



Full Length Article

Allelic Variations and Agronomic Comparisons of Durum Wheat Cultivars under East-Mediterranean Conditions

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Abstract

Durum wheat (*Triticum turgidum* ssp. *durum* Desf.) is a traditional Mediterranean crop and widely produced in Turkey. This study was carried out to compare the allelic variation and agronomic characteristics of durum wheat genotypes during 2015-2016 and 2016-2017 in a randomized complete block design with four replications. A total of 14 durum wheat genotypes including twelve durum wheat cultivars (Güney Yıldızı, Sarı Başak, Sarıçanak 98, Zenit, Burgos, Saragolla, Cesare, Zühre, Levante, Ecem, Svevo, Dumlupınar), one old variety (Kunduru-1149) and a landrace (Karakılçık) were used as plant materials. Allelic variations of the 14 durum wheat genotypes were determined using 11 DNA markers.

According to the results, genotypes were found variable for all investigated traits except grain filling period (GFP), years were found different for all traits except gluten content (GC) and yellowness (B) and genotype×year interaction (G×Y) varied for plant height (PH), vegetative period (VP), days to maturity (DM), grain number per spike (GNS), test weight (TW), thousand kernel weight (TKW), grain yield (GY) and GC. The highest grain yield was obtained from Cesare cultivar over two year data with 5568 kg ha⁻¹ and followed by Burgos and Svevo cultivars with 5080 kg ha⁻¹ and 5027 kg ha⁻¹, respectively. Protein ratio (PR) of the genotypes ranged between 10% to 14.8% and Cesare and Karakılçık had the highest PR. According to the dendrogram, Burgos and Karakılçık genotypes were found similar in terms of the alleles investigated in the study with 86%. Sarı Başak and Dumlupınar genotypes were found the most diverse ones with 49% genetic similarity. 11 allele specific DNA markers interrogated in 20 loci and the allele number per marker was found as 1.8. The average polymorphism information content (PIC) was identified as 72.5%. Cesare cultivar produced bands for eight allele specific markers and Zenit cultivar was the only cultivar that produced allele for Xgwm18 marker. The findings of this study may shed light to breeding programs with field and laboratory performance of these genotypes. © 2019 Friends Science Publishers

Keywords: Allelic variation; Durum wheat; Landraces; Agronomic traits; Quality parameters

Introduction

Durum wheat (*Triticum turgidum* ssp. *Durum* Desf., $2n = 4x = 28$, AABB) is native to Turkey, and is one of the major crops with 3.9 mil. tons production (TÜİK, 2017) while it is the 10th most important crop in the world with 37 mil. tons production (FAO, 2017). It is planted on about 10% of the wheat area of the world mostly in East and North Africa, West Asia, India, North America, Eastern Europe and Mediterranean basin (Kabbaj *et al.*, 2017). Turkey has plenty of genetic resources and favorable regions for durum wheat production and Turkish genetic resources have been contributing to durum wheat breeding programs worldwide.

In Turkey, modern wheat breeding programs were established in 1925 based on selection method to develop cultivars for various ecological regions of the country (Altıntaş *et al.*, 2008). Besides modern and old varieties, Turkey also has durum wheat landraces grown in the small farms besides registered cultivars (Sayaslan *et al.*, 2012). For example, Karakılçık which is one of the landraces have

been grown in small extent in the rural areas of Mediterranean coastal cities and Kunduru-1149 as an old variety has considerable production area in the inner Anatolia. Genetic resources are the most preferred materials to broaden genetic base and increase yield and quality (Dumlupınar *et al.*, 2012) and polymerase chain reaction (PCR) based markers either dominant or co-dominant are powerful tools to study allelic variations.

There are huge differences among durum wheat genotypes, which generally provide bases for high yield and quality. Grain yield, and weight, plant height, and maturity are among the most important agronomic traits while protein rate, yellowness, and gluten content are among the most important quality parameters.

Development of high-yielding and high-quality durum wheat varieties is a major objective in breeding programs and to find the allele specific markers for the desired trait are necessary to have suitable selection (Mir *et al.*, 2012). In recent years, there are plenty of allele specific markers developed by researchers for diseases and

agronomic and quality traits (Roder *et al.*, 1998; Shariflou and Sharp, 1999; Butow *et al.*, 2003; Distelfeld *et al.*, 2006; Randhawa *et al.*, 2014; Bansal *et al.*, 2015).

