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Bozhidar Kyosev
Gergana Desheva

Study on variability, heritability, genetic advance and associations among characters in emmer wheat genotypes (*Triticum dicoccon* Schrank).

Authors' addresses:

Institute of Plant Genetic Resources
"Konstantin Malkov",
Sadovo, Bulgaria.

Correspondence:

Bozhidar Kyosev
Institute of Plant Genetic Resources
"Konstantin Malkov",
2 Druzhiba Str., 4122 Sadovo, Bulgaria.
e-mail: b_kyosev@abv.bg

ABSTRACT

Thirty eight emmer wheat genotypes grown in IPGR-Sadovo, Bulgaria during 2012-2014 were evaluated to estimates of variability, heritability, genetic advance and associations among characters in the randomized block design in three replications. Eight agronomic traits were included in the study. The phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the traits. High PCV and GCV were observed in trait grain weight per spike (PCV=30.36%, GCV=24.93%). High genetic advance combined with high heritability showed characters: spike length, grain weight per spike and thousand grain weight. The highly significant and positive phenotypic correlation was found between grain yield per plant and following components: plant height, grain weight per spike, number of grains per spike and thousand grain weight. The grain weight per spike and plant height had strongest direct effect on grain yield per plant. The number of grains per spike via grain weight per spike and thousand grains weight via grain weight per spike had the highest positive indirect effect on the grain yield per plant.

Key words: GCV, genetic progress, heritability, PCV, path analysis, *Triticum dicoccon*

Introduction

Cultivated emmer wheat *Triticum dicoccon* Schrank is a tetraploid species belonging to the genus *Triticum* with hulled grain. It is one of the earliest domesticated wheat derived from wild emmer (*Triticum dicoccoides* Schweinf.) (Troccoli & Codianni, 2005; Zaharieva et al., 2010). Emmer is an ancient wheat crop which 20 years ago was considered an underutilized or neglected crop and which it seemed was probably going to be completely abandoned because of its low productivity and threshing and other agro technical problems (Perrino & Fares, 2003; Vita et al., 2006). Today the increase in interest in natural and organic products has led to a "rediscovery" of this hulled wheat, which has health characteristics associated with high starch-resistant content (Strehlow et al., 1994; Marconi & Cubadda, 2005). Moreover, it has an aptitude to grow at low temperatures, in soils with limited fertility, and utilizes low input techniques. It is also a source of genes for breeding wheat (e.g. resistance to wheat diseases and drought, root system efficiency)

(Sherma et al., 1981; Blanco et al., 1990; Lage et al., 2006; Konvalina & Moudry, 2007; Konvalina et al., 2012a, 2012b, 2013). The grains contain more crude protein than the grains of modern varieties (Marconi et al., 1999). Whole meal flour is a valuable source of dietary fibre in its insoluble forms, cellulose and hemicellulose, and it contains high quantities of Ph, Zn, Cu, K, Mg and Mn (Marconi & Cubadda, 2005). The attention toward this ancient species has also been renewed by the increasing demand for traditional products, the request for species suitable to be grown in marginal areas and the need to preserve genetic diversity and to develop new genotypes between interspecific crosses (Codianni et al., 2000; Stagnari et al., 2008).

Variability studies are limited in emmer wheat. Variability particularly decides the effectiveness of selection (Subhashchandra et al., 2009). It is fact that the higher the variability among the genotypes betters the chances for further improvement in the crop (Subhashchandra et al., 2009). Genetic information like heritability and genetic advance for different yield contributing traits would be of

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great value enabling the breeder to use best genetic stock for improvement in breeding programme (Yadawad et al., 2015).

