Genetic variability, heritability and genetic advance for important quantitative traits of durum wheat: Part I

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Abstract

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The experiments were conducted under field conditions in the breeding-experimental field of Field Crops Institute - Chirpan in four consecutive years. It was used randomized block design in three replications. The accepted technology for growing durum wheat has been applied. Nine quantitative traits were studied, seven of them being elements of productivity and the other two being related to grain quality. The aim of this study was to establish genetic variability, heritability and genetic advance in five modern durum wheat varieties crossed in a diallel design and their F_1 generations. Significant genetic variability was found among the 15 tested genotypes for all studied traits. The genotype-environment interaction was statistically significant for all traits with predominantly larger PCVs than GCVs.

The traits plant height, productivity tillering, main spike length, grains number per main spike, grains weight per main spike, thousand grain weight were characterized by high heritability (h^2_{BS}%) over 60% and high genetic advance (GA%) over 20%. For the traits characterizing the grain quality of durum wheat was established, moderate heritability and low genetic advance, which makes the effective selection difficult. Additive gene effects control plant height, productivity tillering, main spike length, grains number per main spike, grain weight per main spike and thousand grain weight. An effective selection of genotype by phenotype can be applied to them. This information will be useful in the implementation of breeding programs to improve durum wheat.

Keywords: Genetic variability; Heritability; Genetic Advance; Quantitative traits; Durum Wheat

Introduction

Durum wheat is a food crop that has received considerable attention from researchers around the world. It provokes scientific interest due to the different ways of consumption and its nutritional value. New varieties are being developed and the cultivation technology is being improved. Many researchers are working on morpho-physiological potential and yield elements. However, little has been written about the changes in the agrometeorological conditions in Bulgaria. It is necessary to work in this direction, as well as their impact on durum wheat should be studied. Nevertheless, some of the important findings of the research are related and contribute to the improvement of productivity, the establishment of heritability, the determination of the existing genetic diversity and the association of yield with its elements of yield.

An efficient and effective breeding program requires the study of variability and the existing genetic capabilities of genotypes, so that it can be used to improve yield. Success also depends on the amount of genetic variation present in the crop, but also on its degree, which is inherited from the parents to the generations (Bello et al., 2012). Durum wheat has a large genetic variability, which provides a great pre-

requisite for improving productivity and its elements and grain quality with breeding methods. The assessment of genetic variability is a prerequisite for developing an effective breeding program (Parkash, 2012). The use of genetic distant parents gives a better chance to improve the economic characteristics of the generations. Critical assessment of the nature and degree of variability is a basic prerequisite for formulating effective breeding methods (Krishna et al., 2007). The choice of the most appropriate breeding method for the rational improvement of productivity and its elements in each crop largely depends on genetic variability, the relationship between quantitative and qualitative traits and the determination of the heritability.

A wide range of variability is available in durum wheat genotypes and they allow to improve productivity through targeted breeding. The assessment of genetic variability, which is in the germplasm of wheat is a prerequisite for creating a successful breeding program (Parkash, 2012). The importance of genetic variability is a necessary requirement as it provides not only a basis for breeding but also valuable information on the choice of parents to be used in the hybridization scheme. The improvement in each crop is based on the degree of genetic variation and the degree of improvement depends on the size of the genetic variability (Shirshat et al., 2007). In order to initiate any breeding work, it is necessary to assess the genetic variability present in local genotypes for productivity and its elements. Genotypic and phenotypic coefficients of variation are useful for detecting the amount of variability present in germplasm (Datta & Das, 2013).

Determining heritability is useful for studying the genetic changes of a population subjected to breeding (Falconer, 1981). Broad sense heritability is the ratio of genotypic variance to total variance. Thus, heritability denotes the proportion of phenotypic variance that is due to the genotype that is heritable (Hanson et al., 1956). Assessments of heritability are influenced by various factors: the type of genetic material, the size of the sample, the method of sampling, the conduct of the experiment, the method of calculation, and the relationship between all of these (Fehr, 1987). The selection by a given trait should be easy if the heritability is high. This is because there would be a close match between genotype and phenotype due to the relatively smaller contribution of the environment to the phenotype. High heritability indicates the existence of additive genes in the expression of the trait that can be easily used (Bharadwaj et al., 2007). Assessment of broad sense heritability shows genetic abnormalities with less environmental impact and a potential high efficiency of selecting a particular hybrid with the desired trait (Allard, 1960). However, for a trait with low heredity, selection may be significantly difficult or practically impossible due to

the masking effect of the environment on genotypic effects (Singh, 1991).

