Genetic variability, heritability and genetic advance for important quantitative traits related to the productivity and quality in F_2 generation of durum wheat: Part II

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Abstract

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The aim of this study was to estimate genetic variability, heritability and genetic advance for quantitative traits related to productivity and quality in F_2 segregating generation of durum wheat. On the other hand these parameters will be calculated for every single hybrid combination. The experiments were performed in a randomized block design in three replications under field conditions using the adopted cultivation technology. Modern statistical evaluation methods were applied to the results. The analysis of variance revealed highly significant differences among the genotypes for all traits measured. Phenotypic coefficients of variation were generally higher than genotypic coefficients of variation for all traits studied, indicating the influence of the environment. Plant height, main spike length, grains weight per main spike and thousand kernel weight expressed high heritability coupled with high genetic advance indicating that most likely the heritability is due to additive gene effects. The trait grains number per main spike coupled high heritability and moderate genetic advance and was also controlled by additive genetic effects. An effective selection of genotype by phenotype can be conducted to them. Regarding the traits plant height, main spike length and grains number per main spike GxE was nosignificant. Generally in this research, genetic parameters for the traits were reasonable as expected, because this experiment was conducted for three consecutive years and also evaluation of genotypes was based on genetics variance. High heritability coupled with high or moderate GA% and low GxE interactions indicate that these yield components of durum wheat can be improved by pure line selection. In certain hybrid combination such as: Superdur X Progres (SxP), Progres X Predel (PxPr), Deni X Predel (DxPr), Victoria X Superdur (VxS) and Victoria X Deni (VxD) it is possible with a selection in them to improve pure lines on several traits at the same time, as they coupled high heritability and high genetic advance. This information is very useful for breeders and their programs and would be valuable for improving the genetic diversity of durum wheat and creating new, more productive lines/varieties.

Keywords: heritability; genetic advance; quantitative traits; F_2; durum wheat

Introduction

Durum or macaroni wheat is a raw material in pasta production and, although it is less common than common winter wheat, it is a very important cereal product due to the increasing demand for pasta. In fact it was widely used for human consumption. Durum wheat (2n = 28, AABB, *Triticum turgidum* L. ssp. *Durum*) is the most commonly cultivated form of allotetraploid wheat and is grown on 8% of the world's wheat area (FAOStat, 2016). It is among the ten

most important crops in the world constituting 37 million tons annual production (Ranieri, 2015; Taylor & Koo, 2015). It originates from the Mediterranean region and is used to make pasta and semolina (Ren et al., 2013). Approximately 75% of durum wheat is still grown in the Mediterranean basin in irrigated and rainy environments, which contributes to 50% of world production (Li et al., 2013). According to the main climate scenarios, the expected growth of the average annual temperature is already a reality. Under these conditions, durum wheat production is threatened by the effects of climate change and needs more sustainable development. Grain yield is a polygenic trait; therefore, the breeding of genotypes based solely on grain yield is not very effective, therefore, to increase the efficiency of breeding, the identification by the wheat breeder of the traits contributing to the final yield is crucial (Saeed et al., 2016). Heritability is the assessment of the genetic part on appearance (phenotype). Heritability and the values of genetic advance help us make selection more effective and evaluate selection response (Ijaz et al., 2015).

The degree of genetic variability is considered an important factor, which is an essential prerequisite for successful hybridization aimed at obtaining high-yielding generations. The large range of variability in the population provides an opportunity to select genotypes with a variety of desirable traits (Arya et al., 2013). It is necessary to conduct the research, determine the genetic variability and ways of inheritance for different elements of the yield to derive a successful breeding program. Research on segregating generations is useful for understanding and establishing the effects after hybridization. Heritability describes the degree of transmission of a trait from one generation to the next. Genetic advance can be considered as a final assessment of the improvement according to the applied selection pressure on the materials. High heritability coupled with high genetic advance for different yield elements indicate a better opportunity to select highly productive genotypes (Mangi et al., 2007; Stamatov et al., 2018). The genetic information obtained from these parameters for various traits contributes to increased productivity. The information has great value, allowing breeders to use the best genetic stock to improve the breeding program. Studies of genetic variability in segregating generations in wheat have also been carried out by other authors (Hokrani et al., 2013).