In this study, 14 durum wheat genotypes consisted of 12 modern durum wheat cultivars, one old variety and one landrace were investigated for some agronomic and quality traits for two years and allele specific markers interrogating 11 loci were used to determine allelic variations.

Materials and Methods

Plant Materials

A total of 14 durum wheat genotypes including twelve durum wheat cultivars (Güney Yıldızı, Sarı Başak, Sariçanak 98, Zenit, Burgos, Saragolla, Cesare, Zühre, Levante, Ecem, Svevo and Dumlupınar), one old variety (Kunduru-1149) and a landrace (Karakılçık) were used as plant materials.

Field Trials

Field trials were conducted in 2015-2016 and 2016-2017 cropping seasons in Kahramanmaraş province of Turkey (East-Mediterranean Region of Turkey, located between 37°53' N, 36°58' E with 507 m elevation). The experiments were arranged in a randomized complete block design with four replications. The experiments were planted on 28 December 2015 in the first year, and on 19 January 2017 in the second year. Plot sizes were arranged as 6 m long and 1.2 m width with six plant rows in each plot. In the first year, 70 kg ha⁻¹ of N and P₂O₅ were applied at time of planting and 70 kg ha⁻¹ of N was applied as top dressing on 02 March 2016 while, in the second year 80 kg ha⁻¹ of N and P₂O₅ were applied at time of planting and 70 kg ha⁻¹ of N was applied as top dressing on 10 March 2017. Tribenuron-Methyl 75% was used for weed control, whereas there was no control required for insect pests and diseases. In this study; plant height from soil level to spikes as cm and vegetative period as days between planting to flowering were measured. Grain filling period as days between to flowering to maturity and days to maturity as days between planting to maturity were determined. Also, grain number and weight per spike traits by counting and weighing of 10 spikes randomly collected from the main crops of the each plot, and test weight as kg per hectoliters by weighing of the volume of grains per unit were determined. Grain yield as kg per hectare by weighing the grains obtained from the each plot was determined. All measurements and calculations mentioned above were performed according to (Dumlupınar *et al.*, 2011). Lastly, protein ratio and gluten content were determined by the NIR Spectroscopy (Delwiche, 1995) and yellowness were observed by spectrophotometer (Gardner color view, USA) according to the Hunter B Scale (Anonymous, 2002) for two years.

Molecular Analysis

DNA Sources: Genomic DNA from single seed plants was used for PCR reactions. Four seeds of each genotype were planted in a 10.2 cm diameter pot. Three of the seedlings were removed at the two leaf stage. The entire leaves from the remaining seedling were harvested and placed in a 2.0 mL micro-centrifuge tube for DNA isolation. Leaf tissues were ground into a fine powder in the liquid nitrogen using a sterilized test tube pestle. Hexadecyltrimethylammonium bromide (CTAB) method was used to extract DNA, described as Dumlupınar *et al.* (2016a).

PCR and Fragment Analysis

11 allele specific primers were used to characterize the allelic variation (Table 1). PCR reactions were performed in a volume 20 µL, containing 5 µL of 0.5 µM forward and 0.5 µM reverse primers, 5 µL (80 ng) of genomic DNA, 5 µL of master mix, 0.2 µL Taq DNA polymerase, 0.1 µL MgCl₂, 1.2 µL dNTP, 2 µL reaction buffer, and 1.5 µL ddH₂O were used (Dumlupınar *et al.*, 2016a). The conditions of PCR reactions were carried out with an initial denaturing (94°C, 4 min.), followed by 35 cycles of denaturing (94°C, 1 min): annealing (55°C, 1 min): extension (72°C, 1 min) and a final extension (72°C, 10 min). Fragment analyses were performed using “QIAxcel Advanced System” Fragment Analyzer and the DNA bands finally were obtained.

Data Analyses

The data obtained from the field trials for the consecutive two years was subjected to the ANOVA procedure. Duncan's Multiple Range Test was used to comparisons of mean values (MSTAT-C Manual, 1991). Genetic similarities were estimated for the 14 durum wheat genotypes using Dice's index (Dice, 1945) with NTSYSpc ver. 2.20q (Rohlf, 2005) as described by Dumlupınar *et al.* (2016b). Prior to marker data analysis, a binary data matrix was constructed with each primer set was coded as one or zero as the presence or absence of each fragments generated. A dendrogram was generated using the unweighted pair group method with arithmetic mean (UPGMA) from the similarity matrix. Polymorphism information content (PIC) indices were calculated for each primer using the method described by Weir (1996). $PIC=1-\sum(P_i)^2$, where P_i is the frequency of the ith allele in the 14 durum wheat genotypes.