It is extremely important to understand the gene action and the pattern of inheritance of quantitative traits in order to select an appropriate methodology to improve the breeding program (Vineela et al., 2013). The effective breeding program depends to a large extent on the variation available in the gene pool of productivity enhancing traits. The selection is effective when the degree of variability in the population is large enough. The identification and use of a genotype with a higher genetic potential is a crucial requirement for the production of a more productive durum wheat varieties. Efforts are being made to increase the yield, improve its elements and increase the grain quality. To achieve these goals, a comprehensive study of the genetic mechanisms for controlling the main traits under the influence of different environmental conditions has to be carried out.

Heritability suggests that individuals are more closely related and tend to resemble each other rather than distant ones (Falconer & Mackay, 1996; Rafiq et al., 2010). Heritability assessment helps breeders find the resources needed to effectively refine desired traits and to achieve maximum results within short time and fewer resources (Smalley et al., 2004). There are different ways to calculate heritability. It can be defined in the broad or narrow sense of a plant, an individual plot, or the average of homozygous generation (Nyquist & Baker, 1991). Smalley et al. (2004) reported that they calculated parent-generation heritability in both plants and animals. High genetic advance combined with high inheritance provides the most suitable conditions for a selection. This also indicates the presence of additive genetic effects controlling the trait. Therefore, it implies a reliable improvement of the trait through an appropriate selection. Simultaneous assessment of heritability and genetic advance is more reliable and meaningful than their individual consideration (Nwangburuka & Denton, 2012). Assessment of genetic advance is used in modern breeding programs and in other crops (Stamatov et al., 2020).

The aim of this study is to establish genetic variability, heritability and genetic advance in five modern durum wheat varieties and their F_1 generations. The study will allow breeders to predict the possible advance and improvement of yield, its elements and grain quality. Also to make recommendations on the various traits of successful implementation of a more effective selection in durum wheat.

Materials and Methods

The experiments were conducted under field conditions in the experimental field of the Field Crops Institute – Chir-

pan, Bulgaria. They were sown after the predecessor of spring peas and the accepted technology for growing durum wheat was applied. The meteorological conditions during first three years of research were characterized by higher than the multi-year norm temperatures. The first two harvest years 2014 and 2015 were favorable in terms of soil moisture and precipitation above the perennial average. The third harvest year 2016 was characterized as the hottest and at the same time with 20% less precipitation than the norm. The fourth 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 varieties of durum wheat as parent varieties: four Bulgarian (Victoria, Deni, Progress, Predel) and the Austrian Superdur. The old and the new standards from executive agency for variety testing, approbation and seed control are included. Diallel crosses were performed without reciprocal combinations. The following F_1 hybrid combinations were obtained: Victoria X Deni, Victoria X Superdur, Victoria X Progres, Victoria X Predel, Deni X Superdur, Deni X Progres, Deni X Predel, Superdur X Progres, Superdur X Predel and Progres X Predel. The experiments was carried out by a randomized block design in three replications in the period 2014 - 2017. Each parent and each F_1 generation has been sown handly in two rows. The length of the row is 2 meters, the row spacing is 20 cm. Inside the row, the distance between the individual plants is 5 cm. In the phenophase of full maturity, plants from each replication are harvested for biometric studies. From each parent and each F_1 generation, 20 plants were randomly selected.

The following quantitative traits were observed: plant height (cm); productivity tillering (number); main spike lenght (cm); spikelets number per main spike (number); grains number per main spike (number); grains weight per main spike (g); thousand grain weight (g); grain protein content (%) and grain wet gluten content (%).

Statistical analyses for studied traits was estimated by variance components method based on the combined analyses over four growing seasons. 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 $(\sigma^2_{ph}) = \sigma^2_g + \sigma^2_e$

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

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

The expected Genetic Advance for each trait was calculated as:

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

where, K = 2.06 at 5% selection intensity for trait; σ^2_{ph} = Phenotypic variance for trait or $(\sigma^2_{ph})^{0.5}$ 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

Analysis of variance revealed significant differences in genotypes across all traits (Table 1). The results show an acceptable amount of variability between genotypes. This allows breeders to improve these traits with hybridization and selection. Significant differences in plant height genotypes were reported by Abinasa et al. (2011); Tesfaye et al. (2014), for main spike length and spikelets number per main spike Ali et al. (2008); Abinasa et al. (2011), for thousand grain weight Ali et al. (2008); Akcura (2009). The influence of the year is significant for all characteristics. The genotype X environment interaction (GxE) is also highly significant for all traits except the grain protein content (0.6n.s.) and spikelets number per main spike (1.7*). This shows that genotypes have reacted differently to changes in different agrometeorological conditions.

