Durum	RIL (F$_7$:F$_8$)	72	40.50	30.82	36.53	35.95
Durum	RIL (F$_7$:F$_8$)	73	38.65	40.62	46.27	41.85
Durum	RIL (F$_7$:F$_8$)	74	37.74	40.54	34.60	37.63
Durum	RIL (F$_7$:F$_8$)	75	30.30	40.37	41.53	37.40
Durum	RIL (F$_7$:F$_8$)	76	29.59	30.49	31.30	30.46
Durum	RIL (F$_7$:F$_8$)	77	33.37	30.89	34.63	32.96
Durum	RIL (F$_7$:F$_8$)	78	36.96	33.70	32.07	34.24
Durum	RIL (F$_7$:F$_8$)	79	31.77	36.91	33.10	33.93
Durum	RIL (F$_7$:F$_8$)	80	36.92	40.56	39.83	39.10
Durum	RIL (F$_7$:F$_8$)	81	33.57	30.76	29.43	31.25
Durum	RIL (F$_7$:F$_8$)	82	28.61	30.55	37.70	32.29
Durum	RIL (F$_7$:F$_8$)	83	33.03	33.88	35.43	34.11
Durum	RIL (F$_7$:F$_8$)	84	31.64	15.50	28.73	25.29
Durum	RIL (F$_7$:F$_8$)	85	–	–	12.13	12.13
Durum	RIL (F$_7$:F$_8$)	86	32.43	30.59	9.93	24.32
Durum	RIL (F$_7$:F$_8$)	87	38.15	37.22	37.83	37.73
Durum	RIL (F$_7$:F$_8$)	88	30.93	30.13	34.47	31.84
Durum	RIL (F$_7$:F$_8$)	89	41.45	40.20	40.10	40.58
Durum	RIL (F$_7$:F$_8$)	90	–	–	–	–
Durum	RIL (F$_7$:F$_8$)	91	–	40.87	39.90	40.39
Durum	RIL (F$_7$:F$_8$)	92	23.68	30.75	32.80	29.08
Durum	RIL (F$_7$:F$_8$)	93	27.11	–	28.83	27.97
Durum	RIL (F$_7$:F$_8$)	94	34.09	37.17	35.77	35.68
Durum	RIL (F$_7$:F$_8$)	95	32.46	37.12	42.60	37.39
Durum	RIL (F$_7$:F$_8$)	96	38.91	25.11	32.07	32.03
Durum	RIL (F$_7$:F$_8$)	97	39.74	50.43	41.77	43.98
Durum	RIL (F$_7$:F$_8$)	98	35.05	33.94	38.37	35.79
Durum	RIL (F$_7$:F$_8$)	99	34.71	40.42	37.27	37.47
Durum	RIL (F$_7$:F$_8$)	100	32.71	–	32.17	32.44
Durum	RIL (F$_7$:F$_8$)	101	38.62	50.29	36.03	41.65
Durum	RIL (F$_7$:F$_8$)	102	32.25	34.00	33.73	33.33
Durum	RIL (F$_7$:F$_8$)	103	62.22	–	–	62.22
Durum	RIL (F$_7$:F$_8$)	104	34.15	27.05	27.80	29.67
Durum	RIL (F$_7$:F$_8$)	105	–	–	–	–
Durum	RIL (F$_7$:F$_8$)	106	30.30	33.84	44.93	36.36
Durum	RIL (F$_7$:F$_8$)	107	40.47	37.09	44.30	40.62
Durum	RIL (F$_7$:F$_8$)	108	–	–	–	–
Durum	RIL (F$_7$:F$_8$)	109	32.84	50.44	46.93	43.40
Durum	RIL (F$_7$:F$_8$)	110	35.50	37.21	42.20	38.30
Durum	RIL (F$_7$:F$_8$)	111	23.88	20.74	28.73	24.45
Durum	RIL (F$_7$:F$_8$)	112	36.76	33.92	39.03	36.57
Durum	RIL (F$_7$:F$_8$)	113	24.94	30.36	35.47	30.26
Durum	RIL (F$_7$:F$_8$)	114	28.48	30.43	32.63	30.51
Durum	RIL (F$_7$:F$_8$)	115	28.81	30.30	31.57	30.23

