

## Genetic Analysis of Some Quality Traits in Maize

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**Abstract:** Field experiments were conducted during the 2015 – 2016 growing seasons in Konya, Turkey. Seven inbred lines, 3 testers and 21 F<sub>1</sub> progenies that were produced by line x tester mating design in 2015 were used as materials. Seeds of each genotype were sown by hand to 5 m long rows according to “Randomized Complete Block Design” with three replications with spacing of 70 × 20 cm in second week of May in 2016. Each replicate plot was consisted of two 5 m long rows. Corn cobs of parentages and crosses were harvested manually in October when the moisture content of the grains was approximately 20%. Laboratory analyses were performed during the 2017 – 2018 with seeds of 7 inbred lines, 3 testers and 21 hybrid maize combinations. Crude oil content (COC), crude protein content (CPC), hectolitre weight (HW), starch content (SC) and thousand grain weight (TGW) traits of each genotype were determined. The variance compounds of the population, general combining abilities (GCAs) of the parentages and specific combining abilities (SCAs) of the progenies were calculated. Line 3.2 (CPC; 0.448\*, HW; 8.794\*, TGW; 24.805\*\*), line 3.4 (CPC; 0.054\*, COC; 1.019\*\*, HW; 23.905\*\*), line 14.21 (CPC; 0.176\*\*, COC; 1.297\*\*, HW; 18.349\*\*), line 3.6 (COC; 1.441\*\*, SC; 2.145\*\*), line 14.2 (SC; 1.675\*\*, HW; 21.460\*\*), line 14.26 (SC; 2.566\*\*, TGW; 35.550\*\*) and line 14.20 (CPC; 0.767\*\*) had significant and positive GCAs at several properties. Our results suggested that this population is suitable for developing progenies with appropriate quality traits.

**Keywords:** breeding, GCA, line × tester, SCA, quality in maize

## Mısırdaki Bazı Kalite Özelliklerinin Genetik Analizi

**Öz:** Tarla denemeleri 2015 – 2016 yetiştirme sezonlarında Konya, Türkiye koşullarında yürütülmüştür. Denemede materyal olarak 7 ana, 3 baba hat ve 2015 yılında line × tester yöntemine göre üretilmiş 21 F<sub>1</sub> kombinasyonuna ait tohumluklar kullanılmıştır. Her bir genotipe ait tohumluklar 2016 yılının Mayıs ayının ikinci haftası içerisinde el ile 5 m uzunluğundaki sıralara “Tesadüf Blokları Deneme Deseni” ne göre üç tekrürlü olarak 70 × 20 ekim düzeninde ekilmişlerdir. Her bir parsel 5 m uzunluğunda iki sıradan oluşacak şekilde tasarlanmıştır. Ebeveynlerin ve melezlerin kaçanları Ekim ayı içerisinde tane nem oranları yaklaşık %20 olduğunda hasat edilmişlerdir. Laboratuvar analizleri 2017 – 2018 yıllarında yapılmış, analizlerde 7 ana hat, 3 test edici ve 21 melez mısır kombinasyonuna ait tohumluklar kullanılmıştır. Her bir genotipte ham yağ oranı (HYO), ham protein oranı (HPO), hektolitre ağırlığı (HA), nişasta içeriği (Nİ) ve bin tane ağırlığı (BTA) özellikleri belirlenmiştir. Popülasyonun varyans bileşenleri, ebeveynlerin genel kombinasyon yeteneği (GKY), melezlerin ise özel kombinasyon yeteneği (ÖKY) değerleri hesaplanmıştır. Hat 3.2 (HPO; 0.448\*, HA; 8.794\*, BTA; 24.805\*\*), 3.4 (HPO; 0.054\*, HYO; 1.019\*\*, HA; 23.905\*\*), 14.21 (HPO; 0.176\*\*, HYO; 1.297\*\*, HA; 18.349\*\*), 3.6 (HYO; 1.441\*\*, Nİ; 2.145\*\*), 14.2 (Nİ; 1.675\*\*, HA; 21.460\*\*), 14.26 (Nİ; 2.566\*\*, BTA; 35.550\*\*) ve 14.20 (HPO; 0.767\*\*) nin birçok özellikte pozitif ve önemli GKY değerlerine sahip oldukları izlenmiştir. Denemeden elde edilmiş bulgular denemeye konu popülasyonun arzu edilen kalite kriterlerine sahip melezlerin geliştirilmesine uygun olduğunu göstermiştir.