The aim of current study is to estimate genetic variability, heritability and genetic advance for 9 quantitative traits related to productivity and quality in F_2 segregating generations of durum wheat. On the other hand these parameters will be calculated for every single hybrid combinations.

Materials and Methods

The experiments were conducted under field conditions in the experimental field of the Field Crops Institute - Chirpan. The experiments were sown after the predecessor of spring peas and the accepted technology for durum wheat growing was applied. The meteorological conditions during the three years of research was characterized by higher than the multi-year norm temperatures. The first year 2015 of the study was favorable in terms of soil moisture and precipitation above the perennial average. The second harvest year 2016 was characterized as the hottest and at the same time with 20% less precipitation than the norm. The third harvest year 2017 was characterized by optimal temperatures close to the average for a multi-year period, but with 20% less precipitation than the norm.

The study included five modern durum wheat varieties as parent varieties: Victoria (V), Deni (D), Superdur (S), Progres (P) and Predel (Pr). Victoria, Deni, Progres and Predel varieties was created in Field Crops Institute - Chirpan. Victoria and Predel by combining breeding method and Deni and Progres by mutation-hybridization breeding. The varieties was selected among the new Bulgarian durum wheats, including the old and the new standard of executive agency for variety testing, approbation and seed control and the Austrian variety Superdur. The choice of varieties is based on previous observation on them. All varieties were crossed with each other and a diallel cross was made without reciprocal combinations. From F_1, 20 plants were selected at random from each cross and they were used for F_2 sowing. The following F_2 hybrid combinations were obtained and sown: Victoria X Deni (VxD), Victoria X Superdur (VxS), Victoria X Progres (VxP), Victoria X Predel (VxPr), Deni X Superdur (DxS), Deni X Progres (DxP), Deni X Predel (DxPr), Superdur X Progres (SxP), Superdur X Predel (SxPr) and Progres X Predel (PxPr). They was set in a randomized block design in three replications in three consecutive years: 2015, 2016 and 2017. Each parent was sown in two rows and each F_2 generation in five rows. They was sown by hand in 2 meters long rows. The row spacing is 20 cm, and within the row between the individual plants 5 cm. After the phenophase of full maturity, the necessary plants from each replication was plucked and collected for biometric examinations. 20 plants were randomly selected from each parent, and 30 from each F_2 generation.

The following quantitative traits were observed: plant height (cm), productivity tillering (pcs.), main spike length (cm), spikelets number per main spike (pcs.), grains number per main spike (pcs.), grains weight per main spike (g), thousand kernel weight (g), grain protein content (%) - Kjeldahl

method BDS ISO 20483: 2014 and grain wet gluten content (%) - BDS EN ISO 21415-2: 2008.

The data was subjected for analysis of variance (Steel et al., 1997). The genotypic and phenotypic components of variance were computed according to Burton & Devane (1953). The heritability, genetic advance and genetic advance in percentage of mean was calculated according to Johnson et al. (1955); Allard (1960); Falconer & Mackay (1996).

(1) Genetic Variance (σ^2_g) = Genotype mean square (GMS) – Error Mean Square (EMS) / Number of replication (r)

(2) Environmental Variance (σ^2_e) = Error Mean Square (EMS)

(3) Phenotypic Variance (σ^2_{ph}) = $\sigma^2_g + \sigma^2_e$

Genotypic, Phenotypic and Environmental coefficient of Variation was calculated as:

(4) GCV% = ($\sigma^{2\ 0,5}_g$ / $\overline{x}$) x 100; PCV% = ($\sigma^{2\ 0,5}_{ph}$ / $\overline{x}$) x 100; ECV% = ($\sigma^{2\ 0,5}_e$ / $\overline{x}$) x 100,

where, GCV% = Genotypic Coefficient of variation; σ^2_g = Genotypic Variance; PCV % = Phenotypic Coefficient of variation; σ^2_{ph} = Genotypic Variance; ECV % = Environmental Coefficient of variation; σ^2_e = Environmental Variance.

