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Heritability estimates for milling quality associations of bread wheat in the Northwest Turkey

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Abstract
The milling and baking value of wheat grain is determined by texture and size of grain, especially grain protein quantity and quality. A diallel trial was carried out with parents and their F_2 progeny at in Namık Kemal University, Agricultural Faculty, Field Crops Department research area in Tekirdağ Province of Trakya Region where is located North Part of Turkey during 2012-2013 growing year, to determine the heritability and combining ability of the different milling quality characteristics. High narrow sense heritabilities were found for Zeleny Sedimentation value, the ratio of zeleny sedimentation value to grain protein content (quality index), thousand kernel weight and gluten index. In descending order, thousand kernel weight, the ratio of wet gluten to grain protein content, zeleny sedimentation value, the ratio of zeleny sedimentation value to grain protein content (Quality index) and wet gluten content showed predominance additive gene action with higher GCA estimate values than SCA. In the case of grain hardiness, the SCA values were much higher, indicating non-additive gene action or over-dominance. All genotypes was involved as a parent in almost all the best performing F_2 combinations, but Aldane proved to be the best general combiner, followed by Flamura85, with Selimiye in third place. Among the crosses, Fs/Phl, Sb/Slm and Esp/Sb exhibited the highest positive specific combining ability in most of the prominent traits. These cultivars which have been identified can be incorporated into the breeding programme together with their progeny to improve quality characteristics.

Keywords: Bread wheat, grain quality, additive gen action, combining ability, heritability

Introduction
One important goal in wheat (*Triticum aestivum* L.) breeding is to develop high-yielding cultivars that possess the functional attributes demanded by producers, processors, and consumers. This is no small feat because producers strive for high yielding crops, processors require highly functional flour, and consumers demand and expect excellent sensory qualities in the end products (Seabourn *et al*. 2012) [28]. The total wheat growing area in Turkey is around 8.1 million hectares, with a total wheat production of around 21.8 million tons and yield per hectare of about 2.69 t. Particularly, wheat production is of great socio-economic importance in the Thrace Region, a part of the Balkan Peninsula that covers 23,485 km^2, consisting of Tekirdağ, Edirne, and Kırklareli Provinces and some districts of Istanbul and Çanakkale Provinces. 6.71% of wheat cultivation areas of Turkey were in the Thrace Region, with 11.88% of total national production. National average wheat yield was approximately half of that obtained in the Thrace Region (Bilgin *et al*. 2016) [9].

Many wheat varieties have been released by seed companies and breeding programs in the Thrace Region over the last 60 yr. However, there is still no bread wheat variety in this large region, which has a range of variability in weather and soils that shows enough stability to satisfy farmers, and the milling and manufacturing industry in terms of both grain yield potential and bread-making quality (Başer *et al*. 2005; Erekul *et al*. 2009) [6, 12]. The use of foreign materials that are not well adapted to the region and disregarding grain quality in the breeding process are playing the lead roles in harvesting a low-quality wheat crop in this region and throughout Turkey (Bilgin and Korkut, 2005) [8].

Wheat (*Triticum aestivum* L.) quality is important to bakers and millers alike. The inheritance of the components of quality is complex (Ausemus *et al*. 1967) [3], determined by a number of characteristics influenced by environment, genotype and their interaction (Fischer and Byerlee 1991) [13]. For the effective improvement of quality,

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a plant breeder must have knowledge of the inheritance of quality traits and of the joint inheritance of quality and agronomic traits (Baker *et al*. 1971) [5]. The unexploited gene pool of wheat grown in Thrace Region could be evaluated in order to improve wheat quality in local material through breeding. This could be achieved by identifying progeny from test crosses that have potential to be integrated into the breeding programme. Breeders are interested in parameters that are highly heritable and reproducible (Neacu *et al*. 2009) [23], and this can be estimated from specific crossing models.