Heritability estimates provide an indication of the expected response to selection in a population. Information on the nature and magnitude of heritability in a population is one of the prerequisites for successful breeding programs in selecting genotypes with desirable characters (Amin et al., 1992). There is a direct relationship between heritability and response to selection, which is referred to as genetic progress. The expected response to selection is also called genetic advance (GA). High genetic advance coupled with high heritability estimates offers the most effective condition for selection (Larik et al., 2000; Shukla et al., 2004; Shoukat et al., 2007). Phenotypic and genotypic coefficients of variations, heritability and genetic advance have been used to assess the magnitude of variance in wheat breeding material (Abinasa et al., 2011). Correlation and path coefficient analysis could be used as an important tool to bring information about appropriate cause and effects relationship between yield and some yield components (Khan et al., 2003, 2005). Path coefficient analysis separates the direct effects from the indirect effects through other related characters by partitioning the correlation coefficient (Dixet & Dubey, 1984). Therefore the present study was designed to estimate the degree of genetic variability, heritability, genetic advance and associations among characters in emmer wheat genotypes.

Materials and Methods

The study is carried out in the experimental field of Institute of Plant Genetic Resources “Konstantin Malkov”-Sadovo, Bulgaria during 2012-2014 growing seasons. Thirty nine emmer wheat accessions were examined (Table 1). The accessions were sown in harvest plots each of 1 m² in three replications, in the randomized block design. Each plot consisted of five rows of 1.0 m length with 20 cm and 5 cm spacing between and within rows, respectively. All the agronomical packages and practices were applied to raise healthy crop. At the time of maturity, five competitive plants of each genotype from each replication were randomly selected. Data were registered for number of productive tillers per plant, plant height, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, thousand grain weight and grain yield per plant.

The mean data from all eight characters were used to analysis of variance according to Lidansky (1988). Genotypic and phenotypic variances, genotypic and phenotypic coefficient of variability, broad sense heritability were calculated according to Singh & Chaudhary (1985). Genetic advance in terms of percentage of means was assessed by Brim et al. (1959). Phenotypic correlations were calculated by using phenotypic variances and covariance. Correlation coefficients were calculated as followed by Lidansky (1988) whereas path coefficient analysis was conducted to Dewey & Lu (1959) using phenotypic correlations to assess direct and indirect influences of different yield components (plant height, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike and thousand grain weight) on grain yield per plant.

Results

Analysis of variance

Mean squares of plant height, spike length with awns, spike length without awns, number of spikelets per spike, number of grains per spike, grain weight per spike, thousand grain weight and grain yield per plant showed highly significant differences between genotypes (Table 1).

Phenotypic variance ranged from 0.19 (grain weight per spike) to 153.50 (plant height). Values of genotypic variances ranged between 0.13 (grain weight per spike) and 84.13 (plant height). Environmental variances ranged from 0.06 (grain weight per spike) to 69.37 (plant height) The highest phenotypic, genotypic and environmental variance values of 153.50, 84.13 and 69.37 for plant height and 94.01, 48.29 and 45.71 for number of grains per spike were recorded in the study (Table 2).

The genotypic coefficient of variability (GCV) ranged from 9.61% for plant height to 43.04% for grain yield per plant, whereas, phenotypic coefficient of variability (PCV) ranged from 7.11% plant height to 24.93% for grain weight per spike (Table 2). The recorded of GCV were high (above 20%) for six of investigated characters, moderate for number of spikelets per spike (10.80%) and low for plant height (9.61%). The recorded of PCV was high for grain weight per spike (24.93%) and low for plant height (7.11%) (Table 2).

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Table 1. Minimum, maximum, means, mean squares and standard error of means for eight quantitative characters of thirty eight genotypes (*Triticum dicoccon* Schrank).

Characters	Minimum	Maximum	Means	Mean squares	Standard error of means
Plant height	94.20	162.10	128.99	868.86***	1.15
Spike length with awns	8.12	24.22	16.13	27.62***	0.31
Spike length without awns	5.27	14.95	9.59	11.80***	0.2
Spikelets per spike	18.5	33.4	27.96	20.79***	0.28
Grain weight per spike	0.29	2.81	1.43	0.44***	0.04
Number of grains per spike	18.87	77.2	42.47	190.50***	0.9
Thousand grain weight	16.26	52.86	33.37	136.70***	0.69
Grain yield per plant	1.53	21.27	6.78	11.2*	0.27

*p<0.05, **p<0.01, *** p<0.001

Table 2 . Genetic parameters of various yield components of 38 emmer wheat genotypes