Heritability (h^2_{BS}%) on Entry Mean Basis was calculated as:

(5) h^2_{BS} = σ^2_g / σ^2_{ph}, h^2_{BS}% = (σ^2_g / σ^2_{ph}) x 100

The expected Genetic Advance for each trait was calculated as:

(6) GA = K x (σ^2_{ph})$^{0.5}$ x h^2_{BS} ,

where, K = 2.06 at 5% selection intensity for trait; σ^2_{ph} = Phenotypic variance for trait or (σ^2_{ph})$^{0.5}$ standard deviation of phenotypic variance; h^2 = Broad Sense Heritability of the trait

Genetic Advance as percentage of mean is calculated as:

(7) GA% = (GA / $\overline{x}$) x 100

Results and Discussion

The analysis of the variance revealed that all studied genotypes had significant differences by the studied traits (Table 1). Differences between genotypes were highly significant (p <0.001). This implies a great variation between them, which is of great importance and allows breeders to improve them through selection and breeding. An exception was trait productive tillering. Many researchers found significant differences among genotypes for agronomic characters (Menshawy et al., 2014; Talukder et al., 2014; Mohammad et al., 2015; Kaya & Turkoz, 2016; Desheva & Cholakov, 2014; Karimizadeh et al., 2012; Tripathi et al., 2015). The environment was also highly significant for the studied traits with the exception of productivity tillering and the spikelets number per main spike. The GxE interaction is poorly significant for the characteristics of grains weight per main spike, thousand kernel weight, grain protein content and grain wet gluten content. For the other traits included in the study, the interaction GxE was nosignificant. Nosignificant values indicate that the genotypes for these traits responded in an identical way during the three years of the study.

It is essential for breeders to determine variability using parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2_{bs}%) and genetic advance (GA%). Therefore, the study of the genetic variability of grain yield components among durum wheat genotypes provides a strong basis for selecting desired genotypes to increase yield and improve other agronomic characteristics. Table 2 presents the mean, minimum and maximum values of the studied traits. The plant height had mean value 94.32 cm and was in the range from 79.70 to 102.11 cm. Productivity tillering had mean value 7.92 pcs and ranged from 7.19 to 8.64 pcs. The main spike length had mean value 8.30 cm and ranges from 6.66 to 9.05 cm. The spikelets number per main spike had mean value 22.37 pcs and ranges from 21.58 to 23.75 pcs. The grains number per main spike had mean value 52.85 pcs and ranges from 46.77 to 56.88 pcs. The grains weight per main spike had mean value of 2.56 g and ranges from 2.15 to 2.94 g. The thousand kernel weight had mean value of 48.71 g and was in the

Table 1. Mean squares value from ANOVA for 9 quantitative traits in F$_2$ generation

Traits	Genotype	Environment (Year)	GxE	Error
Plant height	435.91***	121.94***	8.75 n.s.	5.85
Productivity tillering	1.30 n.s	0.78n.s.	0.66 n.s.	0.82
Main spike lenght	4.09***	1.49***	0.07 n.s.	0.15
Spikelets number per main spike	3.58***	0.28n.s	0.33 n.s.	0.55
Grains number per main spike	90.50***	139.36***	15.99 n.s.	13.16
Grains weight per main spike	0.40***	2.19***	0.06*	0.04
Thousand kernel weight	133.98***	1470.06***	7.66**	3.84
Grain protein content	1.86***	7.47***	0.95*	0.85
Grain wet gluten content	11.20***	54.84***	6.42*	3.80

*** Significant at p<0.001; ** Significant at p<0.01; * Significant at p<0.05; n.s. – not significant

range from 42.00 to 54.46 g. The grain protein content had mean value of 11.33% and was in the range from 10.58% to 12.09%. The grain wet gluten content had mean value 30.59% and ranges from 28.62% to 32.50%. The mean values was optimal for durum wheat in our growing conditions. A wide range between the minimum and maximum values has been established. This is indicative for the significant genetic variability between the studied genotypes. Bhushan et al. (2013) and Tambe et al. (2013) reported similar results in terms of scope for all quantitative traits observed in our study.