Griffing (1956) [14] developed a diallel method for determining combining ability of lines and quantifying the nature and magnitude of gene action. In general, for plant breeding, hybrid combinations with high SCA and those with at least one parent with high GCA are the most sought after (Paini *et al*. 1996) [24]. Combining ability describes the breeding values of parental lines to produce hybrids. In addition, diallel analysis gives plant breeders the opportunity to choose the efficient selection method by allowing them to estimate several genetic parameters (Unay

et al. 2004) [33]. These genetic parameters have not been estimated for quality traits of wheat cultivars grown in the Northwest Region (Thrace) of Turkey. In the Region, the wheat industry is still at an infancy stage without a rigorous breeding programme for improving bread making quality. Hence, cultivars with good bread making quality are required. The first aim of this study was to evaluate parents, F_2 progeny from a diallel cross by determining the general combining ability (GCA) and specific combining ability (SCA) of measured traits as well as the GCA: SCA ratio. The second aim was to determine broad sense and narrow sense heritabilities of the quality characteristics as successful selection and rapid progress is dependent on high heritability.

Materials and Methods
Plant Material: Six widely used commercial bread wheat cultivars and one advanced line were selected based on variability of baking quality characteristics (Table 1).

Table 1: Agronomic and quality of bread wheat genotypes used as parents.

Genotypes	Origin	Parantage	Growth type	Quality
Flamura85	Romania	RANNYAYA-12/NADADORES-63//LOVRIN-12	Winter	Good
Aldane	Turkey	Bul2477–2/3/093–44/AU//BEZ	Winter	Good
Selimiye	Turkey	LAU/AGD/3/ODES95//OLV/B16	Winter	Medium
Esperia	Italia	B 16/3*LINEA RUSSA	Winter	Medium
Saraybosna	Croatia	OSJECKA-20/OSK-4.216-2-76	Facultative	Medium
FS	Turkey	Flamura80/Saraybosna	Facultative	Weak
Pehlivan	Turkey	BEZ/TVR/5/CFN/BEZ//SU92/CI13645/3/NAI60/4/EMU'S	Winter	Weak

Among the genotypes identified as parents, half diallel crosses were performed in the 2010/2011 growing season. The experiment was set up with twenty-one F_2 combinations and their 7 parents in randomized complete block design with three replicated in 2012-2013 growing year. Plots consisted of two rows per entry. Rows were five meters in length with interrow and interplant spacing 20 cm and 5 cm, respectively. Sowing was done by hand in 05.11.2012. Composed fertilizer (20.20.0), Urea (46%) and Ammonium Nitrate fertilizers (26%) were applied at 200 kg ha^{-1} for seedbed preparation stage, 180 kg ha^{-1} for tillering stage and 200 kg ha^{-1} for stem elongation stage, respectively. All other cultural practices were applied time to time as and when required.

Experimental Site: The study was conducted in Namık Kemal University, Agricultural Faculty, Field Crops Department research area in Tekirdağ Province of Trakya Region where is located North Part of Turkey. It lies at an altitude of 10m above sea level and at 27° 34' East and 40° 59' North. The Thrace region, a peninsula, is under the typical continental climate. Average rainfall of 476mm was lower than the last fifty year average of 521mm, most of which falls between November and June. The relatively low rainfall (0.2mm) received in June was a negative effect on the filling period. But irregularities in rainfall amounts according to the month are the most characteristic feature of the region. Temperature in summer rise to the maximum of 28.4 °C, while winter temperature may reach as low as -0.3 °C. It has a clayey loamy texture and enters the weak soil group according to soil analysis.

Grain quality analysis
After harvest, the grain samples were cleaned. Physical characteristics of the grain such as thousand kernel weight (TKW) and test weight (TW) were determined following the

official methods of the Approved Methods of the American Association of Cereal Chemists (AACC 2000) [1]. The quantity of grain protein content (GP) (ICC 1995) [18] and grain hardness were determined by a near infrared reflectance spectrophotometer calibrated against Kjeldahl data. Wet gluten quantity (WG) and gluten index (GI) of wheat flours were analyzed according to the revised standard ICC method No. 155 (ICC, 1994) [17] by using the Glutomatic 2200 system (Perten Instruments AB, Huddinge, Sweden). Zeleny sedimentation value (ZS) was determined following ICC method No: 166/1 (ICC 1972) [16]. The quality index (ZS/GPC) was expressed as a ratio between the sedimentation value and the content of grain protein according to Halverson and Zeleny (1988) [15]. The ratio of wet gluten to total protein content (WG/GPC), as measure of wet gluten production per protein unit was according to the equation proposed by Simic *et al*. (2006) [29].