The mean, maximum and minimum values of the studied traits (Table 2) also reveal a large variability in the genotypes. The greatest scope is observed at the plants height. Its average value is 93.2 and this classifies it as medium-high wheat. By falling into this classification, it can be assumed that they will be resistant to lodging and would tolerate higher rates of nitrogen fertilization. Productivity tillering values indicate that genotypes formed a large number of tillers. This is most likely due to the larger nutrient area of the individual plants during hand sowing. For the characteristics main spike length, spikelets number per main spike, grains number per main spike, grains weight per main spike and thousand grain weight, the values are within normal limits

Table 1. Mean squares value from ANOVA for 9 quantitative traits of 15 durum wheat genotypes in F_1 generation

Traits	Genotype	Environment, year	GxE	Error
Plant height	577.3***	145.1***	23.4***	9.2
Productivity tillering	9.3***	16.5***	2.0***	0.8
Main spike length	6.1***	10.9***	0.2***	0.1
Spikelets number per main spike	7.9***	17.2***	0.6 n.s.	0.7
Grains number per main spike	264.5***	426.5***	38.9***	15.5
Grains weight per main spike	0.8***	11.6***	0.2***	0.1
Thousand grain weight	127.4***	1982.5***	25.3***	9.0
Grain protein content	4.6***	77.8***	1.7*	1.1
Grain wet gluten content	14.8***	110.9***	9.8***	3.5

*** Significant at $p<0.001$; ** Significant at $p<0.01$; * Significant at $p<0.05$; ns – not significant

for durum wheat. With the smallest range is the trait grains weight per main spike. According to the classification, the average values of the grain protein content and grain wet gluten content have sufficiently high values. Their scope determines that there are no genotypes with values below the minimum requirements for obtaining high-quality pasta. The determined values indicate that there is sufficient variability between genotypes and they are a source of variable genetic material. Other authors have also reported a wide range of studied characteristics (Paul et al., 2006).

Genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) are presented in Table 2. GCV ranges from 6.09 for the grain wet gluten content to 20.18 for productivity tillering. PCV ranges from 7.81 for the main spike length to 22.79 for the productivity tillering. 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%). According to this classification, low PCV is characterized by the characteristics spikelets number per main spike, grain protein content and grain wet gluten content. Moderate PCVs are typical of plant height, main spike lengh, grains number per main spike and thousand grain weight. High PCVs are characterized by productivity tillering and grains weight per main spike. With regard to GCV, only productivity tillering have high GCV. All other traits are characterized by moderate values, except only the spikelets number per main spike, the grain protein content and the grain wet gluten content that have low values. Abinasa et al. (2011) reported high genetic variability for the yield elements in early generations in wheat. Bhushan et al. (2013) reported that PCV and GCV values were moderate for the spikelets number per main spike. Malbhage et al. (2020) reported obtained moderate PCVs for the characteristics of grains number per main spike and thousand grain weight, as in our case. High GCV and PCV suggest sufficient opportunities for selection of promising elite plants from a certain population for the trait. In general, a moder-

ate and high coefficient of variability indicates that there is a scope of selection and improvement of these traits. Low values indicate the need for creation of variability either by hybridization or mutation followed by selection (Tiwari et al., 2012). The calculated PCV values are greater than the GCV values for all examined traits. This is due to the genotype-environment interaction (Kavitha & Reddy, 2002; Wolde et al., 2016). According to Kandel et al. (2018) when the GCV is greater than the PCV, the environment has no significant effect on the expression of the traits. For traits where the differences are smaller, it can be argued that the environment has not have a large impact. For the traits plant height, the main spike length and spikelets number per main spike, selection based on phenotypic expression can be very effective and may lead to genetic improvement of these traits. Narrower difference between the values of GCV and PCV indicated that the environmental effect was small for the expression of these traits and they are controlled by additive gene effects (Abinasa et al., 2011; Hokrani et al., 2013). In contrast, the large differences in PCV and GCV show the large influence of the environment on the phenotypic expression of the other traits. Thus, the selection was not effective and should not be expected to genetically improve. This suggests that inheritance control is exercised by nonadditive genetic effects and dominance predominates.