Results

The mean squares and F values were obtained from the statistical analysis (Table 2) and the mean data for the investigated traits are given in Table 3. The pictures of the primers Sun209 and Xgwm47 and a dendrogram were generated from the markers data of all genotypes were given in Fig. 1, 2 and 3, respectively. The allelic variations of the genotypes according to the markers are indicated in Table 4.

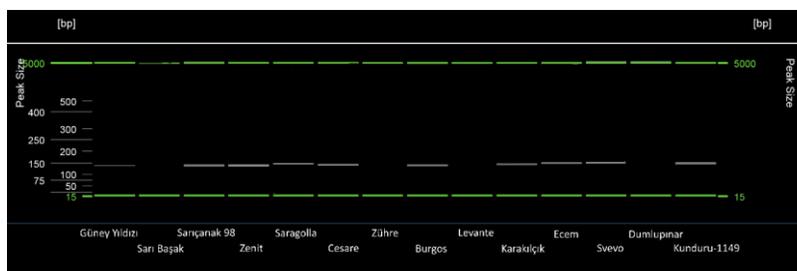


Fig. 1: Visualization of Sun209 Primer of 14 durum wheat genotypes on Fragment Analyzer

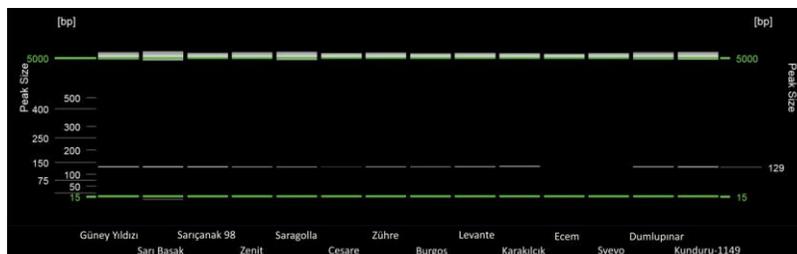


Fig. 2: Visualization of Xgwm47 Primer of 14 durum wheat genotypes on Fragment Analyzer

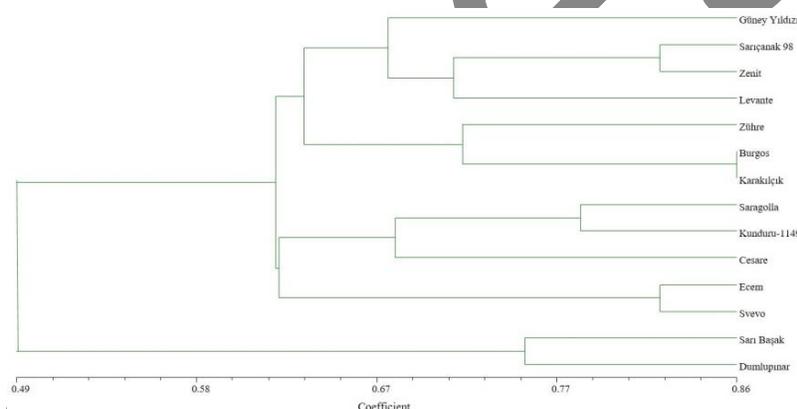


Fig. 3: Dendrogram based on allelic variations of 14 durum wheat genotypes

Genotypes, years and genotype \times year interaction (G \times Y) were found significantly different for plant height (Table 2). Kunduru-1149 had the highest plant height with 129.9 cm and followed by Karakılıçık with 124.0 cm. The shortest ones were Zenit, Saragolla and Cesare (77.6, 85.5 and 85.5 cm, respectively). The mean values for plant height for first and second years were found as 104.5 cm and 88.9 cm, respectively (Table 3). Genotypes, years and G \times Y varied for vegetative period (Table 2). While Karakılıçık and Kunduru-1149 genotypes had the longest VP with 138 days, Sarıçanak 98, Sarı Başak, and Saragolla genotypes were the earliest ones with 127 days. In the first year, the mean vegetative period was 144 days, however 116 days was found in the second year (Table 3). While the grain filling period was found significant for years, there were no significant differences for genotypes and G \times Y (Table 2). Sarı Başak showed the

