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EFFECT OF ENVIRONMENTAL AND GENETIC FACTORS ON THE CORRELATION AND STABILITY OF GRAIN YIELD COMPONENTS IN WHEAT

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More effective breeding and development of new wheat genotypes depend on an intricate analysis of the complex relationships among many different traits. The objective of this paper was to determine the interrelationship, direct and indirect effects, and stability of different yield components in wheat. Forty divergent genotypes were analyzed in a three-year study (2005-2007). Highly significant correlations were found between

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grain yield per plant and all the other traits analyzed except spike length, with the only negative correlation being that with plant height. Path analysis revealed highly significant direct effects of grain number per spike, grain mass per spike and 1000 grain weight on grain yield per plant. Analysis of stability parameters showed that the stability of grain yield per plant depended for the most part on the stability of grain number per spike, grain mass per spike and harvest index. Cluster analysis identified genotypes with a high performance for grain yield per plant and good stability parameters, indicating the possibility of developing wheat varieties with a high potential and high stability for a particular trait.

Key words: correlations, path analysis, stability, wheat.

INTRODUCTION

Manifestation of wheat yield fluctuates widely as a result of its interaction with the environment, because grain yield in wheat is a complexly inherited character and is the product of several contributing factors that affect it directly or indirectly. In the context of yield improvement, when selecting desirable genotypes it is very important to know the nature and extent of variation present within a set of breeding material as well as the interrelationship between each yield component and grain yield and the exact contribution of each component to yield via direct and indirect effects. It is known that the improvement of the genetic architecture of yield must be based on a more intensive study of individual yield components (KHAN and DAR, 2010).

Genotypic and phenotypic correlations are important in determining the degree to which various yield contributing characters are associated (AKRAM *et al.*, 2008). Correlation studies among yield contributing traits may help in indirect selection of yield components. Correlation is a pragmatic approach to developing selection criteria for accumulating an optimum combination of yield contributing traits in a simple genotype (MUNIR *et al.*, 2007). Analysis of traits with a potential impact on grain yield requires that correlations among them should be determined. Getting to know the correlations among traits is of great importance for the process of selection that takes place within a breeding program. Of the many methods that can be utilized for this purpose, analysis of correlation coefficients is one of the most widely used ones.

Correlations themselves express only the degree to which traits are interrelated, while path analysis provides a better picture in analytical terms of yield expression as a result of its components. It does not, however, point to the nature of that dependence. It is necessary to perform the path analysis of correlation coefficients, because this method enables good-quality and complete recognition of the relationships among the investigated components (ZEČEVIĆ *et al.*, 2004).

Against this background, therefore, the objective of the present paper was to estimate the genetic variability and association of different characters and their direct and indirect effects on grain yield per plant as well as the stability of different yield

components with a view to identify genotypes with the best potential for improving yield and its component characters.

MATERIALS AND METHODS

During 2005-2007, a trial was conducted at the Experimental Field of the Institute of Field and Vegetable Crops in Novi Sad. A randomized block design with three replicates was used. Forty wheat genotypes of different geographic origin were used as the experimental material.

The size of the experimental unit was 2 m² and the units were spaced 20 cm apart. The row-to-row distance within each unit was 10 cm and the seeding rate was 350 viable seeds per m². Samples for analyses were taken at full maturity and consisted of 30 plants (10 per replicate). The quantitative indicators spike length – SL (cm), spikelet number per spike – SN, grain number per spike – GN, grain mass per spike – GM (g), and spike index – SI (%) were all determined at the level of the main stem spike. Plant height – PH (cm) was measured from the base of the stem to the tip of the spike. Grain yield per plant – GY (g), 1000-grain weight – TGW (g), and the harvest index – HI (%) were calculated as the average for the whole plant.