**Anahtar Kelimeler:** Islah, GKY, line × tester, ÖKY, mısırdaki kalite

## INTRODUCTION

Cereals are one of the basic elements of trade and provide an important component of human nutrition. Cereal grains are also important sources of energy for domesticated animals (Chanpek et al., 2014). The annual global production of corn surpasses that of all other grains (1 billion tonnes), followed by wheat (751 million tonnes) and rice (482 million tonnes) (Anonymous 2017). Dent corn – *Zea mays indentata* Sturt.– is a cereal from *Gramineae* and belong to *Maydeae* (Emeklier, 2012). Maize is an industrial crop that provides a source of starch, syrup, glucose, gluten and oil. The economic and nutritional value of maize grains is mainly due to its high starch (73%), protein (9%) and oil (4%) contents (Musila et al., 2010). Nearly 49% of grown maize is currently being utilised as raw material in the

animal feed industry. Maize has a wide variety of uses (Mahesh et al., 2013) and so developing higher quality maize is gaining intense scientific interest (Ding et al., 2011). Plant breeding has been very successful in producing higher - yielding maize genotypes. By exploiting genetic variation in corn, the composition of the kernel has been altered to improve both the quantity and quality of starch, protein and oil (Singh et al., 2014). Sprague and Tatum (1942) defined GCA as the ‘average of a line in hybrid

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**Geliş Tarihi:** 14 Haziran 2019

**Kabul Tarihi:** 13 Aralık 2019

combination' and defined SCA as the 'deviation of certain crosses from expectation on the basis of the average performance of the line. Nagma et al., (2014) reported that the combining ability of an inbred line is the factor that ultimately determines its usefulness in the production of hybrid and synthetic plants; thus, GCA values of parentages used in breeding programmes must be known by breeders (Machkiowa et al., 2011). Analysis of the combining ability is one of the most powerful approaches for identifying the best combiners to be used in crosses, either to accumulate functional genes. Knowing the combining ability also helps one understand the genetic architecture of various attributes, which enables breeders to design effective breeding plans to develop valuable lines (Singh et al., 2017). Effective parental selection is very important for producing high - quality, single - cross hybrids. Breeders normally focus on producing inbred parents with high GCAs and hybrids with high SCAs (Patil et al., 2012). The present study aims to provide insights into methods for increasing desirable traits related to grain quality of maize (COC, CPC, HW, SC, TGW) and provides materials to different usage areas of industry.

## MATERIALS AND METHODS

### Plant Materials

In our trials, we used seven inbred lines [**Origin:** Turkey; **Generation:** S7; **Maturity Group:** Late) 3.2, 3.4, 3.6, 14.2, 14.20, 14.21 and 14.26], three testers [FRMo 17 (USA), FRB 73 (USA) and ADK 451 (Turkey)] and 21 hybridised  $F_1$  progenies.

### Field Experiment

The seven inbred lines and 3 testers were crossed to produce 21  $F_1$  hybrid progenies following the line  $\times$  tester mating design developed by Kempthorne (1957) in 2015 growing season. The various maize accessions were grown in a randomized complete block design with three replications in 2016. Seeds of each genotype were sown by hand in the second week of May with a spacing of 70  $\times$  20 cm. Each replicate plot of a particular accession consisted of two 5 m long rows. Cultural practices, as described by Kirtok (1998), were followed.

Corn cobs from parents and crosses were harvested manually in October when the moisture content of the grains was approximately 20%.