longest grain filling period with 44 days, in contrast Karakılıçık had the shortest period with 35 days. The mean GFP for the first and second years were found as 41 days and 38 days, respectively (Table 3). The days to maturity values varied for genotypes, years and G \times Y (Table 2). While Kunduru-1149 and Dumlupınar genotypes were the latest ones with 175 days to maturity, Güney Yıldızı, Sarıçanak 98 and Zühre genotypes were the earliest with 167 days to maturity. The mean vegetations for first and second years were found as 187 days and 154 days, respectively (Table 3). There were significant variations among the durum wheat genotypes, years and G \times Y for grain number per spike (Table 2). While Sarıçanak 98 has the highest GNS with 58.8, Kunduru-1149 had the lowest values with 35.4. The mean GNS values were identified as 48.5 and 36.0 for year one and two, respectively. The genotypes and years were different for GWS (Table 2).

Table 1: Details of 11 used primers in this study

No	Primer Name	Primer Sequences 5' to 3'	Reference	Marker-type	Expected Loci (bp)
1	Sun1	CGTCCCTGAAGAGAGAAAGAA ATAGGCACAACCCCTAAC	Shariflou and Sharp, 1999	Co-dominant	219, 233, 260, 271, 275, 285 and 289
2	Sun104	TGCTATGTGCGTGATGATGA TTACATGCTCCAGCGACTTG	Randhawa <i>et al.</i> , 2014	Dominant	225
3	Sun209	AG CTATGAGCTTCGCTATTG GTGATTGGTTCGGATTACTTA	Bansal <i>et al.</i> , 2015	Co-dominant	148
4	Sun479	CAAATGAAATGTGATCCTGTT TCATCTAACCAGCAATGGTAT	Bansal <i>et al.</i> , 2015	Co-dominant	200
5	Bx7 ^{OE}	CCTCAGCATGCAAACATGCAGC CTGAAACCTTTGGCCAGTCATGTC	Butow <i>et al.</i> , 2003	Co-dominant	563
6	UHW89	TCTCCAAGAGGGGAGAGACA TCTCCAAGAGGGGAGAGACA	Distelfeld <i>et al.</i> , 2006	Co-dominant	122
7	Xgwm18	TTGCTACCATGCATGACCAT TTCACCTCGATTGAGGTCTCT	Roder <i>et al.</i> , 1998	Co-dominant	182
8	Xgwm47	TTGCTACCATGCATGACCAT TTCACCTCGATTGAGGTCTCT	Roder <i>et al.</i> , 1998	Co-dominant	150
9	Xgwm66	CCAAAGACTGCCATCTTTCA CATGACTAGCTAGGGTGTGACA	Roder <i>et al.</i> , 1998	Co-dominant	137
10	Xgwm68	AGGCCAGAATCTGGAATG CTCCCTAGATGGGAGAAGGG	Roder <i>et al.</i> , 1998	Co-dominant	166
11	Xgwm131	AATCCCCACCGATTCTTCTC AGTTCGTGGGTCTCTGATGG	Roder <i>et al.</i> , 1998	Co-dominant	157

Table 2: Mean squares and F values of genotype, year and G×Y interaction for yield components subset of 14 durum wheat genotypes and two years

Source of Variation	PH	VP	GFP	DM	GNS	GWS	TW	TKW	GY	PR	GC	B
	Mean Squares											
R	71.77	5.74	6.24	10.73	42.51	0.17	4.48	16.05	431.83	0.16	1.56	0.31
G	2090.1	116.7	36.5	66.5	395.2	0.32	97.1	30.9	37616	15.5	13.6	37.5
Y	6814.0	24219.7	292.5	29385.5	4440.2	43.3	388.5	6806.2	331916	18.0	0.38	0.27
G×Y Int.	228.7	30.5	28.6	22.4	32.8	0.18	24.8	47.2	5023	0.22	0.66	0.25
	F Values											
G	53.18**	9.27**	1.53 ^{ns}	6.74**	24.8**	2.62**	11.4**	2.61**	22.1**	74.7**	63.0**	205.3**
Y	173.3**	1922.3**	12.25**	3023.5**	278.7**	345.8**	45.8**	575**	195.1**	86.4**	1.8 ^{ns}	1.49 ^{ns}
G×Y Int.	5.82**	2.42**	1.20 ^{ns}	2.27**	2.06*	1.47 ^{ns}	2.93**	3.99**	2.95**	1.0 ^{ns}	3.0**	1.39 ^{ns}
CV (%)	6.47	2.71	12.3	1.84	9.45	17.1	3.98	8.14	9.25	3.53	4.18	1.74