Characters	Genotypic variance	Phenotypic variance	Environmental variance	Phenotypic coefficient of variability, %	Genotypic coefficient of variability, %	Heritability, %	Genetic advance, % of means
Plant height	84.13	153.50	69.37	9.61	7.11	54.81	10.84
Spike length with awns	8.28	11.06	2.77	20.62	17.85	74.93	31.83
Spike length without awns	3.64	4.52	0.88	22.17	19.89	80.48	36.76
Spikelets per spike	5.83	9.12	3.29	10.80	8.64	63.96	14.23
Grain weight per spike	0.13	0.19	0.06	30.36	24.93	67.47	42.19
Number of grains per spike	48.29	94.01	45.71	22.83	16.36	51.37	24.16
Thousand grain weight	40.68	55.34	14.66	22.29	19.11	73.51	33.76
Grain yield per plant	1.25	8.52	7.27	43.04	16.50	14.69	13.03

Heritability and genetic advance expressed as percentage of mean

In the present study heritability estimated ranged from 14.69% to 80.486 % (Table 3). High estimates of heritability (above 60%) in broad sense were recorded for five characters studied (spike length with awns – 74.93%, spike length without awns – 80.48%, spikelets per spike - 63.96%, grain weight per spike - 67.47% and thousand grain weight - 73.51%). The expected genetic advance expressed as a

percentage of the mean varied between 10.84% for plant height and 42.12% for grain weight per spike. Genetic advance as percentage of mean was high for grain weight per spike (42.12%) followed by spike length without awns (36.76%), thousand grain weight (33.76%), spike length with awns (31.83%) and number of grains per spike (24.162%). Genetic advance was moderate for spikelets per spike (14.23%) and plant height (10.84%) (Table 2).

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Correlations between investigated characters

Pearson's correlation coefficients between 8 characters are presented in Table 3. Plant height showed significant positive correlation with all investigated traits. Spike length with awns correlated positively with spike length without awns (0.653), spikelets per spike (0.474), grain weight per spike (0.217) and number of grains per spike (0.341), while spike length without awns was in significantly positive relationship with spikelets per spike (0.629), grain weight per spike (0.435), number of grains per spike (0.563) and grain yield per plant (0.274). Spikelets per spike also correlated positively with grain weight per spike (0.381) and number of grains per spike (0.498). Grain weight per spike showed significantly positive correlation number of grains per spike (0.691), thousand grain weight (0.760) and grain yield per

plant (0.620). The correlation between number of grains per spike and grain yield per plant was positive and significant at the 0.01 level. Thousand kernel weight correlated positively with grain yield per plant (0.393) (Table 3).

Multiple linear regressions based on all accessions

The results of stepwise regression analysis were calculated by considering the grain yield per plant as the dependent variable and plant height, spike length without awns, grain weight per spike, number of grains per spike and thousand grain weight as the independent variables (Table 4). The standard linear regression for grain yield per plant (Y) was:

$$Y = -2.928 + 0.092 * X_1 - 0.326 * X_2 + 6.840 * X_3 - 0.077 * X_4 - 0.166 * X_5$$

Table 3. Phenotypic (r_{ph}) correlation coefficients of investigation yield components in emmer wheat

Variable	Plant height	Spike length with awns	Spike length without awns	Spikelets per spike	Grain weight per spike	Number of grains per spike	Thousand grain weight	Grain yield per plant
Plant height	1							
Spike length with awns	0.414**	1						
Spike length without awns	0.565**	0.653**	1					
Spikelets per spike	0.340**	0.474**	0.629**	1				
Grain weight per spike	0.530**	0.217*	0.435**	0.381**	1			
Number of grains per spike	0.539**	0.341**	0.563**	0.498**	0.691**	1		
Thousand grain weight	0.219*	-0.066	0.014	-0.035	0.760**	0.153	1	
Grain yield per plant	0.562**	0.124	0.274**	0.153	0.620**	0.456**	0.391**	1

** . Correlation is significant at the 0.01 level (2-tailed).

* . Correlation is significant at the 0.05 level (2-tailed).