To reveal which traits had high variability, it is necessary to consider PCV and GCV (Arphita et al., 2017). The coefficients of variation account only for the degree of the general variation of the trait. They cannot explain which was heritable and non-heritable (Basavaraj et al., 2017). The results for PCV and GCV was presented in Table 2. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values were classified (Sivasubramanian & Menon, 1973) as low (<10%), moderate (10-20%) and high (> 20%). The highest PCV had the trait grains weight per main spike. In terms of classification, he was classified with moderate value. Indicated moderate PCV was the traits: main spike length, thousand kernel weight, plant height, productivity tillering and grains number per main spike. The other traits in the study was with low PCV. In terms of GCV, main spike length had the highest value. Its value was within the moderate GCV. Other traits that had expressed moderate GCV values was: grains weight per main spike, thousand kernel weight and plant height. The other traits studied had low values for PCV. Dashora et al. (2020) reported that the main spike length and thousand kernel weight had high values for PCV and GCV, as in our case. For the traits grain protein content and grain wet gluten content Chatzav et al. (2010) revealed low PCV and GCV, as in our case. In all cases of our study, PCV is greater than GCV. The differences between PCV and GCV was small for most traits. Exceptions was the traits of productivity tillering, grain protein

content and grain wet gluten content where these differences was considerable. For the plant height, main spike length and thousand kernel weight, the differences in PCV and GCV values were very small and nonconsiderable. The calculated PCV values was greater than the GCV values for all examined traits. This was as a consequence of the influence of the environment on their expression (Dashora et al., 2020). On the other hand the PCV values for most characteristics were closer than the corresponding GCV values showing little environment effect on their expression. Similar results for the studied traits were also observed by Tsegaye et al. (2012). Shah et al. (2015); Wolde et al. (2016); Kabir et al. (2017) reported similar results for this traits. There were no traits with high PCV and GCV in the study. Most traits, however, was characterized by moderate values. GCV expresses the true genetic potential of the studied traits in durum wheat. GCV shows a high presence of variability for the studied traits with mean values. With them, the selection can be more efficient, as it was directly proportional to the GCV. As quantitative traits, they was affected by the growing environment. It is necessary to conduct such a study for several years and in different locations.

Phenotypic variance, genotypic variance, environmental variance and genetic advance was presented in Table 3. With their help, broad sense heritability and genetic advance as a percentage of the mean values was calculated. The magnitude of the genotypic variance was higher than the environment variance for the traits: plant height, main spike length, spikelets number per main spike, grains number per main spike, grains weight per main spike and thousand kernel weight (Table 3). This determines that genotypic variance was a major contributing factor to phenotypic trait variation. In the other traits, the variance of the environment was higher and it had a greater role in the phenotypic variation. Heritability assessment was used as a predictive tool to express the reliability of phenotypic value. High heritability helps to implement an effective selection in a certain trait. High values of heritability indicate that the manifestation of the traits

Table 2. Variation coefficient, means values and its ranges for 9 quantitative traits in F$_2$ generation

Traits	Min-Max	Mean	PCV %	GCV %	ECV %
Plant height	79.70-102.11	94.32	12.95	12.69	2.56
Productivity tillering	7.19-8.64	7.92	12.29	4.93	11.26
Main spike lenght	6.66-9.05	8.30	14.58	13.81	4.68
Spikelets number per main spike	21.58-23.75	22.37	5.58	4.50	3.30
Grains number per main spike	46.77-56.88	52.85	11.81	9.61	6.86
Grains weight per main spike	2.15-2.94	2.56	15.59	13.62	7.57
Thousand kernel weight	42.00-54.46	48.71	14.11	13.52	4.02
Grain protein content	10.58-12.09	11.33	8.85	5.76	6.72
Grain wet gluten content	28.62-32.50	30.59	8.18	5.13	6.38