R: Replication, G: Genotype, Y: Year, G×Y Int.: Genotype × Year Interaction, PH: plant height (cm), VP: vegetative period (days), GFP: grain filling period (days), DM: days to maturity (days), GNS: grain number per spike (grains), GWS: grain weight per spike (g), TW: test weight (kg hl⁻¹), TKW: thousand kernel weight (g), GY: grain yield (kg ha⁻¹), PR: protein ratio (%), GC: gluten content (%), B: Yellowness (%), CV: Coefficient of variation
Significance: ** $P < 0.01$, * $P < 0.05$ and ns: not significant

Table 3: Mean data over two years for plant height (PH), vegetative period (VP), grain filling period (GFP), days to maturity (DM), grain number per spike (GNS), grain weight per spike (GWS), test weight (TW), thousand kernel weight (TKW), grain yield (GY), protein ratio (PR), gluten content (GC) and yellowness (B) belong to 14 durum wheat genotypes

	PH	VP	GFP	DM	GNS	GWS	TW	TKW	GY	PR	GC	B	
Years	**	**	**	**	**	**	**	**	**	**	ns	ns	
	2015-16	104.5a	144a	41a	187a	48.5a	2.68a	74.9a	50.0a	5002a	13.3a	11.1	24.5
	2016-17	88.9b	116b	38b	154b	36.0b	1.44b	71.2b	34.4b	3913b	12.5b	11.0	24.4
		**	**	ns	**	**	**	**	**	**	**	**	
Genotypes	Güney Yıldızı	89.5ef	128de	39	167e	42.1b	1.97bcd	71.3de	38.7c	4169de	13.08bc	11.1cd	24.4e
	Sarı Başak	89.4ef	127de	44	171cd	43.5b	2.07bcd	73.3cd	43.0ab	4711bc	10.0g	8.3h	27.1b
	Sarıçanak 98	88.0ef	127e	40	167e	58.8a	2.28ab	75.7bc	42.5abc	4660bc	12.4de	10.7def	23.7f
	Zenit	77.6g	128de	41	169de	40.7b	1.92bcd	69.4ef	41.5abc	3819e	12.22e	10.2f	24.7de
	Burgos	88.4ef	130bcde	41	171cd	43.0b	2.13abcd	78.4ab	43.6a	5080b	13.3b	11.8b	23.2g
	Saragolla	85.5f	127e	41	167e	52.3a	2.50a	73.5cd	42.2abc	4927b	11.4f	9.4g	28.3a
	Cesare	85.5f	131cde	40	171cd	51.2a	2.28ab	79.7a	44.0a	5568a	14.8a	11.8b	25.4c
	Zühre	93.4de	128de	40	167e	41.9b	1.92bcd	72.5cde	42.3abc	4360cd	12.23e	10.4ef	24.9d
	Levante	86.3f	129cde	39	168e	44.7b	2.09bcd	74.2cd	39.5bc	4368cd	12.27de	10.5ef	24.9d
	Karakılçık	124.0a	138a	35	173abc	24.8e	2.20abc	67.8f	38.9c	2861f	14.8a	12.7a	18.7h
	Ecem	100.0c	134a	38	172bcd	41.8b	1.78d	74.5cd	41.6abc	4922b	14.5a	11.8b	25.1cd
	Svevo	97.0cd	133bc	39	172bcd	41.3b	1.94bcd	72.5cde	43.3ab	5027b	14.4a	12.8a	23.3fg
	Dumlupınar	120.1b	133cb	42	175a	37.1cd	1.97bcd	67.3f	44.5a	3761e	12.7cd	11.5bc	23.5fg
	Kunduru-1149	129.9a	138a	37	175a	35.4d	1.79cd	71.7de	44.9a	4160de	12.1e	10.8de	24.9d
	Mean	96.7	130.7	39.7	170.3	42.7	2.06	72.9	42.2	4457	12.9	10.9	24.4