The phenotypic, genotypic and environment variance are presented in Table 3. The highest phenotypic variance was found for plant height followed by the grains number per main spike, and the lowest for grains weight per main spike. The genotypic variance is highest for plant height followed by the grains number per main spike, lowest in grains weight per main spike. The highest variance of the environment has the grains number per main spike followed by the plants height and the thousand grain weight. The lowest variance of the environment is characterized by the grains weight per main spike. These variances were used to calculate heritability and expected genetic advance.

Table 2. Variation coefficient, means values and its ranges for 9 quantitative traits of 15 durum wheat genotypes in F$_1$ generation

Traits	Min-Max	Mean	PCV, %	GCV, %	ECV, %
Plant height	79.6-104.1	93.2	15.12	14.77	3.25
Productivity tillering	6.9-10.2	8.3	22.79	20.18	10.59
Main spike length	6.4-9.5	8.6	16.80	16.27	4.18
Spikelet's number per main spike	20.7-23.9	22.4	7.81	6.92	3.63
Grains number per main spike	43.4-58.7	53.1	18.68	17.15	7.41
Grains weight per main spike	2.0-2.9	2.6	22.02	18.79	11.47
Thousand grain weight	39.3-51.4	47.1	14.77	13.33	6.36
Grain protein content	14.5-16.9	16.0	9.32	6.71	6.47
Grain wet gluten content	29.2-33.9	31.8	8.47	6.09	5.88

Heritability is an important parameter in selection an effective method for improving genotypes. The selection of a single elite plant in early generations can be very effective for a trait that is highly inheritable compared to a trait that is less inheritable. Broad sense heritability for the nine quantitative traits is given in Table 3. Heritability ranges from 51.71% for grain wet gluten content to 95.38% for plant height. The heritability values were classified (Johnson et al., 1955) as low (<30%), moderate (30-60%) and high (> 60%). With medium heritability are the two traits associated with grain quality. Lowest heritability on the basis of grain wet gluten content was reported by the authors Bilgin et al. (2010). In our research all traits related to the productivity have a high heritability. Such results for traits related to productivity have been reported by other authors (Dwidevi et al., 2002; Ali et al., 2008; Kumar et al., 2013). They also suggest that selection by the traits productivity tillering, plant height, thousand grain weight can improve yield. Khan et al. (2010) reported high heritability of productivity tillering, as in our case. For the traits grains number per main spike and thousand grain weight Rashidi (2011) reported high broad sense heritability. High heritability was found for the traits plant height, productivity tillering and grains number per main spike (Ajmal et al., 2009). The calculated high heritability suggests that the expression of traits is weakly influenced by environmental conditions. Therefore, direct selection of phenotypes in the early segregated generations on these traits would be successful and could lead to good results. The moderate values of heritability found for the two traits related to grain quality suggest that the environment has a great influence on the expression. With them, the direct selection would be ineffective due to the influence of the environment. Heritability alone does not provide enough genetic information to improve genotypes through selection. The combination of heritability and genetic advance and GCV provides much greater reliability and it is much more useful in breeding improvement work (Johnson et al., 1955).

The expected genetic advance (GA) is low for all traits except plant height and grains number per main spike and thousand grain weight (Table 3). High heritability and low expected genetic advance suggest the influence of non-additive genetic effects (Salman et al., 2014). Salman et al. (2014) reported that for traits, productivity tillering, main spike length, and spikelets number per main spike, high heritability was found combined with low expected genetic advance (GA), as in our case. Baranwal et al. (2012) reported that in their studies they received high genetic advance for the trait grains number per main spike. Genetic advance presented as a percentage of mean (GA%) is much more defining (Table 3). GA% ranged from 9.02 for grain wet gluten content to 36.81 for productivity tillering. The estimates of genetic advance and genetic advance as percent of mean were classified (Johnson et al., 1955) as low (<10%), moderate (10-20%) and high (> 20%). Low GA% characterizes both traits related to grain quality. Low values for GA% at the grain protein and wet gluten content were also reported by the authors (Bilgin et al. 2010). The moderate GA% characterizes the spikelets number per main spike. The other studied traits have a high GA%. Morteza et al. (2018) found that the characteristics of grains weight per main spike and the grains number per main spike have a high GA%. Malbhage et al. (2020) reported a high GA% in durum wheat for the productivity tillering, as in our case.