### Laboratory Analysis

All laboratory analyses were performed during 2017 - 2018. Cobs of parents and crosses were air - dried after harvesting under standard room conditions. Whole grains were used to determine Hectolitre Weight (HW) and Thousand Grain Weight (TGW). Milled grain samples were used to determine Crude Oil Content (COC), Crude Protein Content (CPC) and Starch Content (SC). Percent Crude Oil

Content (COC) was determined following Khan et al. (2016) via the soxhlet method. Percent Crude Protein Content (CPC) was determined following the procedures used by Mosse (1990) using a Leco Truspec CHNS elemental analyser. Hectolitre weight values ( $\text{kg h}^{-1}$ ) were determined with a PM - 400 hectolitre weight scale. Percent Starch Content (SC) was determined according to Alan et al. (2011). Four replicates of 100 randomly collected seeds were counted. Each seed group replicate was weighed. The obtained values were converted to Thousand Grain Weight (TGW). We used SPSS version 20.0 to statistically analyse all data. We performed analysis of variance for a randomised complete block design. We calculated the heritability components [ $\sigma^2$  (Variance) GCA (General Combining Ability),  $\sigma^2$  (Variance) SCA (Specific Combining Ability), RV (Relative Variance),  $\sigma^2$  (Variance) A (Additive),  $\sigma^2$  (Variance) D (Dominance),  $\sqrt{D/A}$ ], GCAs (General Combining Abilities) of the parentages and SCAs (Specific Combining Abilities) of the progenies as described by Singh and Chaudhary (1979) and Hussain and Sulaiman (2011). The Relative Variance (RV) was calculated as described by Fasahat et al. (2016). The t-test being used to test the significance of the GCAs (General Combining Abilities) and SCAs (Specific Combining Abilities)

## RESULTS AND DISCUSSION

### Variance Components

Results of the analysis of variance for all attributes are summarised in Table 1. For each feature, its variation among genotypes was statistically significant ( $P < 0.01$ ), suggesting a remarkable amount variation that promoted the investigation of the genotypes.

When variations among variance components of the population in the trial were investigated, we observed that  $\sigma^2\text{SCA} > \sigma^2\text{GCA}$  for the traits COC, CPC and TGW and  $\sigma^2\text{D} > \sigma^2\text{A}$  for the traits COC and TGW.  $\sigma^2\text{GCA} > \sigma^2\text{SCA}$  for HW and SC and that in all  $\sigma^2\text{As}$  was  $> \sigma^2\text{Ds}$  (Table 2). The RVs ranged from 0.260 to 0.832. The RV of the SC trait was higher than it was for any of the other traits, followed by HW, CPC and COC. The minimum RV value was obtained for the TGW attribute. The observation that  $\sigma^2\text{D} > \sigma^2\text{A}$  of the TGW and COC traits indicated high dominance effects on these properties; high  $\sqrt{D/A}$  values support these results as well (Table 2). Dominant gene effects were not observed for most of the other attributes (except for TGW and COC). For attributes (traits) under the influence of GCA, additive gene effects operate, whereas for traits under the influence of SCA, non - additive, dominant and / or epistasis gene affecting HW and SC properties in the population we studied were under the influence of additive genes, effects operate (Tan, 2010; Rodrigo et al., 2012; Tongbram

Table 1. Analysis of variance for features at the parents and their F1 progenies of maize

Sources	d.f.	COC (%)	CPC (%)	HW (kg.hi <sup>-1</sup> )	SC (%)	TGW (g)
Replications	2	0.885	0.106*	17332.052**	2.455	23238.460**
Genotypes	30	459.456**	58.874**	129368.835**	804.735**	378399.756**
Error	60	18.915	1.930	62517.580	57.671	323730.780
Total	92	479.256	60.910	209218.467	864.861	725368.995
CV (%) <sup>1</sup>		11.68	2.10	4.41	1.55	23.54

\*\* P < 0.01; COC: Crude Oil Content ; CPC: Crude Protein Content ; HW: Hectolitre Weight; SC: Starch Content; TGW: Thousand Grain Weight

<sup>1</sup> Coefficient of variation.