Significance: ** $P < 0.01$, * $P < 0.05$, and ns: not significant

Table 4: Allelic variation of 14 durum wheat genotypes

No	Primer Name	Güney Yıldızı	Sarı başak 98	Sarıçanak 98	Zenit	Saragolla	Cesare	Zühre	Burgos	Levante	Karakılçık	Ecem	Svevo	Dumlupınar	Kunduru Loci -1149	PIC Values(%)	
1	Sun1			+	+	+	+	+	+	+	+	+	+	+	+	Waxy <i>Wx-A1</i>	86
2	Sun104															Stripe Rust <i>Yr51</i>	87
3	Sun209	+		+	+	+	+		+			+			+	Stem Rust <i>Sr49</i>	49
4	Sun479							+				+	+	+		Stem Rust <i>Sr49</i>	87
5	Bx7 ^{OE}						+			+						Gluten Strength	79
6	UHW89			+	+	+	+	+				+				High Protein Content <i>Gpc-B1</i>	82
7	Xgwm18				+											Stripe Rust	99
8	Xgwm47	+	+	+	+	+	+	+	+	+				+		Stripe Rust	27
9	Xgwm66								+							Powdery Mildew	99
10	Xgwm68	+	+	+	+	+	+	+	+	+	+	+	+	+		Thousand Kernel Weight	27
11	Xgwm131	+	+	+	+	+	+	+	+	+	+	+	+	+		Stripe Rust <i>Yr39</i> , Heat Tolerance(chlorophyll content and Chlorophyll fluorescence)	76

While Saragolla cultivar had 2.5 g grain weight per spike, Ecem cultivar had the lowest grain weight with 1.78 g. The grain weight per spike value was higher in the first year as 2.68 g than second year as 1.44 g (Table 3). There were significant differences among durum wheat genotypes, years and G×Y for test weight (Table 2). Cesare cultivar was the highest for the TW with 79.7 kg hl⁻¹, while Kunduru-1149 and Dumlupınar genotypes had 67.3 kg hl⁻¹ and 67.8 kg hl⁻¹ test weights, respectively. The test weight for the first year was 74.9 kg hl⁻¹, while 71.2 kg hl⁻¹ in the second year (Table 3). The genotypes, years and G×Y were found as variable for thousand kernel weight (Table 2). Kunduru-1149 had the highest TKW with 44.9 g, followed by Dumlupınar and Cesare genotypes with 44.5 and 44.0 g TKW, respectively. The genotypes Güney Yıldızı and Karakılçık had the lowest TKW values with 38.7 and 38.9 g, respectively. The mean thousand kernel weight values for first and second years were identified as 50.0 g and 34.4 g, respectively (Table 3). The grain yield was found different for genotypes, years and G×Y (Table 2). The highest grain yield was obtained from Cesare cultivar for two years data with 5568 kg ha⁻¹, followed by Burgos and Svevo cultivars with 5080 and 5027 kg ha⁻¹, respectively. The lowest grain yield values were obtained from Karakılçık with 2861 kg ha⁻¹, followed by Dumlupınar and Zenit with 3761 and 3819 kg ha⁻¹, respectively. The mean grain yield value was 5002 kg ha⁻¹ in the first year and 3913 kg ha⁻¹ in the second year (Table 3). Genotypes and G×Y varied for gluten content (Table 2). Svevo and Karakılçık genotypes had the highest GC values (12.8% and 12.7%, respectively), while Sarı Başak cultivar had the lowest gluten content with 8.3%. The gluten content values for the both years were almost same with 11.1% in the first year and 11.0% in the second year (Table 3). The yellowness was found significant for genotypes (Table 2). Saragolla cultivar has the highest B value with 28.3%, while the lowest B value was obtained from Karakılçık with 18.7%. The B values of the genotypes for both first and second year were 24.5% and 24.4%, respectively (Table 3).

According to the dendrogram distributions, Burgos and Karakılçık genotypes were found the most similar genotypes in terms of the alleles investigated in the study

with 86% similarity. However, Sarı Başak and Dumlupınar genotypes were separated from others with 49% genetic similarity (Fig. 3).