The analysis of variance (ANOVA) and estimates of the components of variance due to genotype (σ^2_G), genotype by environment ($\sigma^2_{G \times Y}$), and error (σ^2_e) were calculated according to COMSTOCK and MOLL (1963). The interdependence of the traits was determined using Pearson's correlation coefficient, while direct and indirect effects were assessed by path analysis (DEWEY and LU, 1959). Stability statistics of EBERHART and RUSSEL (1966), i.e., genotype means, regression coefficients (bi), and deviations from regression (Sdi^2), were calculated and the last two statistics were tested against 1 and 0, respectively. The agglomerate hierarchy cluster analysis was used to group the genotypes according to similarity of trait (GY) and stability parameters (bi and Sdi^2) into closely linked clusters and to separate the different genotypes into more distant clusters, i.e. clustering according to the degree of similarity by Euclidean distance application. The data were statistically processed using the SPSS (1994) and GenStat (2006) software packages.

RESULTS AND DISCUSSION

Analysis of variance showed that all sources of variation were highly significant in all nine quantitative traits under study (Tab.1). Generally speaking, the G × Y interaction was low but significant (data not shown). The significance of the interaction for the nine traits resulted from the different ability of the genotypes to adjust their yield components to environmental factors, primarily as a result of genetic differences.

The components of variance (%) for each quantitative trait illustrate the relative contribution of each source of variation to total variance. As environmental factors are always variable in space and time, their variability is most often the greatest (MLADENOV *et al.*, 2001). In the present study, however, this was not the case. The G × Y interaction effect, which accounted for 6.0 to 34.9% of the total variance, was most notably indicative of similarities between the study years. The

components of genotype variance, which ranked from 42.8 to 86.4%, explained most of the total variance for each quantitative trait and at the same time indicated the possibility for improving the analyzed traits in the population (BAKER *et al.*, 1971). The significance of the G \times Y interaction in relation to the genetic effects can be represented through the $\sigma^2_{G/Y}$ $\sigma^2_{G \times Y}$ variance component ratio. A ratio of >1.0 is indicative of a great influence and stability of genetic factors in relation to the variability associated with the G \times Y interaction (Tab.1).

Table 1. Significance and mean squares for variance analysis in 2005-07

Source of variation	Df	SN	GM	GN	GY	PH	SL	TG M	HI	SI
Genotype(G)	39	**	**	**	**	**	**	**	**	**
Year (Y)	2	**	**	**	**	**	**	**	**	**
G \times Y	78	**	**	**	**	**	**	**	**	**
Error	240	ns	ns	ns	ns	ns	ns	ns	ns	ns
σ^2_G (%)		57.4	53.8	45.8	46.2	86.4	53.0	60.3	71.0	42.8
$\sigma^2_{G \times Y}$ (%)		28.8	30.8	31.3	34.9	6.0	20.0	28.7	23.7	28.6
σ^2_e (%)		13.8	15.4	22.9	18.9	7.6	27.0	11.0	5.3	28.6
$\sigma^2_{G/Y} / \sigma^2_{G \times Y}$		2.0	1.7	1.5	1.3	14.5	2.6	2.1	3.0	1.5

SN - spikelet number per spike, GM – grain mass per spike, GN - grain number per spike, GY - grain yield per plant, PH - plant height, SL – spike length, TGW - 1000 grain weight, HI - harvest index, SI - spike index, ns, ** - nonsignificant and significant at $P < 0.01$

The relationships for all quantitative traits were ranked from 1.3 to 14.5. The values of the analyzed traits ranged widely, with the range among the cultivars being greater than that between the years in the case of all the traits concerned (Tab. 2). Such wide variation of means was to be expected given the large differences among the cultivars.

Correlations among the different traits in our study are shown in Table 3. GY was highly significantly correlated with most of the traits analyzed; the only exception being SL. GY was negatively correlated only with PH. PH was significantly correlated with SL. The correlation between PH and SI was significant and negative, while the correlations between PH and GN, GM and HI were negative and highly significant. No correlation was found between GN and TGW. These results confirm the findings of AKRAM *et al.* (2008), KHAN and DAR (2010) and contrast with the findings of MUNIR *et al.* (2007) Correlations among traits depend on genetic and environmental factors. Pleiotropic gene effects and gene linkage are the main reasons for the existence of genetic correlations among traits (FALCONER and MACKAY, 1996)

Table 2. Cultivar and environment mean values for 9 traits of 40 wheat genotypes grown in 2005-07