and Baskheti, 2014). Therefore, we speculate that genes whereas COC, CPC and TGW were under the influence of non – additive genes. Similarly, Singh et al. (2017) and Mahesh et al. (2013) revealed that  $\sigma^2_{GCA} > \sigma^2_{SCA}$  for SC and  $\sigma^2_{SCA} > \sigma^2_{GCA}$  for COC and CPC traits. Likewise, Ding et al. (2011) and Iqbal et al. (2007) reported that  $\sigma^2_{SCA} > \sigma^2_{GCA}$  for HW and TGW traits. The variance components of every trait depend on the genetic makeup of the population. Different gene effects / actions can affect inheritance of characters in a population as well. Additive variance associated with the average effects of individual genes measures the breeding value of the population and can always be changed via selection (Sofi et al. 2007). Populations are more suitable for selective breeding if they possess properties with higher  $\sigma^2_A$  and for heterosis (Hs) breeding if they possess higher  $\sigma^2_D$ . Based on previous studies, this population is suitable for selective breeding for HW, SC and CPC and suitable for Hs breeding for obtaining COC and TGW. Li et al. (2017) reported that if the degree of dominance ( $\sqrt{D/A}$ ) for any character in the population is between 0.20 (inclusive) and 0.80, then partial dominance occurs, whereas dominance occurs if  $0.80 \leq \sqrt{D/A} < 1.20$  and super dominance occurs if  $\sqrt{D/A} \geq 1.20$ . Therefore, super dominance for COC and TGW got attention with higher  $\sigma^2_D$ . Dominance is very effective in populations that include genotypes with different genetic bases (Nagma et al. 2014). Dominance variance is associated with intra – allelic gene interactions at segregating loci and so measures breeding behaviour of alleles of heterozygotes, a fact that Table 2. Variance components of the population for each traits

can be practically applied in heterosis breeding (Sofi et al. 2007). Sometimes, additive and non–additive gene effects operate together in establishing some traits. Relative variance is a criterion used to determine the rate of additive and non–additive gene effects on specific traits. Relative variance values closer to 1.0 indicate more additive gene effects than non–additive gene effects (Fasahat et al. 2016). In the population we studied, additive gene effects were more effective in producing the SC trait than the COC, CPC and HW traits, whereas non – additive genes effects were more effective in producing the TGW trait (Table 2).

#### General Combining Ability

Estimates for GCAs and SCAs for five attributes in 21 crosses are presented in Table 3. Most inbred lines exhibited significant and positive GCAs in various traits: lines 3.2, 14.21 and 3.4 in CPC, lines 3.6, 14.20, 14.21 and 3.4 in COC, lines 3.4, 14.2, 14.21 and 3.2 in HW, and lines 14.26, 3.6 and 14.2 in SC. Only lines 14.26 and 3.2 had significant and positive GCAs in TGW. Lines 3.4 and 14.21 had significant and positive GCAs at COC, CPC and HW traits; these parentages had significant and negative GCAs at SC trait as well. A remarkable similarity was observed of GCAs of lines 3.4 and 14.21 at different features. Tan (2010) reported that combining ability is the ability to transfer desired parental traits to F<sub>1</sub> progenies. Therefore, breeders must know the GCAs of parents used in breeding programmes (Machkiowa et al. 2011). Nagma et al. (2014) reported that the combining ability of an inbred line is the ultimate factor determining its use in the production of

Traits	$\sigma^2_{GCA}$	$\sigma^2_{SCA}$	Relative Variance			
			$[2\sigma^2_{GCA} / (2\sigma^2_{GCA} + \sigma^2_{SCA})]$	$\sigma^2_A$	$\sigma^2_D$	$\sqrt{D/A}$
COC (%)	1.083	5.413	0.286	2.165	5.413	1.581
CPC (%)	0.198	0.313	0.558	0.395	0.313	0.889
HW (kg/l)	620.014	331.582	0.789	1240.027	331.582	0.517
SC (%)	3.319	1.340	0.832	6.639	1.340	0.449
TGW (g)	198.724	1131.391	0.260	397.447	1131.391	1.687

COC: Crude Oil Content ; CPC: Crude Protein Content ; HW: Hectolitre Weight; SC: Starch Content; TGW: Thousand Grain Weight

hybrid and synthetic varieties. The inbred parents 3.4, 14.21 and 3.6 exhibited significant and positive GCAs in COC; in addition, the lines 3.2, 14.2, 14.20 and 14.26 exhibited significant and negative GCAs, which indicated the potential of the parents for effectively transmitting genetic materials essential for a given attribute to their progenies (Topal et al., 2004) and so indicated the potential of them to produce high or low oil content genotypes. The SCAs of the hybrids of lines 3.4, 14.21 and 3.6 were significant and positive as well (Table 3). Singh et al. (2014) reported that high quality maize oil is particularly suitable for human consumption. The oil of maize is considered to be better than most of other edible oils due to its fatty acid composition and its stability during storage and cooking. Maize kernels are composed of 3 – 4% oil. However, more than 7% oil has been reported from high oil content genotypes (Singh et al., 2014). Oil from maize has a greater feed efficiency than normal maize when fed to animals. Maize oil contains 2.25 times more calories than starch