The markers used in the study were allele specific markers. In this study, the allele number per marker was found as 1.8. A comparison was made on the basis of expected primer sizes for 14 durum wheat genotypes. According to this comparison, all durum wheat genotypes under study had alleles for *waxy* genes except from Güney Yıldızı and Sarı Başak cultivars (Table 4). Saragolla, Cesare, Karakılçık, Svevo and Kunduru-1149 genotypes contained alleles for *Yr51*. The other markers related with stripe rust such as Xgwm18 had alleles for only Zenit, while Xgwm47 had alleles for all cultivars except Ecem and Svevo cultivars (Fig. 2). On the other hand, Xgwm68 marker which is related with stripe rust resistance gene (*Yr59*) and heat tolerance gene (Xgwm131) produced alleles for all durum wheat genotypes. The closely linked markers were found as Sun209 and Sun479 for *Sr49*. While marker Sun209 amplified the alleles for Güney Yıldızı, Sarıçanak 98, Zenit, Saragolla, Cesare, Burgos, Karakılçık, Ecem, Svevo and Dumlupınar, Sun479 marker had alleles on Zühre, Karakılçık, Ecem, Svevo and Dumlupınar genotypes. The Bx7^{OE} marker was related with gluten strength produced alleles only for Cesare and Levante cultivars. Among the durum wheat genotypes, Sarıçanak 98, Zenit, Saragolla, Cesare, Zühre and Ecem included alleles for UHW89 marker which was related with high protein content gene *Gpc-B1*. Burgos cultivar was the only cultivar with powdery mildew resistance revealed with Xgwm68 marker (Table 4). The PIC values of the markers were found between 27% and 99%. While Xgwm66 and Xgwm18 markers indicated 99% PIC values, Xgwm68 had the lowest PIC value as 27% (Table 4).

Discussion

Plant breeders and breeding programs worldwide have achieved success on grain yield and components with quality traits in recent years. With improvements in biotechnology, plant breeders have been able to use marker assisted selection (MAS) in breeding programs besides agro-morphological traits.

According to the results of two years experiments in this study, the landrace Karakılçık and old variety Kunduru-1149 had the highest plant heights as expected. The modern cultivars had moderate plant heights and this situation might be due to dwarfing genes that lacks in landraces. In previous works, this was explained by genotype effect and the high heritability of plant height (Collaku, 1994; Royo *et al.*, 2010) which confirms our results.

The phenological traits VP, GFP and DM varied for durum wheat genotypes Kunduru-1149 which is result of selection from a landrace population. In addition, Dumlupınar derived from a cross of Kunduru-1149 as one of the parents had the longest growing period, followed by Karakılçık. The modern cultivars had shorter durations and it was considered that genotypic effect and climate changes affected the phenological traits. Alghabari *et al.* (2014) reported that different genotypic responses were observed under heat stress for longer periods and Farooq *et al.* (2009) also determined climatic effects were observed on phenological growing stages which were in line with our findings. In this study, the durum wheat genotypes varied for yield and yield components such as GNS, GWS, TW, TKW and GY. The modern cultivars especially Cesare cultivar had the highest yield and yield components followed by Saragolla in terms of GNS and GWS. Soriano *et al.* (2016) reported that genotype effect was explained the total variation for yield and yield components by 16% to 37% in modern durum wheat cultivars and mediterranean landraces. Hruby (1993) determined that TKW was strongly influenced by the growing season. Bilgin *et al.* (2008) indicated for durum wheat that higher TKW values resulted with higher grain yields and reported a positive proportional of gain yield to TKW, TW, GNS and GWS which is considered as TW and TKW depended on growing season and location and during the growing season grain yield depended on the GNS and GWS and agro-ecological conditions. Kara *et al.* (2008) reported a genetic influence on yield and yield components of Turkish durum wheat genotypes in different growing periods and locations. In addition, Royo *et al.* (2007) reported variations among Spanish and Italian originated durum wheat genotypes and date of release and determined a huge variation between modern and old genotypes. The previous works were in agreement with our findings in terms of yield and yield components. The quality parameters (PR, GC and B) were measured and variations were observed from durum wheat genotypes in this study. The protein ratio and gluten content of the landrace Karakılçık was the highest unlike the other agronomical traits. It can be suggested that it has a potential to be a donor for PR and GC in the further wheat breeding programs. The modern cultivars Cesare, Ecem, Svevo also showed better performance about PR and GC. In this study, Saragolla had the highest B values, suggesting that it may be considered as potential parent in the breeding programs. In previous studies, Maria *et al.* (2017) reported a variation based on origins of durum

wheat genotypes and it was affected by genotype, environmental and genotype \times environmental effects. The protein content of Turkish durum wheat genotypes previously reported ranged from 10.9% to 13.8% under different environments (Genç *et al.*, 1993; Sözen and Yağdı, 2005; Sakin *et al.*, 2011a, b). In addition, aforesaid findings were in line with Sayaslan *et al.* (2012) who reported protein ratio ranging between 10.7% and 16.8%. Hence, it can be suggested that the quality parameters may be affected by genotype and environmental effect.