Statistical analysis
The data after compilation were subjected to simple analysis of variance technique (Steel and Torrie 1980) [32] using statistical package 'MSTATC' to see whether significant differences existed among the wheat genotypes for further analysis. An ANOVA was done on the F_2 generation for each characteristic evaluated. Traits showing significant differences were subjected to combining ability analysis Method 2, Model 1 as proposed by Griffing (1956) [14]. The GCA and SCA, as well as the relationship between these two values, were evaluated. GCA is used to designate the average performance of a line in hybrid combination. SCA is used to identify cases in which certain combinations do relatively better or worse than would be expected on the basis of the average performance of the lines involved (Sprague and Tatum 1942) [31]. The GCA:SCA ratio indicates whether GCA or SCA effects are predominant and which factor plays a more important role in exercising genetic

control. This ratio also indicates whether a character is mainly under the control of additive or non-additive (dominant) gene action (Sing *et al*. 1986) [30]. To confirm the above findings, the additive gene action was calculated by estimating the components of variance and expressing them in a ratio (2GCA/2GCA+SCA). The closer this ratio is to unity, the greater the predictability based on general combining ability alone (Baker 1978) [4]. Heritability is in fact a regression coefficient of genotypic values (G) on phenotypic values (P) and is defined as the ratio of genotypic to phenotypic variance

(Wricke and Weber 1986) [35]. GCA, SCA, additive gene action, broad and narrow sense heritabilities were estimated using computer software 'AGD-R (2015) Version 2.0' developed by Rodriguez *et al*. (2015).

Results and Discussion
The ANOVA is given in Table 2. As expected, a significant replication effect was found for GI, TKW, ZS, ZS/GPC and grain protein content. A significant genotype effect was shown for all traits examined.

Table 2: Analysis of variance of milling quality characteristics for parents and F$_2$ progeny

Source of variation	D.F.	TKW	TW	WG	GI	ZS	GH	WG/P	ZS/P	GPC
Replication	2	3.15*	0.25	0.08	5.04**	3.86*	0.505	0.62	3.61*	4.01*
Genotypes	27	10.65**	5.05**	6.17**	37.10**	20.09**	7.187**	4.62**	13.78**	8.50**
Error	54									

Analysis of variance of the combining ability for quality characteristics

Source of variation	D.F.	TKW	TW	WG	GI	ZS	GH	WG/P	ZS/P	GPC
GCA	6	39.94**	16.15**	19.50**	117.33**	76.96**	16.57**	15.62**	51.51**	24.92**
SCA	21	2.28**	1.88*	2.36**	14.17**	3.84**	4.51**	1.48	3.00**	3.81**

Aldane, Flamura85 and Selimiye performed very well for all the quality characteristics (Table 3). Aldane, Flamura85 or Selimiye was involved as a parent in most of the best performing F$_2$

combinations. Some heterosis was evident in the F$_2$ progeny, especially for GI and ZS, where the Fs/Phl and Sb/Slm crosses performed significantly better than both parents.

Table 3: The averages of the parental genotypes over 3 replications, and the best performing crosses

Traits	Flamura85 (F85)	Esperia (Esp)	Saraybosna (Sb)	Aldane (Ald)	F/S (Fs)	Selimiye (Slm)	Pehlivan (Phl)	Best crosses
TKW	48.03	48.77	40.33	48.47	35.53	51.10	50.13	F85/Sn; Fs/Phl
TW	83.00	82.20	80.20	82.53	78.93	83.87	83.60	Esp/Sn
WG	34.03	30.73	35.77	37.97	36.70	37.67	38.83	Sn/Fs; Fs/Slm
GI	92.67	85.33	55.33	88.67	59.33	84.00	58.67	Fs/Phl; Esp/Fs
ZS	55.33	44.00	43.33	67.67	43.33	53.67	43.33	Sn/Slm; Esp/Sn
GH	52.33	50.33	54.00	53.33	52.00	53.33	52.67	F85/Fs;Esp/Slm
WG/GPC	2.57	2.45	2.78	2.61	2.80	2.85	2.88	Sn/Fs; Esp/Sn
ZS/GPC	4.18	3.51	3.37	4.66	3.30	4.06	3.22	Sn/Slm;Fs/Phl
GPC	13.23	12.53	12.87	14.53	13.14	13.23	13.50	Fs/Slm; Sn/Fs