is less influenced by the environment and more by the genotype. Breeders can select individual plants and use simple selection methods based on the phenotypic manifestations of the traits. The heritability values was presented in Table 3. The heritability values were classified (Johnson et al., 1955) as low (<30%), moderate (30-60%) and high (> 60%). Broad sense heritability ranges from 16.10% to 96.08%. Most of the studied traits was characterized with high heritability. The highest heritability was the trait plant height. Other traits with high heritability was the thousand kernel weight, main spike length, grains weight per main spike, grains number per main spike and the spikelets number per main spike. Moderate heritability was the two traits related to the grain quality. Productivity tillers had a very low value for heritability. Kahrizi et al. (2010); Gulnaz et al. (2011); Ullah et al. (2011); Ijaz et al. (2013); Memon et al. (2018) reported that in their studies they obtained high heritability for the plant height. High heritability related to thousand kernel weight was reported in some previously conducted studies (Tazeen et al., 2009; Tsegaye et al., 2012). The results obtained by us coincide with those of Patil & Koujalagi (2018) that high heritability was characterized for the traits plant height, spikelets number per main spike, grains number per main spike, main spike length and thousand kernel weight. According to Ullah et al. (2018) traits plant height and thousand kernel weight had a high heritability. Shah et al. (2018) reveals that in the traits productivity tillering, plant height and grains number per main spike, heritability was with high value. Knowledge of heritability is essential and helps breeders determine the degree of improvement by selection (Robinson et al., 1949). High heritability does not usually guarantee great success. In order for the selection to achieve great success, it is necessary to take into account genetic advance (Bhargava et al., 2003; Vashistha et al., 2013). This determines that genetic advance is another important parameter for a selection that helps breeders (Shukla et al., 2004).

Genetic advance is a useful indicator of the progress that can be expected as a result of the selection made in the respective population. The estimates of genetic advance as percent of mean values were classified (Johnson et al., 1955) as low (<10%), moderate (10-20%) and high (> 20%). In our study, genetic advance as percentage of mean (GA%) ranged from 4.08% to 26.94%. With high genetic advance was characterized the traits like main spike length, thousand kernel weight, plant height and grains weight per main spike. With moderate GA% is the trait grains number per main spike. The traits productivity tillering, spikelets number per main spike, grain protein content and grain wet gluten content was with low GA%. According to Tsegaye et al. (2012) maximum expected genetic advance as percentage of

mean values was observed for thousand kernel weight and main spike length and minimum was for grain protein content. High genetic advance was reported for the traits plant height, productivity tillering, grains number per main spike and thousand kernel weight, while for the traits spikelets number per main spike and main spike length was moderate (Patil & Koujalagi, 2018). Bhardwaj (2018) reveals that the main spike length is characterized with high GA%, and the grains number per main spike with moderate, as in our case. Jamil et al. (2017) found that the thousand kernel weight is characterized with high GA%. The traits plant height, grains number per main spike, grains weight per main spike and thousand kernel weight was characterized with high genetic advance (Rathwa et al., 2018).

The coupled of heritability with genetic advance indicates the predominance of additive or non-additive genetic effects in the control of traits. These traits can be improved with a simple selection. High heritabiliity and low genetic advance suggest the action of non-additive genetic effects. In this situation, the environment had an influence, not the genotype, and a selection would not be successful. In contrast, the combination of high heritability with high genetic advance indicates that the trait is controlled by additive genetic effects and an effective selection can be conducted Singh & Narayanan (1993). The traits plant height, main spike length, grains weight per main spike and thousand kernel weight were determined to coupled high heritability and high genetic advance. Therefore, they was controlled by additive gene effects and it is possible to carry out an effective selection of genotype by phenotype. The grains number per main spike coupled high heritability with moderate genetic advance. The traits productivity tillering, spikelets number per main spike, grain protein content and grain wet gluten content coupled moderate or low heritability with low genetic advance. Therefore, non-additive genetic effects play a key role in their manifestation and the selection of these traits will be difficult and ineffective. Haq et al. (2008) find that for the trait grains number per main spike, high heritability was coupled with high genetic advance. Ijaz et al. (2013) reported an established high heritability coupled with high genetic advance for the traits plant height and thousand kernel weight, as in our case. Patil & Koujalagi (2018) found that the traits plant height, grains number per main spike and thousand kernel weight coupled high heritability with high genetic advance, as in our case. Kaddem et al. (2014) reported that for the traits main spike length and grains weight per main spike, high heritability coupled with high genetic advance prevailed. Almajidy et al. (2017) conclude that traits plant height, grains number per main spike and grains weight per main spike showed high heritability coupled with