Path coefficient analysis

The results in the investigation indicated that grain weight per spike had the greatest positive effect (1.197) on yield grain per plant, followed by plant height (0.369) (Table 5). The effect of the others traits were negative direction towards reducing the yield. Especially thousand grain weight had a prominent effect on yield grain per plant in negative direction with (-0.561). Spike length (with and without awns) and spikelets per spike had minimum negative direct effect on the yield (-0.051, -0.119 and -0.199), respectively.

Thousand grain weight and number of grains per spike had positive indirect effect on yield grain per plant via grain weight per spike, (0.909 and 0.826) respectively.

Grain weight per spike affected on the grain yield negatively via thousand grain weight (-0.426). The indirect effect of plant height through grain weight per spike was positive (0.634). Spike length also had indirect positive effect on the grain yield per plant via grain weight per spike (0.520 and 0.456).

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Table 4. Result of stepwise regression analysis for grain yield per plant (Y) in emmer wheat

	Unstandardized Coefficients		Standardized Coefficients	R Square	Adjusted R Square
	B	Std. Error	Beta		
(Constant)	-2.928	3.080			
Plant height (X1)	0.092	0.021	0.389		
Spike length without awns (X2)	-0.326	0.131	-0.236	0.501	0.478
Grain weight per spike (X3)	6.840	1.727	1.012		
Number of grains per spike (X4)	-0.077	0.046	-0.255		
Thousand grain weight (X5)	-0.166	0.073	-0.420		

Table 5. Direct (Bold and Underline) and indirect effect of 7 characters (independent variables) on grain yield per plant (dependent variable) in 35 wheat genotypes. The last column shows genotypic correlations (r_{ph}) of independent variables with grain yield plant

Variable	Direct and indirect effect							Total indirect effect	r_{ph}
	Plant height	Spike length with awns	Spike length without awns	Spikelets per spike	Grain weight per spike	Number of grains per spike	Thousand grain weight		
Plant height	<u>0.369</u>	-0.021	-0.067	-0.068	0.634	-0.162	-0.123	0.193	0.562
Spike length with awns	0.153	<u>-0.051</u>	-0.078	-0.094	0.260	-0.102	0.037	0.175	0.124
Spike length without awns	0.209	-0.034	<u>-0.119</u>	-0.125	0.520	-0.169	-0.008	0.393	0.274
Spikelets per spike	0.126	-0.024	-0.075	<u>-0.199</u>	0.456	-0.149	0.020	0.352	0.153
Grain weight per spike	0.196	-0.011	-0.052	-0.076	<u>1.197</u>	-0.207	-0.426	-0.577	0.620
Number of grains per spike	0.199	-0.018	-0.067	-0.099	0.826	<u>-0.300</u>	-0.086	0.756	0.456
Thousand grain weight	0.081	0.003	-0.002	0.007	0.909	-0.046	<u>-0.561</u>	0.952	0.391

Discussion

In present study, 38 genotypes of emmer wheat were studied to assess their genetic potential. Highly significant differences and wide ranges of variation for all characters indicated the presence of sufficient variability among the genotypes (Alam et al., 2013; Desheva & Cholakov, 2014). The mean squares for genotypes were significant ($p < 0.05$ and $p < 0.001$) for all traits studied. The amount of genotypic and phenotypic variability that exist in a species is the utmost importance in breeding better varieties and in initiating a

breeding program. Relatively higher phenotypic variance values of 153.07 for plant height and 48.29 for number of grains per spike were recorded in the study. Similarly, the genotypic variances for these traits were also high, indicating that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these traits (Degewione et al., 2013). Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population (Abinasa et al., 2011). Phenotypic coefficient of variability and GCV values of approximately more than 20% are

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regarded as high whereas values less than 10% are considered low and values in between as medium (Deshmukh et al., 1986). In the present study high PCV and moderate GCV were observed in traits: spike length with awns (PCV=20.62%, GCV=17.85%), spike length without awns (PCV=22.17%, GCV=17.85%), grain weight per spike (PCV=30.36%, GCV=24.93%), number of grain per spike (PCV=22.83%, GCV=16.36%), thousand grain weight (PCV=22.29%, GCV=19.11%) and grain yield per plant (PCV=43.04%, GCV=16.50%). Moderate PCV and low GCV were found for spikelets per spike (PCV =10.80% and GCV=8.64%) Low PCV and GCV showed plant height (PCV =9.61% and GCV=7.11%). The PCV values were higher than GCV values for all the traits which reflect the influence of environment on the expression of traits. These findings were in agreement with those of Gashaw et al. (2010), Abinasa et al. (2011), Desheva & Cholakov (2014), Kumar et al. (2014), Desheva & Kyosev (2015).