An ANOVA of the combining ability of the different quality traits is also given in Table 2. GCA was significant for all the traits. This is in agreement with data presented by Verma *et al*. (2016) [34] showing a highly significant GCA for GPC, WG and GH, Khodadadi *et al*. (2012) [19] who reported a significant GCA for TKW, TW and ZS, and a report by Sadeghi *et al*. (2012) [27] indicating that GCA was significant for GI. This indicates that these various traits are controlled mainly through additive gene

action.
SCA was significant for test weight. Highly significant SCA was evident for TKW, WG, GI, ZS, GH, GPC and ZS/GPC. Similar findings were reported by Yıldırım (2005) [36] for TKW, WG, GI, GPC and ZS and by Khodadadi *et al*. (2012) [19] for TW and GH. The SCA could be an indication of heterotic effects in these traits.

Table 4: GCA effects of quality traits, with ranking (first, second and third) of most suitable genotypes for improving milling traits

Parents	TKW	TW	WG	GI	ZS	GH	WG/GPC	ZS/GPC	GPC
Flamura85	1.84**[(3)]	0.22	-0.76*	4.60**[(3)]	1.69**[(3)]	0.17	-0.04*	0.15**[(3)]	-0.07
Esperia	0.99*	0.25	-3.13**	7.64**[(2)]	-3.27**	-1.50**	-0.13**	-0.10**	-0.53**
Saraybosna	-3.25**	-0.83**	1.01**[(2)]	-8.51**	-2.01**	0.76**[(1)]	0.05**[(2)]	-0.18**	0.11
Aldane	1.12*	0.01	0.71*[(3)]	9.19**[(1)]	8.66**[(1)]	-0.09	-0.05*	0.49**[(1)]	0.51**[(1)]
F/S	-5.27**	-1.24**	0.54	-7.88**	-2.86**	-0.05	0.02	-0.24**	0.10
Selimiye	2.03**[(2)]	0.79**[(2)]	1.35**[(1)]	2.86**	2.25**[(2)]	0.43*[(2)]	0.10**[(1)]	0.17**[(2)]	0.01
Pehlivan	2.53**[(1)]	0.80**[(1)]	0.29	-7.88**	-4.46**	0.28	0.05*[(3)]	-0.30**	-0.13*

In Table 4 the GCA effects of the quality traits are listed. To produce the best progeny, parental lines with the highest GCA for a specific trait should be used. Pehlivan proved to be the best general combiner for seed size characters such as TKW and TW. To improve any of these characteristics, Pehlivan should be one of the parental lines. Selimiye was the best combiner for WG,

and second best for ZS, GH and ZS/GPC. Aldane was the best combiner for GI, ZS, ZS/GPC and GPC, and third best for WG. Saraybosna was the best combiner for GH, and second best for WG and WG/GPC. Esperia was the second best combiner for GI. Flamura85 was the best third combiner for TKW, GI and ZS/GPC.

Table 5: SCA effects of quality traits and the best combiners to produce desirable progeny are indicated for milling characteristics