In the present study, high to medium GA% combined with high heritability were found for the traits plant height, productive tillering, main spike length, grains number per the main spike, grains weight per main spike and thousand grain weight. These characteristics have moderate GCV, only productivity tillering have high GCV. Earlier scientists like Afridi et al. (2014) and Arya et al. (2018) also reported high heritability and high GA% estimates for grain number per main spike. Malbhage et al. (2020) reported high heritability and medium to high genetic advance in durum wheat for the traits: productivity tillering, plant height, main spike

length and thousand grain weight. According to Morteza et al. (2018) traits productivity tillering, grains weight per main spike, grains number per main spike and thousand grain weight coupled high genetic advance and high heritability, they are controlled by additive genetic effects and effective selection is possible. Al-Tabbal & Fraihat (2012) report that the traits grains number per main spike, grains weight per main spike, spikelets number per main spike and plant height coupled high heritability and high GA%. For these traits, the results found show that genetic control in their expression is simply inherited and determined by several major genes with additive gene effects. The studies of Bilgin et al. (2010) report that the trait grain wet gluten content has low heritability and low GA%, while for the grain protein content the heritability is medium combined with low GA% (as in our case for grain protein content). High heritability values followed by high genetic advance showed the presence of additive gene action (Johnson et al. 1955; Kashif et al. 2003; Salman et al. 2014). Therefore, conducting an individual selection for traits with combined high heritability and high GA% would be effective for their improvement. According to Johnson et al. (1955) the combination of high values for heritability and genetic advance gives the selection great reliability. Therefore, selection based on traits with high and medium GA% leads to improved genotypes on these traits. According to Panse (1957) if a character is modified by non-additive gene effect, it may give high heritability but low genetic advance, whereas, if it is modified by additive gene action, high heritability along with high genetic advance provided good scope for further improvement. Ilyas et al. (2019) report that high to medium heritability combined with low GA% suggests dominance (non-additive) gene action and these traits can be used for heterosis breeding. Repeating the experiments for several consecutive years sheds enough light on the reasons controlling the inheritance of the studied traits. Tracking the next generation F_2 will provide a much clearer and more complete assessment of the expression of traits.

Conclusion

There is a presence of significant genetic variability among the 15 tested genotypes on all studied traits. The genotype-environment interaction with predominantly larger PCVs than GCVs at all traits has been statistically significant. The traits plant height, productivity tillering, main spike length, grains number per main spike, grains weight per main spike and thousand grain weight are characterized by high heritability (h^2_{BS}%) over 60% and high genetic advance (GA%) over 20%. For the traits characterizing the grain quality of durum wheat was established, moderate heritability and low genetic advance, which makes the effective selection difficult. Additive gene effects control the characteristics of plant height, productivity tillering, main spike length, grains number per main spike, grains weight per main spike and thousand grain weight. Therefore, an effective selection of genotype by phenotype can be applied to them. This information will be useful in the implementation of breeding programs to improve durum wheat.

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Table 3. Component of variance (σ²), broad-sense heritability (h^2_{BS} %) and genetic advance (GA) in F_1 generation for 15 genotypes of durum wheat

Traits	Variance σ²			h^2_{BS} %	GA	GA as % of mean
	σ^2_{ph}	σ^2_{g}	σ^2_{e}			
Plant height	198.53	189.36	9.17	95.38	27.69	29.71
Productivity tillering	3.61	2.83	0.78	78.40	3.07	36.81
Main spike length	2.11	1.98	0.13	93.81	2.81	32.46
Spikelet's number per main spike	3.07	2.41	0.66	78.43	2.83	12.62
Grains number per main spike	98.50	83.01	15.49	84.27	17.23	32.43
Grains weight per main spike	0.33	0.24	0.09	72.85	0.86	33.05
Thousand grain weight	48.46	39.48	8.98	81.46	11.68	24.78
Grain protein content	2.24	1.16	1.08	51.82	1.60	9.95
Grain wet gluten content	7.26	3.75	3.51	51.71	2.87	9.02

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