(based on dry weight) and possesses a beneficial composition of fatty acids (oleic and linoleic acids). Starch and oil concentrations have been shown to be negatively correlated in corn. For this population; If the aim of a breeding programme is to increase the oil content, then lines with positive GCAs in COC must be used. However, if the aim of a breeding programme is to increase SC, then parents with low GCAs in COC should be used. Therefore, appropriate GCA values for lines depend on the aims of the specific breeding programme. We observed high inheritance of the CPC trait in the lines 3.4, 3.2 and 14.21, which proves that these parents have the potential to produce hybrids containing high amounts of proteins. The hybrids of these parental lines also exhibited high SCAs (Table 2). Schaefer (1946) reported that proteins are essential nutrients required for proper nutrition in animals. In addition to providing nutrition for animals, products of proteins can be used as secondary materials in industrial

Table 3. Estimation of GCA in parents and SCA in the F1 progenies for all traits

GCA (parents)	COC (%)	CPC (%)	HW (kg.hi <sup>-1</sup> )	SC (%)	TGW (g)
3.2	-1.125**	0.448**	2,002*	-4.135**	24.805*
3.4	1.019**	0.054*	5,442**	-0.281*	-7.168
3.6	1.441**	-0.200**	-3,664**	2.145**	1.723
14.2	-1.592**	-0.749**	4,885**	1.675**	-49.875**
14.20	-0.714**	0.767**	0,510	-0.516**	-1.167
14.21	1.297**	0.176**	4,177**	-1.455**	-3.868
14.26	-0.325**	-0.495**	-13,352**	2.566**	35.550**
FRMo 17	-0.321**	0.147**	3,913**	-0.654**	-1.297
FRB 73	0.937**	-0.400**	1,294	-0.611**	-22.002
ADK 451	-0.616**	0.253**	-5,207**	1.264**	23.300*
<b>SCA (combinations)</b>					
3.2 × FRMo 17	0.154*	-0.027**	0,440	-1.000**	-13.670**
3.2 × FRB 73	-1.003**	0.806**	-2,256**	-0.164	42.209**
3.2 × ADK 451	0.849**	-0.779*	1,816**	1.163**	-28.539*
3.4 × FRMo 17	3.910**	0.051**	-2,005**	0.860**	21.363**
3.4 × FRB 73	-2.214**	-0.330**	-0,900*	0.313*	-30.060**
3.4 × ADK 451	-1.695**	0.279**	2,905**	-1.174**	8.698
3.6 × FRMo 17	-2.013**	-0.086**	-1,271**	-0.562**	31.618**
3.6 × FRB 73	1.597**	0.173**	2,400**	0.334*	-38.090**
3.6 × ADK 451	0.416**	-0.086**	-1,129**	0.228	6.473
14.2 × FRMo 17	0.121	-0.881**	-0,760	0.305*	11.364
14.2 × FRB 73	-1.037**	0.122**	0,144	-0.461**	31.759**
14.2 × ADK 451	0.916**	0.759**	0,616	0.156**	-43.123**
14.20 × FRMo 17	-0.357**	0.462**	3,829**	-2.163**	-25.362**
14.20 × FRB 73	0.519**	-0.690**	0,400	1.369**	24.875*
14.20 × ADK 451	-0.162*	0.228**	-4,229**	0.794**	0.488
14.21 × FRMo 17	-2.268**	0.089**	0,784	2.171**	5.874
14.21 × FRB 73	4.141**	-0.009	-1,344**	-0.762**	-38.982**
14.21 × ADK 451	-1.873*	-0.080**	0,560	-1.409**	33.108**
14.26 × FRMo 17	-1.168**	-0.278**	-8,716**	4.410**	8.232
14.26 × FRB 73	-3.625**	-0.743**	-6,144**	3.391**	47.707**
14.26 × ADK 451	-0.073	-0.991**	-8,240**	4.261**	62.313**