Crosses	TKW	TW	WG	GI	ZS	GH	WG/GPC	ZS/GPC	GPC
F85/Esp	-2.708*	0.509	0.429	2.982	1.482	0.352	0.020	0.113	0.057
F85/Sb	4.962**	0.124	-0.345	4.463*	-1.778	0.759	0.012	-0.085	-0.183
F85/Ald	1.392	-0.046	0.888	-9.907**	0.222	-1.389**	0.066	0.018	-0.013
F85/Fs	-0.419	-0.269	-0.645	2.167	0.074	2.574**	-0.105	-0.079	0.294
F85/Slm	0.188	-0.024	0.140	2.093	0.963	0.093	0.004	0.069	0.028
F85/Phl	2.581*	0.094	-0.234	-13.167**	-3.333*	-1.093*	0.062	-0.154	-0.380*
Esp/Sb	-0.549	1.294	2.166*	0.759	5.185**	-0.574	0.082	0.265*	0.443*
Esp/Ald	-0.453	0.124	-0.568	-2.944	-0.815	-1.389**	-0.028	-0.016	-0.054
Esp/Fs	2.203	0.969	-2.801**	9.797**	-1.296	-2.093**	-0.142*	-0.006	-0.380*
Esp/Slm	2.777*	-0.454	-0.749	6.389**	-4.074**	1.426**	0.023	-0.198	-0.380*
Esp/Phl	-0.164	-0.335	-1.157	-1.537	-0.037	0.907	-0.022	0.070	-0.320
Sb/Ald	0.584	-1.128	-1.375	9.204**	-3.407*	0.019	-0.099	-0.234*	-0.028
Sb/Fs	-0.360	-0.017	2.625**	-7.722**	-0.889	-0.685	0.087	-0.188	0.513**
Sb/Slm	-1.319	0.561	0.977	4.537*	7.333**	0.500	0.035	0.491**	0.180
Sb/Phl	-2.294	0.946	-0.231	-0.389	0.370	0.315	-0.087	-0.062	0.339*
Ald/Fs	-0.631	1.013	-0.108	6.574**	1.111	0.500	0.027	0.142	-0.183
Ald/Slm	0.744	0.791	-0.423	2.833	3.000*	-0.648	-0.011	0.254*	-0.117
Ald/Phl	0.603	-0.291	-0.197	9.241**	0.704	1.167*	0.001	0.098	-0.091
Fs/Slm	-1.934	-0.032	2.910**	-17.426**	0.519	-0.019	0.078	-0.140	0.657**
Fs/Phl	3.692**	1.020	-1.897*	11.982**	3.889**	0.796	-0.097	0.348**	-0.217
Slm/Phl	0.132	0.065	-1.445	0.574	-4.556**	-1.019*	-0.049	-0.274*	-0.283

Table 5 gives the SCA effects of the quality traits for all the crosses. The SCA effect is an indication of the heterosis (interaction) for a specific trait. Although Paroda and Joshi (1970) [25] and Morojele and Labuschagne (2013) [21] stated that a marked decrease in the magnitude of the SCA in the F_2 population were found, good results could still be obtained in F_2. The best specific combinations to produce progeny with desirable milling characteristics, were Fs/Phl, Esp/Sb and Sb/Slm. The combinations Fs/Slm and Sb/Fs can be used to develope desirable progenies for GPC. F85/Sb proved to be the best cross to improve thousand kernel mass.

The calculated values for the GCA, SCA and GCA: SCA ratios, are listed in Table 6. This ratio reveals whether the different characters show an additive or non-additive gene action. A GCA: SCA ratio with a value greater than one, indicates additive gene action, whereas a GCA:SCA ratio with a value lower than one, indicates dominant gene action. In descending order, the following characteristics showed predominance additive gene action with higher GCA estimate values than SCA: TW, TKW, WG/GPC, ZS, ZS/GPC and WG. High additive gene action indicates higher heritability and less environmental influences. Sadeghi *et al.* (2012) [27] also found predominance for additive gene effects for TKW, ZS and WG. In contrast to our data, Ahmad *et al.* (2017) reported TW to be the only character with more non-additive than additive gene action. The remainder of the characteristics showed very little variation between the GCA and SCA, possibly implicating dominance or non-additive gene action.