Table 3 (*continued*)

Genotype	Line	Line name	TKW_Val15 (g)	TKW_Val16 (g)	TKW_Val17 (g)	TKW_mean (g)
Durum	RIL (F$_7$:F$_8$)	116	28.84	30.49	33.13	30.82
Durum	RIL (F$_7$:F$_8$)	117	24.38	30.58	29.73	28.23
Durum	RIL (F$_7$:F$_8$)	118	33.02	33.63	37.40	34.68
Durum	RIL (F$_7$:F$_8$)	119	39.37	40.57	42.27	40.74
Durum	RIL (F$_7$:F$_8$)	120	42.32	40.54	38.13	40.33
Durum	RIL (F$_7$:F$_8$)	121	38.43	30.75	39.27	36.15
Durum	RIL (F$_7$:F$_8$)	122	34.83	40.20	37.83	37.62
Durum	RIL (F$_7$:F$_8$)	123	35.22	40.88	43.83	39.98
Durum	RIL (F$_7$:F$_8$)	124	–	20.33	22.93	21.63
Durum	RIL (F$_7$:F$_8$)	125	35.76	34.12	38.97	36.28
Durum	RIL (F$_7$:F$_8$)	126	–	40.25	44.10	42.18
Durum	RIL (F$_7$:F$_8$)	127	35.32	40.54	35.77	37.21
Durum	RIL (F$_7$:F$_8$)	128	38.25	40.32	36.57	38.38
Durum	RIL (F$_7$:F$_8$)	129	35.72	40.36	34.20	36.76
Durum	RIL (F$_7$:F$_8$)	130	28.74	33.80	27.73	30.09
Durum	RIL (F$_7$:F$_8$)	131	31.36	37.06	41.63	36.68
Durum	RIL (F$_7$:F$_8$)	132	44.17	–	36.97	40.57
Durum	RIL (F$_7$:F$_8$)	133	25.44	30.20	22.80	26.15
Durum	RIL (F$_7$:F$_8$)	134	32.29	30.81	33.73	32.28
Durum	RIL (F$_7$:F$_8$)	135	–	–	–	–

Table 4

HMW-GS (*Glu-A1* and *Glu-B1* loci) and gliadin (*Gli-B1* locus) composition of two parents and 135 durum wheat RI lines derived from the interspecific cross between the common wheat accession 02-5B-318 and the durum cv. Saragolla.

Genotype	Line	Line name	*Glu-A1*	*Glu-B1*	*Gli-B1*
Common	Parent	02-5B-318	2*	7 + 9	γ-42
Durum	Parent	Saragolla	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	1	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	2	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	3	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	4	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	5	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	6	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	7	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	8	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	9	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	10	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	11	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	12	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	13	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	14	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	15	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	16	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	17	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	18	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	19	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	20	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	21	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	22	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	23	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	24	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	25	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	26	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	27	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	28	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	29	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	30	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	31	null	6 + 8	γ-45

Table 4 (*continued*)

Genotype	Line	Line name	Glu-A1	Glu-B1	Gli-B1
Durum	RIL (F$_7$:F$_8$)	32	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	33	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	34	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	35	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	36	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	37	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	38	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	39	2*	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	40	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	41	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	42	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	43	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	44	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	45	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	46	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	47	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	48	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	49	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	50	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	51	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	52	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	53	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	54	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	55	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	56	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	57	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	58	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	59	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	60	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	61	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	62	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	63	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	64	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	65	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	66	2*	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	67	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	68	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	69	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	70	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	71	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	72	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	73	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	74	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	75	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	76	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	77	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	78	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	79	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	80	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	81	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	82	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	83	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	84	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	85	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	86	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	87	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	88	2*	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	89	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	90	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	91	null	7 + 9	γ-42

Table 4 (*continued*)