Trait	Range				Mean (n=120)	CV (%)
	Cultivar (n=40)	CV (%)	Year (n=3)	CV (%)		
GY	2.8-5.6	17.6	4.3-5.0	8.6	4.5	22.4
SN	15.8-21.3	7.6	17.5-19.1	4.8	18.6	9.5
GN	30.2-55.7	12.4	39.3-43.6	5.5	41.1	15.5
GM	1.1-2.2	17.6	1.5-1.8	8.5	1.7	21.6
PH	64.5-125.2	18.1	89.2-94.2	3.0	92.3	18.5
SL	7.1-11.4	12.2	7.7-9.5	10.9	8.8	16.5
TGW	25.7-50.9	13.3	38.8-42.9	5.0	40.8	15.7
HI	0.29-0.49	13.2	0.41-0.43	2.2	0.42	14.0
SI	0.69-0.82	3.5	0.77-0.78	0.9	0.78	4.2

SN - spikelet number per spike, GM – grain mass per spike, GN - grain number per spike, GY - grain yield per plant, PH - plant height, SL – spike length, TGW - 1000 grain weight, HI - harvest index, SI - spike index, CV – coefficient of variation

Table 3. Correlations among different traits of wheat

	GN	GM	PH	SL	TGW	HI	SI	GY
SN	0.60**	0.56**	-0.21	0.35*	0.19	0.11	0.18	0.47**
GN		0.64**	-	0.17	-0.07	0.53**	0.21	0.55**
			0.60**					
GM			-	0.11	0.72**	0.72**	0.68**	0.97**
			0.45**					
PH				0.40*	-0.05	-	-0.31*	-
						0.76**		0.42**
SL					-0.02	-0.27	-0.13	0.09
TGW						0.46**	0.70**	0.77**
HI							0.67**	0.73**
SI								0.71**

SN - spikelet number per spike, GM – grain mass per spike, GN - grain number per spike, GY - grain yield per plant, PH - plant height, SL – spike length, TGW - 1000 grain weight, HI - harvest index, SI - spike index *, ** significant at P<0.05 i 0.01

According to HRISTOV *et al.* (1999, 2008), a higher contribution of the genetic base to the phenotypic expression of PH offers great possibilities for achieving plant height that matches the projected ideotype in the process of breeding. Due to the existing correlations, the shortening of the stem results in a shorter spike but also produces a better HI, the theoretical upper limit of which has been put at 0.6 (AUSTIN *et al.*, 1980). The tendency of maintaining the achieved HI at the existing level while increasing the total above-ground biomass has contributed to the development of high-yielding varieties for southeastern Europe (MLADENOV *et al.*, 2006). The

improvement of GY depends greatly on GN and GM, which means that the characteristics of the spike are of great importance for the further advancement of wheat breeding (HRISTOV *et al.*, 2006). However, although the correlation between GN and TGW is not significant, the negative nature of it reflects the great complexity of correlations among traits and the need to achieve a very fine balance in the values of particular traits. The achievement of an optimum GN is most notably dependent on achieving better spikelet fertility, especially in the lower half of the spike, as most often very few grains are formed there (HRISTOV *et al.*, 2008). SI is highly significantly correlated with HI, which is understandable given that both these traits are under the dominant influence of GM. The presence of a highly significant link between GN and HI and the absence of such connection with SI suggests that grain production on secondary spikes is not satisfactory and should be improved.

Correlations among traits were further analyzed using the path-coefficient approach, which involves further dividing the correlation coefficients into direct and indirect ones through alternative traits or pathways. GY, as a complex outcome of different traits and the best estimate of the genetic yield potential, was viewed as the dependent variable, while GN, GM, PH, SL, TGW, HI and SI were the independent variables. This kind of approach provides a different picture than correlation analysis does.