high genetic advance. Therefore, these traits should be given top priority during selection in durum wheat breeding. High heritability of grains number per main spike and thousand kernel weight coupled with high genetic advance reveal that additive gene effects was important in determining these traits and could be improved through selections. High heritability values coupled with low genetic advance indicate the influence of dominant and epistatic effects (Basciftci et al., 2013). In a study establish heritability and genetic advance of 50 durum wheat genotypes sown on two different dates, Rathwa et al. (2018) found that the traits plant height, grains number per main spike, grains weight per main spike, and thousand kernel weight coupled high heritability with high genetic advance. In all cases, on the three sowing dates, the main spike length and the grains number per main spike coupled high heritability with high genetic advance (Ranoliya et al., 2017). Dragov (2017) finds that non-additive genetic effects play a greater role in inheritance in the grains number per main spike. It was conclude that it is possible to had an effective selection, but it must start in the later segregating generations. Dragov (2020a) reports that non-additive genetic effects play a major role in the inheritance of grain wet gluten content and effective selection for this trait will be difficult and should begin in later segregating generations. Dragov (2020) determines that for the trait grain protein content, a selection of phenotype by genotype is possible, but it must begin in the later segregating generations.

The results obtained in this study support the results of our study for F_1 generation for the same genotypes and traits. An exception was the trait of productivity tillering, which in the F_1 generation was characterized with high heritability and high genetic advance and was determined to be controlled by additive genetic effects. This is largely due to environmental conditions. For the traits plant height, main spike length, grains weight per main spike and thousand kernel weight, the results obtained was identical and they complement the study of the same genotypes in F_1. We can conclude that they

are controlled by additive genetic effects and it is possible to conduct an effective selection of genotype by phenotype. This is very indicative of increasing the yield of durum wheat. Some authors define the traits like plant height, main spike length, grains weight per main spike and the thousand kernel weight for basic elements of productivity and they can increase grain yield. Therefore, it can be expected that a selection on these traits would increase productivity. Aydin et al. (2010) suggest that plant height was primary selection criteria for improving grain yield in wheat. Dashora et al. (2020) determined that a selection based on the grains number per main spike and main spike length can significantly increase the grain yield of durum wheat. According to Basciftci et al. (2013) thousand kernel weight and grains number per main spike can successfully improve the yield of durum wheat. From the study by Shah et al. (2018) it can be seen that the productivity tillering and thousand kernel weight correlated positively with the yield and their increase will improve the productivity. Ullah et al. (2018) reveal that the trait thousand kernel weight is crucial for obtaining high productivity varieties. Determining genetic variability, heritability and genetic advance in F_2 has been conducted by a number of other authors (Ijaz et al., 2013; Hussain et al., 2013; Ijaz et al., 2015; Yadawad et al., 2015; Saleem et al., 2016; Memon et al., 2018. ; Patil & Koujalagi 2018; Somro et al., 2019; Khan et al., 2020). On other hand, Jaiswal et al. (2020) examines heritability and genetic advance in F_1 and F_2 generations obtained from a diallel cross.

Due to the nature of F_2 generation, the researchers investigated hybrid combinations separately for heritability and genetic advance. With the view of breeding, it is generally important which traits can be manipulated by a selection to obtain better genotypes on them. On the other hand, it is possible to obtain specific information in which cross a selection could be applied and, accordingly, the pure lines obtained from it to be improved. Viewed in both directions, any such information will be extremely useful for improving

Table 3. Component of variance (σ²), broad sense heritability (h²$_{BS}$ %) and genetic advance (GA) in F$_2$ generation