Genotype	Line	Line name	Glu-A1	Glu-B1	Gli-B1
Durum	RIL (F$_7$:F$_8$)	92	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	93	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	94	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	95	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	96	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	97	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	98	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	99	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	100	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	101	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	102	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	103	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	104	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	105	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	106	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	107	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	108	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	109	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	110	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	111	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	112	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	113	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	114	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	115	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	116	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	117	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	118	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	119	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	120	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	121	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	122	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	123	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	124	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	125	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	126	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	127	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	128	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	129	null	6 + 8	γ-42
Durum	RIL (F$_7$:F$_8$)	130	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	131	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	132	null	7 + 9	γ-42
Durum	RIL (F$_7$:F$_8$)	133	null	6 + 8	γ-45
Durum	RIL (F$_7$:F$_8$)	134	null	7 + 9	γ-45
Durum	RIL (F$_7$:F$_8$)	135	null	6 + 8	γ-45

(null 2*/ 6 + 8 HMW-GS). Testers included in the analyses were the common wheat cv Chinese Spring and three hexaploid lines (Tester 1, 2, 3).

Colour use is required for Fig. 1 in print.

Supplementary Table 1 lists SNP markers located in the confidence intervals of mapped QTLs for GPC, which were searched for a putative function related to wheat seed storage proteins quality and quantity (protein synthesis/accumulation). Each SNP is annotated with the corresponding marker name, identification code, SNP type, nucleotide sequence/length, and chromosomal position on the durum wheat genetic linkage map developed by Giancaspro et al. [2].

Supplementary Table 2 lists SNP markers located in the confidence intervals of mapped QTLs for GYS, which were searched for a putative function related to wheat productivity (grain yield components). Each SNP is annotated with the corresponding marker name, identification code,
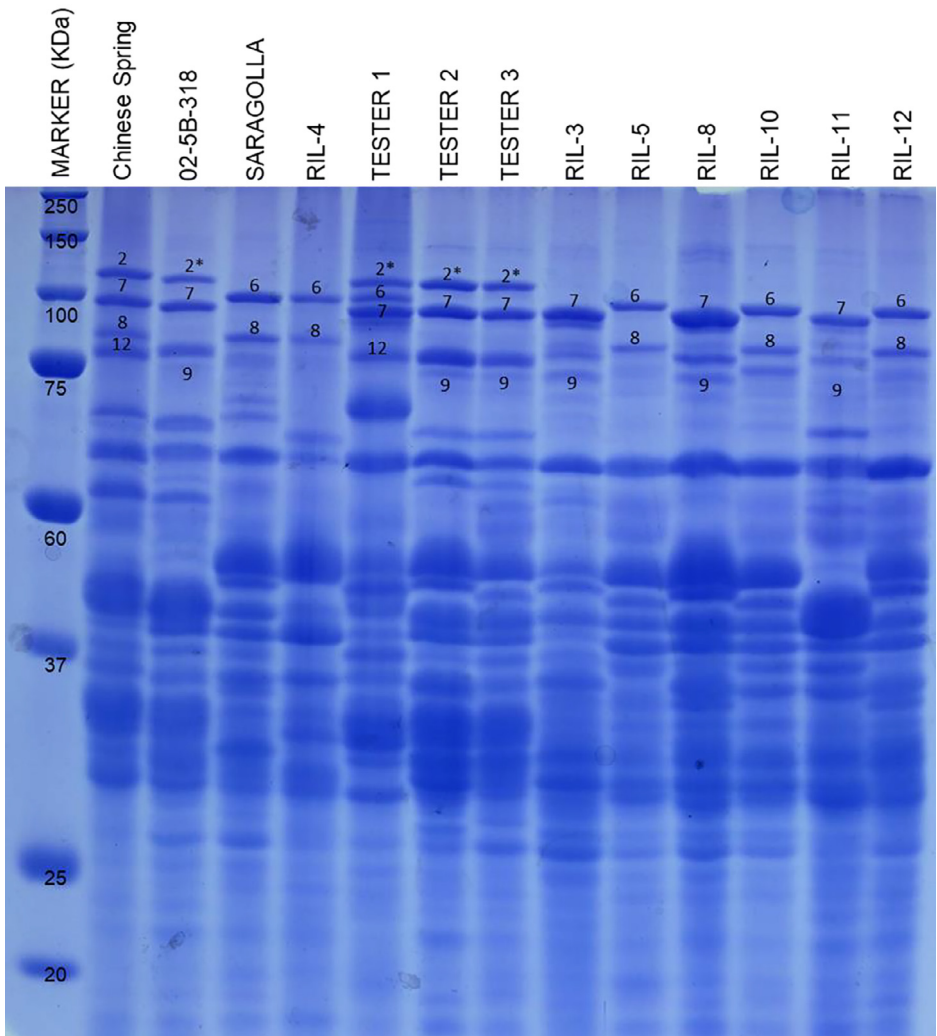
Fig. 1. SDS-PAGE of seed extracts from the two parents and some durum RILs of "02-5B-318 × Saragolla" population. RILs were screened for the HMW glutenin subunits encoded by *Glu-A1* (2*/null) and *Glu-B1* (7 + 9/6 + 8) loci. Common wheat cv Chinese Spring and other hexaploid testers (1, 2, 3) are also reported as controls.