Figure 1 shows the direct and indirect effects of nine different traits associated with yield. GN, GM and TGW had the greatest direct effect on GY. These results were in agreement with those of JOSHI (2005) and KHAN and DAR (2010). It would be ideal if all three of these traits could be improved simultaneously without any compensatory effect. As this is very difficult to achieve, an effort is made to increase GN and GM while maintaining TGW at an optimum level for a particular agroecological region. The manipulation of certain morphological spike characteristics is enabled by relatively easy measurements and the fact that genetic control is dependant on a smaller number of genes (MARTINEK and BEDNAR, 1998). Increasing GN is dependant on the duration of spike formation and the efficiency of photosynthesis during that period (ABBATE *et al.*, 1995), which, together with mineral nutrition, has a direct impact on the intensity of organic matter formation and a larger number of functional florets per spikelet (MIRALLES and SLAFER, 2007). SN had a direct negative influence on GY, which differs from the highly significant positive correlation (Tab.3). The problem of seed set in a spike, especially in the area near its base (GUIDOBALDI and MAICH, 2001), negatively affects grain number per spike. Although the direct effect is not significant, it must be given greater attention, because it indicates that the appearance of sterile spikelets reduces the total yield considerably.

HI and SI, according to our analysis, had no significant direct effect on GY (Fig. 1). The correlation and its significance between HI and GN and HI and PH (Tab. 3) as well as the considerably higher indirect influence of HI on GY via GN suggest that HI as a more complex factor has certain advantages when choosing the selection criterion. This is because HI incorporates all of the aboveground biomass, while SI covers only a minor portion of it. Because of this, SI can only be used as an

additional selection criterion with the aim being to obtain a more accurate picture of the relationships among individual spike components (HRISTOV *et al.*, 2008).

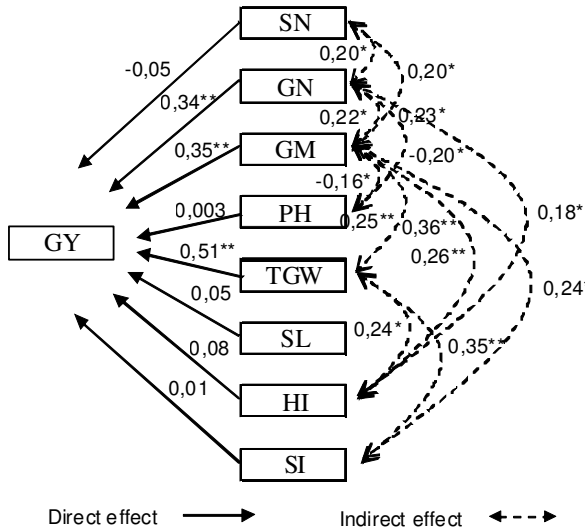


Figure 1. Direct and indirect effects of different wheat traits on grain yield per plant
 SN - spikelet number per spike, GM – grain mass per spike, GN - grain number per spike, GY - grain yield per plant, PH - plant height, SL – spike length, TGW - 1000 grain weight, HI - harvest index, SI - spike index
 *,** significant at $P < 0.05$ i 0.01 , (nonsignificant indirect effects not shown)

Since yield stability is one of the characteristics of yield, genotypes with a complex of positive traits must have good biological plasticity and stability of traits that influence total grain yield. With this in mind, it is necessary to determine the interrelationship of the stability of total grain mass per plant and the stability of the traits being analyzed as well as their interdependence. Table 4 shows the correlations among the regression coefficients as indicators of stability of different wheat traits. GM and GN were highly significantly correlated. These two traits along with HI were highly significantly correlated with GY. Similar findings have been reported by MLADENOV (1996). Although simple correlation analysis has shown that most of the traits are highly significantly correlated with GY, the present analysis shows that GY stability is affected only by the stability of GM, GN and HI. Interestingly, there was a significant correlation between the stability of GN and HI, which suggests that GN has a greater influence on HI stability than GM does.

Table 4. Correlations among bi coefficient of different wheat traits

	GM	GN	GY	PH	SL	TGW	HI	SI
SN	-0.026	-0.091	0.244	0.077	-0.008	-0.103	0.026	0.016
GM		0.521**	0.630**	0.160	0.307	0.164	0.281	-0.124
GN			0.430**	-0.269	0.128	0.196	0.362*	0.099
GY				0.028	0.174	0.078	0.469**	-0.108
PH					0.055	0.196	0.066	0.256
SL						0.252	0.009	0.051
TGW							-0.159	0.264
HI								0.166

SN - spikelet number per spike, GM – grain mass per spike, GN - grain number per spike, GY - grain yield per plant, PH - plant height, SL – spike length, TGW - 1000 grain weight, HI - harvest index, SI - spike index *,** significant at $P < 0.05$ i 0.01