\* P < 0.05; \*\* P < 0.01; COC: Crude Oil Content ; CPC: Crude Protein Content ; HW: Hectolitre Weight; SC: Starch Content; TGW: Thousand Grain Weight

applications. For example, corn gluten meal is one of the products used in producing corn starch, which is comprised of approximately 60% protein. Due to the insolubility of corn protein in water, corn is usually used for animal feeds rather than for human consumption (Schafer, 1946). Sun et al., (2018) reported that oligo – peptides prepared from corn gluten meal protects mitochondria against oxidative damage caused by ROS. Because corn protein potentially provides many commercially useful products, more scientific research is needed on producing corn hybrids that can supply proteins for commercial markets. The inbred lines 3.2, 14.21, 14.2 and 3.4 exhibited significant and positive GCAs in trait HW, which indicates that the combinations of these parents would be useful for providing progenies with high HW. Some progenies of these lines exhibited significant and positive SCAs as well. HW in maize is linked to kernel maturity, integrity and uniformity and so it is not only an important index of grain quality but also an important factor for determining the market corn grades for milling, exporting and other purposes. In addition to the chemical compounds inherent to maize kernels, physical factors (e.g. endosperm hardness, kernel size, water content) and kernel type have also been found to significantly correlate with HW (Ding et al., 2011). High HW indicates high grain size, endosperm hardness and protein content. A selection program focused on one of those traits may provide information to the breeder about the other factors that correlate with such traits. Better information on HW may also enable breeders to evaluate populations more efficiently and provide better information to breeders on traits other than those being specifically investigated. The lines 14.2, 3.6 and 14.26 exhibited significant and positive GCAs in SC; line 14.26 also exhibited significant and positive GCA in the TGW trait. All progenies of line 14.26 had significant and positive SCAs in SC as well. We observed a remarkable relationship between SC and TGW attributes in the inbred line 14.26. Some progenies of the lines 3.6 and 14.2 also exhibited significant and positive SCAs in SC. Based on these results, lines 3.6, 14.2 and 14.26 were good combiners (GCs) for SC and lines 3.2 and 14.26 were GCs for TGW. Corn kernels contain about 77% starch. Corn starch is a major ingredient used in cooking and in many industrialised food products (Mahesh et al., 2013). Maize starch has a wide range of usage areas industry, such as providing a source of synthetic polymers in food packaging (Wang et al., 2017), an alternative source for starch for celiac patients, etc. (Chnapek et al., 2014). Linear correlations have been observed among traits the CPC and HW, COC and CPC, CPC and HW and SC and TGW in many studies (Dorsey – Redding et al., 1991; Saleem et al., 2008; Aliu et al., 2012). We found that lines 3.4, 14.21 and 14.26 also exhibited significant and positive GCAs for traits the COC – CPC – HW, COC – CPC – HW and SC – TGW. Correlations of GCAs of some of the traits can provide benefits to the breeders, interested in selection with more criteria in shorter times.

#### **Specific Combining Ability**

Some of the crosses and combinations of parentages (by GC or poor combiner [PC]) are summarised at Table 3. While