Traits	Variance σ²			h²$_{BS}$ %	GA	GA as % of mean
	σ²$_{ph}$	σ²$_{g}$	σ²$_{e}$			
Plant height	149.20	143.35	5.85	96.08	24.18	25.63
Productivity tillering	0.98	0.16	0.82	16.10	0.33	4.08
Main spike lenght	1.46	1.31	0.15	89.70	2.23	26.94
Spikelets number per main spike	1.56	1.01	0.55	64.95	1.67	7.47
Grains number per main spike	38.94	25.78	13.16	66.20	8.51	16.10
Grains weight per main spike	0.16	0.12	0.04	76.39	0.63	24.53
Thousand kernel weight	47.22	43.38	3.84	91.86	13.00	26.70
Grain protein content	1.01	0.43	0.58	42.30	0.87	7.71
Grain wet gluten content	6.27	2.46	3.80	39.31	2.03	6.63

the breeding program of durum wheat. Table 4 presents the heritability and genetic advance for each cross separately in F_2 for each trait studied. Examining the results of the crosses on the studied traits, can be seen that. Plant height had seven crosses coupled high heritability with high genetic advance. Productivity tillering had no crosses coupled high heritability and high genetic advance. Eight of them coupled low heritability and low genetic advance. For main spike length, four crosses coupled high heritability and high genetic advance. For spikelets number per main spike, no crosses coupled high heritability and high genetic advance had been reported. Grains number per main spike had five crosses coupled high heritability and high genetic advance. Thousand kernel weight had eight crosses were coupled high heritability and high genetic advance. In both traits related to grain quality (grain protein content and grain wet gluten content), there were no crosses coupled high heritability and high genetic advance. Regarding the trait grain protein content content, six crosses coupled low heritability and low genetic advance, and five for grain wet gluten content (Table 4). This was in line with the results obtained above, where heritability and genetic advance by traits were discussed (Table 3). The results in Table 4 reveal that the Victoria X Deni (VxD) hybrid combination coupled high heritability with high genetic advance on four traits: plant height, main spike length, grains number per main spike and grains weight per main

spike. The cross Victoria X Superdur (VxS) coupled high heritability with high genetic advance on four traits: plant height, main spike length, grains weight per main spike and thousand kernel weight. The cross Victoria X Progres (VxP) coupled high heritability with high genetic advance on two traits: main spike length and thousand kernel weight. The cross Victoria X Predel (VxPr) coupled high heritability with high genetic advance on three traits: plant height, main spike length and thousand kernel weight. The cross Deni X Superdur (DxS) coupled high heritability with high genetic advance on three traits: plant height, grains number per main spike and grains weight per main spike. The cross Deni X Progres (DxP) coupled high heritability with high genetic advance on three traits: plant height, grains weight per main spike and thousand kernel weight. The cross Deni X Predel (DxPr) coupled high heritability with high genetic advance on three traits: grains number per main spike, grains weight per main spike and thousand kernel weight. The cross Superdur X Progres (SxP) coupled high heritability with high genetic advance on four traits: plant height, grains number per main spike, grains weight per main spike and thousand kernel weight. This cross also coupled high heritability with moderate genetic advance for the trait grain protein content. The cross Superdur X Predel (SxPr) coupled high heritability with high genetic advance on two traits: grains weight per main spike and thousand kernel weight. The cross Pro-

Table 4. Heritability and genetic advance of 10 hybrid combinations for 9 quantitative traits

Traits		VxD	VxS	VxP	VxPr	DxS	DxP	DxPr	SxP	SxPr	PxPr
PH	h²%	99.2	98.8	33.4	98.9	97.6	95.1	56.2	97.5	92.7	95.7
	GA%	28.2	47.7	2.1	31.3	26.9	21.8	4.9	41.8	18.5	26.2
PT	h²%	52.5	33.7	0.13	60.6	3.3	26.3	13.4	12.3	0.9	3.3
	GA%	14.0	7.3	0.02	14.6	1.0	5.9	3.6	2	0.2	0.5
MSL	h²%	93.7	90.7	91.4	90.9	54.4	6.0	64.0	26.3	3.2	61.9
	GA%	49.5	40.9	45.9	37.2	7.3	0.6	10.0	2.7	0.3	8.1
SNMS	h²%	91.6	52.2	38.5	45.5	65.9	74.2	72.3	5.5	5.9	47.7
	GA%	13.8	6.3	3.1	2.4	8.1	11.3	8.1	0.5	0.5	4.2
GNMS	h²%	82.5	1.5	55.3	62.4	84.8	0.4	88.8	69.6	61.7	85.5
	GA%	21.2	0.2	15.6	7.7	29.8	0.1	31.3	20.5	10.2	30.1
GWMS	h²%	93.0	75.5	19.7	61.8	85.5	78.3	89.9	87.2	81.5	78.5
	GA%	31.0	23.8	4.2	7.7	31.1	29.4	33.7	47.6	33.6	24.5
TKW	h²%	52.9	86.9	96.5	89.2	74.9	93.4	90.2	96.3	85.5	97.9
	GA%	5.2	22.4	20.8	21.8	15.4	28.3	23.4	49.3	24.1	42.9
GPC	h²%	11.8	24.3	37.2	36.3	54.3	56.3	4.9	76.6	41.5	10.0
	GA%	1.8	3.5	6.4	6.7	11.8	11.0	0.7	18.7	6.4	1.7
GWGC	h²%	41.9	0.6	60.2	47.2	38.2	57.5	2.4	48.3	11.6	2.7
	GA%	7.4	0.1	12.1	8.2	7.7	12.4	0.3	8.7	1.4	0.4