SNP type, nucleotide sequence/length and chromosomal position on the durum wheat genetic linkage map developed by Giancaspro et al. [2].

Supplementary Table 3 lists SNP markers located in the confidence intervals of mapped QTLs for TKW, which were searched for a putative function related to wheat productivity (grain yield components). Each SNP is annotated with the corresponding marker name, identification code, SNP type, nucleotide sequence/length and chromosomal position on the durum wheat linkage genetic map developed by Giancaspro et al. [2].

2. Experimental Design, Materials and Methods

Data reported in this article describe the genetic variability for quantity (grain protein content, GPC) and composition (HMW-GS, gliadins) of seed storage proteins, and two yield components - grain yield per spike (GYS) and thousand kernel weight (TKW) - in 135 lines of a durum wheat RIL population obtained by crossing the common wheat accession 02-5B-318 (derived from the Chinese cv. Sumai-3) and the élite durum cv. Saragolla, and advancing single F_2 plants to the F_7 by single seed descent (SSD) [1,2,7–10]. GYS, TKW and GPC data were collected from plants grown in replicated trials in the fields of Valenzano (Metropolitan City of Bari, BA, Italy) for three years (2015, 2016, 2017) using a randomized block design with three replications. Each plot consisted of 1 m rows, 30 cm apart, with 80 seeds sown in each plot and supplemented with 10 g/m^2 nitrogen.

GYS was calculated by dividing the total grain yield per row on the number of spikes per row (about 70–80 spikes). TKW was acquired from a 15 g seed sample per each line, as the average of two technical replicates. GPC was measured by NIR spectroscopy on a 2 g sample of whole-meal flour using a SpectraAlyzer device. The instrument was calibrated with a set of 25 whole-meal flour samples of *T. turgidum* ssp. *durum*, ssp. *dicoccum*, and ssp. *dicoccoides* with known protein concentration and moisture, previously calculated according to official standard methods. For each wheat line, GPC was expressed as the percentage of proteins on a dry weight basis, averaged between two technical replicates. In detail, protein content on dry matter (GPC% d.m.) was calculated with the following formula: [Tot. GPC% / (100 − H%)] × 100.

Parents and durum RILs were characterized for protein subunits encoded by the HMW-GS loci *Glu-A1* and *Glu-B1* and the gliadin locus *Gli-B1*, which are crucial for bread-making quality. Gliadins were extracted from 30 μg of single-seed flour by following the protocol by Payne et al. [3]. HMW-glutenin subunits were determined on grain extracts according to the method of Bushuk and Zillman [4]. Protein subunits were identified based on their relative mobility in SDS-PAGE vertical electrophoresis, and HMW-GS composition was scored according to Payne's catalogue [11]. Progenies were classified for carrying alleles coming from 02-5B-318 or Saragolla. The common wheat parent 02-5B-318 carried the *1Ax2** allele of *Glu-A1* gene encoding the 2* HMW-GS, the *Bx7* and *By9* alleles of *Glu-B1* gene encoding 7 + 9 HMW-GS, and the allele for γ-42 gliadin at *Gli-B1* locus. The durum wheat parent Saragolla had the following alleles combination: non-coding *Glu-A1* locus*; Bx6* and *By8* alleles of *Glu-B1* gene encoding 6 + 8 HMW-GS, and the allele for γ-45 gliadin at *Gli-B1* locus. Gel imaging acquisition and software analyses were performed by DigiDoc (Bio-Rad Laboratories).