Table 6: GCA: SCA ratio and additive gene action determined for milling quality characteristics

Traits	GCA	SCA	GCA:SCA	Additive gene action
Thousand kernel weight (TKW)	8.848	2.609	3.391	0.87
Test weight (TW)	0.535	0.058	9.224	0.95
Wet gluten (WG)	2.233	1.481	1.508	0.75
Gluten index (GI)	60.949	62.113	0.981	0.66
Zeleny sedimentation (ZS)	20.666	6.948	2.974	0.86
Grain hardiness (GH)	0.489	0.991	0.493	0.50
Wet gluten to protein ratio (WG/GPC)	0.006	0.002	3.000	0.86
Sedimentation to protein ratio (ZS/GPC)	0.077	0.028	2.750	0.85
Grain protein content (GPC)	0.093	0.098	0.949	0.66

Table 6 shows the estimated components of variance expressed as a ratio. The closer the ratio is to one, the greater the prediction of general combining ability (additive gene action) alone. The predictability of TKW, TW, ZS, WG/GPC and ZS/GPC, are mostly based on the GCA. WG showed equally high value, indicating that GCA also plays an important role in this character. These characters are easier to improve through selection, for the GI and GPC predictability was based on both GCA and SCA. The fact that the ratio of GCA/SCA is very close to 1 suggests that it plays a role in the inheritance of this character in the additive gene action as well as the non-additive gene action. GH showed the lowest value, thus, of all the characteristics, SCA had the most significant influence on this trait, indicating that the heterotic effects of GH are most sensitive to environmental influences. This is in agreement with the GCA: SCA ratios. Heritability is partitioned into narrow and broad sense. These are tabulated in Table 7.

Table 7: Broad and narrow sense heritability estimates for milling quality characteristics

Traits	Narrow sense (h_n^2)	Broad sense (h_b^2)
Thousand kernel weight (TKW)	0.669	0.768
Test weight (TW)	0.378	0.398
Wet gluten ratio (WG)	0.485	0.646
Gluten index (GI)	0.615	0.929
Zeleny sedimentation (ZS)	0.743	0.868
Grain hardiness (GH)	0.347	0.699
Wet gluten to protein ratio (WG/P)	0.483	0.554
Sedimentation to protein ratio (ZS/P)	0.692	0.815
Grain protein content (GPC)	0.478	0.730

Heritability of a trait is important to a plant breeder, because it reflects its response to selection. Both of them are classified by Dabholkar (1992) [10] as low (0.05-0.10), medium (0.1-0.3) and high (0.30 and above). The narrow sense heritability (phenotypic variance due to additive genetic variability) differed from as high as 0.743 for ZS to 0.347 for GH. Sedeghi *et al.* (2012) [27] reported that for ZS heritability, the additive component was higher than the dominance component. This indicates that selection for higher ZS should give a good response. High narrow sense heritabilities were also found for ZS/GPC, TKW and GI. Selections for these traits to produce superior progeny are much easier because the environmental effects are non-significant.

The broad sense heritabilities (phenotypic responses for which genetic differences are responsible) were relatively high for most of the characteristics. GI had the highest value, followed by ZS, ZS/GPC, TKW, GPC, GH, WG and WG/GPC. The lowest heritability was estimated for TW as in the work of Morojele and Labuschagne (2013) [22]. In broad sense heritability the environment plays a significant role in the expression of the phenotype. In contrast to the findings in this study, high heritabilities were found for test weight by Bhatt and Derera (1975) [7], for grain protein by Kutlu (2012) [20], and for grain hardiness by Ekiz (1996) [11].

Conclusions

All genotypes was involved as a parent in almost all the best performing F_2 combinations, but Aldane, Selimiye and Flamura85 also performed very well for the important characteristics. Overall, Aldane proved to be the best general combiner, followed by Flamura85, with Selimiye in third place. Among the crosses, Fs/Phl, Sb/Slm and Esp/Sb exhibited the highest positive specific combining ability in most of the prominent traits. In descending order, the following characteristics showed predominance additive gene action with higher GCA estimate values than SCA: TW, TKW, WG/GPC, ZS, ZS/GPC and WG. In the case of GH, the SCA values were much higher, indicating non-additive gene action or over-dominance. The response rates when selecting for this characteristic would be very low in F_2. The additive gene action results confirmed the low response. Good success will be achieved when selections are performed for Zeleny sedimentation value, TKW, ZS/GPC and GI with high heritabilities. These characters all express more additive gene action in the form of high GCA rather than SCA as indicated earlier. In case of TW, although GCA/SCA is very close to 1, but its heritability was very low. Characteristics with high SCA, like GH, had very low heritability with large influences from the environment.

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