PH-Plant height; PT-Productivity tillering; MSL-Main spike length; SNMS-Spikelets number per main spike; GNMS-Grains number per main spike; GWMS-Grains weight per main spike; TKW-Thousand grain weight; GPC-Grain protein content; GWGC-Grain wet gluten content; VxD-Victoria x Deni;VxS-Victoria x Superdur;VxP-Victoria x Progres;VxPr-Victoria x Predel; DxS-Deni x Superdur; DxP-Deni x Progres; 25-Deni x Predel; SxP-Superdur x Progres; SxPr-Superdur x Predel; PxPr-Progres x Predel; ; h²%-Broad Sense Heritability; GA%-Genetic Advance as percentage of mean.

gres X Predel (PxPr) coupled high heritability with high genetic advance on four traits: plant height, grains number per main spike, grains weight per main spike and thousand kernel weight. The cross Superdur X Progres (SxP) is extremely valuable, as there was a possibility of making a selection aimed at improving four traits related to productivity and one trait related to grain quality. The Progres X Predel (PxPr), Deni X Predel (DxPr), Victoria X Superdur (VxS) and Victoria X Deni (VxD) crosses was also valuable as it was possible to make a selection to improve simultaneously four basic elements of productivity. Possible simultaneous improvement for three traits was observed in the crosses Deni X Predel (DxPr), Deni X Progres (DxP), Deni X Superdur (DxS) and Victoria X Predel (VxPr). Coupled high heritability with high genetic advance is a proof that additive genetic effects play a greater role in the inheritance of these crosses for the respective traits. Invetsigating the individual hybrid combinations was of great benefit for the effective implementation and guidance of the selection to improve the newly created pure lines.

Conclusion

The analysis of variance revealed highly significant differences among the genotypes for all traits measured. Phenotypic coefficients of variation were generally higher than genotypic coefficients of variation for all traits studied, indicating the influence of the environment. Plant height, main spike length, grains weight per main spike and thousand kernel weight expressed high heritability coupled with high genetic advance indicating that most likely the heritability is due to additive gene effects. The trait grains number per main spike coupled high heritability and moderate genetic advance and was also controlled by additive genetic effects. An effective selection of genotype by phenotype can be conducted to them. Regarding the traits plant height, main spike length and grains number per main spike GxE was nosignificant. Generally in this research, genetic parameters for the traits were reasonable as expected, because this experiment was conducted for three consecutive years and also evaluation of genotypes was based on genetics variance. High heritability coupled with high or moderate GA% and low GxE interactions indicate that these yield components of durum wheat can be improved by pure line selection. In certain hybrid combination such as: Superdur X Progres (SxP), Progres X Predel (PxPr), Deni X Predel (DxPr), Victoria X Superdur (VxS) and Victoria X Deni (VxD) it is possible with a selection in them to improve pure lines on several traits at the same time, as they coupled high heritability and high genetic advance. This information is very useful for breed-

ers and their programs and would be valuable for improving the genetic diversity of durum wheat and creating new, more productive lines/varieties.

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