A durum wheat SNP-based genetic linkage map developed by Giancaspro et al. [2] was used for QTL detection. The high-density map consisted of 4,366 SNPs surveyed from the 81,587 sequences of the 90 K iSelect array by Illumina CSProR (San Diego, CA, USA) described by Wang et al. [12]. ANOVA was conducted for GYS, TKW and GPC traits with standard procedures using X-Stat software [13], and genetic variance (σ^2_G) and broad-sense heritability (h^2_B) evaluated using the variance component estimates. Pearson phenotypic correlation coefficients were calculated between GPC, GYS and TKW by using MSTAT-C statistical software [14]. QTL mapping was performed according to the Inclusive Composite Interval Mapping (ICIM) method [5] implemented in QGene 4.0 software [6]. Scanning interval of 2 cM between markers, and putative QTL with a window size of 10 cM were used as criteria for QTLs detection. The number of marker cofactors for background control was set by forward regression with a maximum of five controlling markers. Putative QTLs were defined as two or more trait-associated markers at LOD ≥ 3. Trait-associated SNPs at LOD ≤ 2 were considered not significant. Suggestive QTLs were classified as one or more trait-associated SNP markers at the subthreshold of 2.0 < LOD < 3.0. The following criteria were used for classification of additive effects: positive additive effects were associated with increased trait values from Saragolla alleles, whereas negative additive effects were contributed by 02-5B-318 alleles.

For the identification of candidate genes, sequences of SNP markers mapping in the confidence intervals of QTLs for GPC, GYS and TKW were blasted using TBLASTX algorithm (http://ncbi.nlm.nih.gov/BLAST) against the wheat draft genome sequence of the tetraploid *dicoccoides* accession Zavitan [15], the durum cv. Svevo [16], and the hexaploid cv. Chinese Spring [17]. Only alignments scoring $\geq$80% identity, $>10^{-7}$ *E*-value and sequences involved in metabolic pathways related to protein content and yield components were considered as putative candidate genes.

Ethics Statements

No ethics statement.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data Availability

SNP markers located in the confidence intervals of mapped QTLs for grain protein content (GPC), yield per spike (YPS) and thousand-kernel wheight (TKW) in 135 durum RILs (Original data) (Mendeley Data).

CRediT Author Statement

Angelica Giancaspro: Methodology, Investigation, Formal analysis, Visualization, Writing – original draft; **Stefania Lucia Giove:** Investigation, Validation, Data curation; **Ilaria Marcotuli:** Validation; **Agata Gadaleta:** Conceptualization, Methodology, Resources, Project administration, Funding acquisition, Supervision, Writing – review & editing.

Acknowledgments

References

[1] A. Giancaspro, S.L. Giove, S.A. Zacheo, A. Blanco, A. Gadaleta, Genetic variation for protein content and yield-related traits in a durum population derived from an inter-specific cross between hexaploid and tetraploid wheat cultivars, Front. Plant Sci. 10 (2019) 1509, doi:10.3389/fpls.2019.01509.

[2] A. Giancaspro, S.L. Giove, D. Zito, A. Blanco, A. Gadaleta, Mapping QTLs for Fusarium Head Blight resistance in an interspecific wheat population, Front. Plant Sci. 7 (2016) 1381, doi:10.3389/fpls.2016.0138124.

[3] P.I. Payne, C.N. Lawn, E.E. Mudd, Control by homoeologous group 1 chromosomes of the high-molecular-weight subunits of glutenin, a major protein of wheat endosperm, Theor. Appl. Genet. 58 (3–4) (1980) 113–120, doi:10.1007/BF00263101.