In this study, the Dice's genetic diversity values based on allele specific markers was found very diverse (Fig. 3) and PIC values were identified between 27% and 99% (Table 4). The dendrogram was consisted of two major clusters. The variation of the genotypes may be explained by the origin of the genotypes used in this study. However, Karakılçık and Burgos genotypes showed the most similar relationships (86%) although originated from different origins (Fig. 3 and Table 4).

In previous works on durum wheat genotypes, Ren *et al.* (2013) reported a low genetic diversity in the cultivars released in the 1960s and 1970s and a rapid increase in genetic diversity after 1970s in worldwide germplasm collection of durum wheat. Also, PIC values of 18% and 22% in a worldwide collection of durum wheat genotypes were revealed by SNP (single-nucleotide polymorphism) markers. Moreover, Moragues *et al.* (2007) indicated that the genetic diversity of 63 durum wheat landraces were determined as 24% and 70% of PIC values for AFLP and SSR markers, respectively derived from Mediterranean basin. In another study, Maccaferri *et al.* (2003) investigated genetic diversity of the durum wheat genotypes obtained collected from Mediterranean countries using SSR markers with a mean diversity index (DI) as 56%.

The Sun1 marker related with waxy *Wx-A1* gene amplified the alleles in 12 out of 14 genotypes at 219 bp in this study. In previous works, the lengths of waxy *Wx-A1* allele were found as 230 bp and 265 bp (Maryami *et al.*, 2014) and 219 bp, 233 bp, 260 bp, 271 bp, 275 bp, 285 bp and 289 bp (Shariflou and Sharp, 1999). In addition, Maryami and Fazeli (2015) determined that the 204 bp band related with *Wx-D1 a/b* and Maryami *et al.* (2014) determined the alleles at 230 bp and 265 bp related with *Wx-A1a* and *Wx-A1b* genes, respectively. In this study, the stripe rust related markers Sun104, Xgwm18 and Xgwm47 produced alleles at 225 bp, 182 bp and 150 bp, respectively as expected. It was reported that marker Sun104 related with *Yr51* stripe rust resistance gene (Randhawa *et al.*, 2014) and Xgwm18 was related with stripe rust *Yr51* resistant gene (Yan *et al.*, 2003). In addition, Xgwm47 marker was associated with stripe rust *Yr64* and *Yr66* and powdery mildew resistance (Cowger *et al.*, 2012).

In this study, stem rust related markers Sun209 and Sun479 were produced bands at 148 bp and 200 bp as expected. In previous work, Bansal *et al.* (2015) reported that the 148 bp and 200 bp bands were amplified using

Sun209 and Sun479 markers, respectively, were related with *Sr49* gene and those markers could be used in marker assisted selection. The markers associated with gluten strength (Bx7^{OE}) generated alleles for only two genotypes and produced bands at 563 bp. Butow *et al.* (2003) reported that Bx7^{OE} is a co-dominant marker and associated with improved dough strength. Cho *et al.* (2017) indicated that Bx7^{OE} marker produced alleles at 520 bp in one genotype and 563 bp in two genotypes in Korean wheat genotypes. Liang *et al.* (2010) also used the Bx7^{OE} marker and 3.5% of the genotypes produced bands at 800 bp in CIMMYT bread wheats.

The high protein content related marker UHW89 produced alleles at 122 bp as expected on durum wheat genotypes in this study. Distelfeld *et al.* (2006) reported an association between UHW89 and high protein content and alleles at 122 bp and 126 bp. The Xgwm68 marker was associated with thousand kernel weight and produced bands for all the genotypes used in the study and produced bands at 166 bp. Cheng *et al.* (2015) reported a relationship between thousand kernel weight and Xgwm68 marker. The Xqwm131 marker was associated with heat tolerance (chlorophyll content and chlorophyll fluorescence) and produce alleles for all genotypes in the study at 157 bp. Pandey *et al.* (2015) reported a significant association for the Xgwm31 marker and physiological traits in a previous work. According to our genetics data, it can be proposed that our findings were generally in agreement with the previous studies.

Conclusion

Firstly, we have considered that Cesare and Saragolla cultivars were promising based on agro-morphological traits, whereas Karakılıç was promising for quality traits (PR and GC). The dendrogram showed that Karakılıç and Saragolla genotypes exhibited the most similar genetic structure. In contrast, Dumlupınar and Sarı Başak cultivars were the most diverse genotypes from others. While the Cesare cultivar produced bands for eight allele specific markers, Zenit cultivar was the only cultivar producing one allele for Xgwm18 marker. The findings of this study could contribute to breeding programs for improving durum wheat varieties.

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