progenies 14.21 (+GC) × FRB 73 (+GC) and 3.4 (+GC) × FRMo 17 (–GC) had significant, positive and high SCAs in COC; 3.2 (–GC) × FRMo 17 (–GC) and 3.6 (+GC) × ADK 451 (–GC) had significant, positive and low SCAs. Tester FRMo 17 took part in two of the combinations as a GC with a negative orientation. Parentages that have opposite gene actions from each other, had progenies with significant and positive SCAs in COC (Table 3). The progenies 3.2 (+GC) × FRB 73 (–GC) and 14.2 (–GC) × ADK 451 (+GC) showed significant, positive and high SCAs in CPC, whereas 3.4 × FRMo 17 and 14.21 × FRMo 17 showed significant, positive and lower SCAs in CPC. Unlike COC; tester FRMo 17 was a GC with positive orientation among some progenies at CPC (Table 3). Following progenies were observed with remarkable SCAs in HW. Progenies 14.20 (PC) × FRMo 17 (+GC) and 3.2 (+GC) × ADK 451 (–GC) showed significant, positive and high SCAs, whereas 14.21 (+GC) × ADK 451 (–GC) and 3.4 (+GC) × ADK 451 (–GC) showed significant, positive and lower SCAs. The progeny of 14.20 (PC) × FRMo 17 (+GC) had the highest SCA, though a poor combiner parent. The progenies 14.21 × ADK 451 (–GC) and 3.2 × ADK 451 (–GC) were also remarkable progenies with good and negative oriented parents. The observation of SCAs in the SC of progenies showed that 14.26 (+GC) × FRMo 17 (–GC) and 14.26 (+GC) × ADK 451 (+GC) showed significant, positive and high SCAs, whereas the progenies 14.2 (+GC) × ADK 451 (+GC) and 14.2 (+GC) × FRMo 17 (–GC) had significant, positive and lower SCAs. All parentages of these four progenies were good combiners therewithal a good combiner FRMo 17, had a negative orientation (Table 3). We observed several progenies with remarkable SCAs. The ones that had significant, positive and the highest SCAs were progenies 14.26 (+GC) × ADK 451 (+GC), 14.26 (+GC) × FRB 73 (–PC), 14.20 (–PC) × FRB 73 (–PC) and 3.4 (–PC) × FRMo 17 (–PC) and three of the previous progenies with the highest SCAs had PC in their gene pools. The SCAs of progenies 14.21 × FRB 73 and 14.20 × FRMo 17 were significant and positive. Fasahat et al., (2016) reported that progenies with high SCAs, where both parents were GCs may indicate the occurrence of additive × additive gene actions with respect to the trait in question. High value hybrids between good and poor general combiner parents may be attributed to favourable additive effects from the GC parent and to favourable epistasis effects from the poor general combiner parent. High performance from hybrids between low × low parents may be due to dominance × dominance types of non – allelic gene interactions, resulting in over dominance. Many of our progenies had significant positive or negative SCAs. We observed that parents of some progenies exhibiting significant and positive SCAs showed dominance/epistasis gene actions in HW and TGW traits. Furthermore, the TGW trait was also under the influence of non – additive genes. The same was not observed for the HW attribute because one of the parentages of our progenies exhibited additive gene action many times. This may explain why  $v^2$  GCA >  $v^2$  SCA in the TGW trait, whereas remarkable epistasis effects of tester. The influence of high GCA can confer stability to a genotype, but high SCA levels

for any trait (which occurs under dominance × dominance gene effects) can be used more effectively in SCA breeding studies. Therefore, Tan (2005) reported that lines that have greater genetic distance are better combiners. According to the scientific literature and our results, parentages in our experimental population had a wide range of genetic variation.

#### CONCLUSIONS

According to the results; line 3.2 (CPC; 0.448\*, HW; 8.794\*, TGW; 24.805\*\*), line 3.4 (CPC; 0.054\*, COC; 1.019\*\*, HW; 23.905\*\*), line 14.21 (CPC; 0.176\*\*, COC; 1.297\*\*, HW; 18.349\*\*), line 3.6 (COC; 1.441\*\*, SC; 2.145\*\*), line 14.2 (SC; 1.675\*\*, HW; 21.460\*\*), line 14.26 (SC; 2.566\*\*, TGW; 35.550\*\*) and line 14.20 (CPC; 0.767\*\*) had significant and positive GCAs at several properties. In the study many of the progenies had significant and positive SCAs at many properties as well. Progeny 3.2 × ADK 451 [COC (0.849\*\*); HW (1,816\*\*); SC (1,163\*\*)], 14.20 × FRB 73 [COC (0,519\*\*); SC (1,369\*\*); TGW (24.875\*\*)], 3.4 × FRMo 17 [COC (9,910\*\*); CPC (0.051\*\*); SC (0,860\*\*); TGW (21.363\*\*)] and 3.6 × FRB 73 [COC (1.597\*\*); CPC (0.173\*\*); HW (2.400\*\*); SC (0,334\*)] had significant and positive SCAs many of the progenies as well. Our results suggested that this population is suitable for developing progenies with appropriate quality traits.

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