The coefficient of variation indicated only the extent of variability present in the characters and does not indicate the heritable portion. This could be ascertained from heritability estimates which in broad sense include both additive and non-additive gene effects and in narrow sense include the proportion of heritable variation which is due to additive component (Lush, 1949). The knowledge of heritability is helpful in assessing merits and demerits of a particular trait as it enables the plant breeder to decide the course of selection procedures to be followed under a given situation. Estimates of broad sense heritability were high for: spike length with awns (74.93%), spike length without awns (80.48%), spikelets per spike (63.96%), grain weight per spike (67.47%) and thousand grain weight (73.51%). According to Gashaw et al. (2010) characters with high heritability are predominantly controlled by genetic factors. Thus, we could anticipate genetic advance under selection for these characters from different types and intensities of selection. Moderate broad sense heritability estimates (30-60%) were exhibited for the number of grains per spike (51.37%) and plant height (54.81%), while low for grain yield per plant (14.69%). The heritability value alone provides no indication of the amount of genetic progress that would result in selecting the best individual, but heritability estimates along with the genetic advance is considered more useful (Ajmal et al., 2009; Farshadfar & Estehghari, 2014). In our investigation characters like spike length (with and without awns), grain weight per spike and thousand grain weight showed high

heritability coupled with high genetic advance indicating the chance of effective selection of these traits for improvement of grain yield because the heritability is due to additive gene effects.

The association of structural elements of yield with grain yield and the interrelationships among the components assumes special importance as the basis for selecting high yielding genotypes. In this study, the correlation between grain yield per plant and plant height; spike length without awns, grain weight per spike, number of grains per spike and thousand grain weight was positively significant. Multiple linear regression method is used to determine the role of yield components in increasing the yield and selection efficiency by means of few traits as the effective indicator to obtain breeding aims (Siahbidi et al., 2013). Results showed that, plant height; spike length without awns, grain weight per spike, number of grains per spike and thousand grain weight remained in the final model.

Path coefficient analysis helps to determine the contribution of various components of yield to overall grain yields in the genotypes under study. It provides an effective way of finding out direct and indirect sources of correlation (Khaliq et al., 2004; Khan et al., 2005 and Mohsin et al., 2009). The results in the investigation indicated that grain weight per spike had the greatest direct positive effect (1.197) on yield grain per plant, followed by plant height (0.369). These traits showed positive correlations with grain yield. As a result, these characters could be considered as main components for selection in a breeding program for higher grain yield. The effect of the others traits were negative direction towards reducing the yield. The direct effects of thousand grains weight and number of grains per spike on yield grain per plant were also negative and high (-0.561; -300). Thousand grain weight and number of grains per spike had the highest positive indirect effect on yield grain per plant via grain weight per spike, (0.909 and 0.826) respectively.

Correlation and path coefficient analysis can be used as an important tool to bring information about appropriate cause and effects relationship between yield and some yield components (Khan et al., 2003).

Conclusion

The present study showed the existence of wide ranges of variations for all of the traits among emmer wheat genotypes. The PCV values were higher than GCV values for all the

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traits which reflect the influence of environment on the expression of traits. Characters like spike length (with and without of awns), grain weight per spike and thousand grain weight showed high heritability coupled with high genetic advance indicating the chance of effective selection of these traits for improvement of grain yield because the heritability is due to additive gene effects. Grain weight per spike and plant height had the direct positive effect and correlation with yield grain per plant. These characters could be considered as main components for selection in a breeding program for higher grain yield.

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