[4] W. Bushuk, R.R. Zillman, Wheat cultivar identification by gliadin electropherograms. I. Apparatus, method and nomenclature, Can. J. Plant Sci. 58 (2) (1978) 505–515, doi:10.4141/cjps78-076.

[5] H. Li, G. Ye, J. Wang, A modified algorithm for the improvement of composite interval mapping, Genetics 175 (2007) 361–374, doi:10.1534/genetics.106.066811.40.

[6] R. Joehanes, J.C. Nelson, QGene 4.0, an extensible Java QTL-analysis platform, Bioinformatics 24 (2008) 2788–2789, doi:10.1093/bioinformatics/btn523.

[7] V. Lionetti, A. Giancaspro, E. Fabri, S.L. Giove, N. Reem, O.A. Zabotina, A. Gadaleta, A. Blanco, D. Bellincampi, Cell wall traits as potential resources to improve resistance of durum wheat against *Fusarium graminearum*, BMC Plant Biol. 15 (2015) 6, doi:10.1186/s12870-014-0369-1.

[8] A. Giancaspro, V. Lionetti, S.L. Giove, D. Zito, E. Fabri, N. Reem, O.A. Zabotina, E. De Angelis, L. Monaci, D. Bellincampi, A. Gadaleta, Cell wall features transferred from common into durum wheat to improve Fusarium Head Blight resistance, Plant Sci. 274 (2018) 121–128, doi:10.1016/j.plantsci.2018.05.016.

[9] A. Gadaleta, P. Colasuonno, S.L. Giove, A. Blanco, A. Giancaspro, Map-based cloning of QFhb.mgb-2A identifies a *WAK2* gene responsible for Fusarium Head Blight resistance in wheat, Sci. Rep. 9 (2019) 6929, doi:10.1038/s41598-019-43334-z.

[10] R. Parada, C. Royo, A. Gadaleta, P. Colasuonno, I. Marcotuli, I. Matus, D. Castillo, A. Costa de Camargo, J. Araya-Flores, D. Villegas, A.R. Schwember, Phytoene synthase 1 (*Psy-1*) and lipoxygenase 1 (*Lpx-1*) genes influence on semolina yellowness in wheat mediterranean germplasm, Int. J. Mol. Sci. 21 (2020) 4669, doi:10.3390/ijms21134669.

[11] P.I. Payne, G.J. Lawrence, Catalogue of alleles for the complex gene loci, Glu-A1, Glu-B1, and Glu-D1 which code for high-molecular-weight subunits of glutenin in hexaploid wheat, Cereal Res. Commun. 11 (1983) 29–35.

[12] S.W. Wang, D. Forrest, K. Allen, A. Chao, S. Huang, B.E. Huang, et al., Characterization of polyploid wheat genomic diversity using a high-density 90,000 single nucleotide polymorphism array, Plant Biotechnol. J. 12 (2014) 787–796, doi:10.1111/pbi.12183.

[13] B. Jones, *X-STAT*, in: Wiley (Eds.), Journal of the Royal Statistical Society. Series C (Applied Statistics), London 38 (2) (1989) 392–395.

[14] R. Freed, S.P. Eisensmith, S. Goetz, D. Reicosky, V.W. Smail, P. Wolberg, MSTAT-C: A Software Program for the Design, Management, and Analysis of Agronomic Research Experiments, East Lansing: Michigan State University, 1991.

[15] R. Avni, M. Nave, O. Barad, K. Baruch, S.O. Twardziok, H. Gundlach, Wild emmer genome architecture and diversity elucidate wheat evolution and domestication, Science 357 (346) (2017) 93–97, doi:10.1126/science.aan0032.

[16] M. Maccaferri, N.S. Harris, S.O. Twardziok, R.K. Pasam, H. Gundlach, M. Spannagl, et al., Durum wheat genome highlights past domestication signatures and future improvement targets, Nat. Genet. 51 (2019) 885–895, doi:10.1038/s41588-019-0381-3.

[17] R. Appels, K. Eversole, C. Feuille, B. Keller, J. Rogers, N. Stein, et al., Shifting the limits in wheat research and breeding using a fully annotated reference genome, Science 361 (2018) 6403, doi:10.1126/science.aar7191.