The results for classification of genotypes and their stability statistics are shown in Table 5. Cluster analysis groups genotypes according to their phenotypic similarities. The similarity was based on the means and responses across the environments. The latter component included both coefficients of regression (bi) and variance of deviations (Sdi^2). The dendrogram can be divided into four major clusters. Cluster I is comprised of four subclusters that contain genotypes with GY values that are at or above the average and satisfactory parameters of stability. Cluster II comprises genotypes that have low stability and GY values that are considerably above the average. The third (III) cluster, comprised of two subclusters, incorporates genotypes with below-average GY values and unsatisfactory parameters of stability (bi, Sdi^2), while the fourth (IV) contains genotypes that have GY values that are considerably below the average but are also characterized by high stability. The cluster analysis did not specifically deal with genotypes that adapt better to favorable or unfavorable environmental conditions (MLADENOV *et al.*, 2001). The objective was to obtain a general picture of the genotype's interaction with their environment and select those with a high average value for a given trait and a satisfactory level of stability. Within Cluster I, of particular note are genotypes from Subcluster D, which have excellent stability, although their average GY is at the level of the general average. Of great importance for further research is the identification of as many as seven genotypes in Subcluster A that had excellent stability and the highest average GY values over the course of the study.

The present findings are in agreement with those of HRISTOV *et al.* (2010), which indicate that it is possible to develop cultivars with a high potential and good stability for a given trait. The high average values of genotypes from Subcluster C and Cluster II suggest that these genotypes should be further observed given the potential they have shown. According to GHADERI *et al.* (1980), grouping genotypes into clusters is based on genotypic behavior that cannot be measured by stability parameters. For example, it is possible for two groups of genotypes with opposite values of a given trait to have similar stability, as was the case with Subcluster A ($\bar{X} = 5.36$ g) and Cluster IV ($\bar{X} = 3.47$ g) in our study. In such cases, the selection of

desirable genotypes must be based on a careful analysis of a large number of parameters, and cluster analysis can in that case point to the nature of the phenotypic response in different environments (CARVER *et al.*, 1987). In view of this, the formation of clusters depends to a great extent on the choice of genotypes as well as on environmental factors.

Table 5. Characterization of four groups of cultivars generated from cluster analysis of GY and parameters of stability during a three-year period

Cluster descriptor	Clusters							
	I				II	III		IV
	A	B	C	D		E	F	
Mean ¹ of <i>bi</i>	0.55	1.13	0.98	0.14	1.97	2.56	1.64	0.82
Mean ² of <i>Sdi</i>	0.08	0.18	1.04	0.09	0.16	0.31	0.48	0.06
Mean of GY (g)	5.36	4.71	5.11	4.40	5.28	3.43	3.92	3.47
No of genotypes	7	5	2	4	7	3	6	6

¹Mean of absolute deviation *bi* from 1 ²Mean of absolute deviation *Sdi*² from 0

CONCLUSION

Highly significant correlations were found between grain yield per plant and all the other traits analyzed except spike length. The correlation with plant height was the only negative one. Path analysis revealed highly significant direct effects of grain number per spike, grain mass per spike and 1000 grain weight on grain yield per plant. Correlation analysis of stability parameters among different traits showed that the stability of grain yield per plant was affected only by the stability of grain number per spike, grain mass per spike and harvest index. Using cluster analysis, seven genotypes were identified that had good stability along with the highest average values of grain yield per plant during the study.

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EFEKAT EKOLOŠKIH I GENETIČKIH FAKTORA NA KORELACIJE I STABILNOST KOMONENTI PRINOSA KOD PŠENICE

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I z v o d

Efikasnije oplemenjivanje i stvaranje novih genotipova pšenice uslovljeno je kompleksnom analizom složenih odnosa velikog broja različitih svojstava. Cilj ovog rada je bio da se utvrde međusobni odnosi, direktni i indirektni efekti kao i stabilnost različitih komponenti prinosa kod pšenice. Analizirano je 40 divergentnih genotipova u toku trogodišnjeg ispitivanja (2005-2007). Utvrđena je visoko značajna korelativna veza između mase zrna po biljci i većine analiziranih svojstava, izuzev dužine primarnog klasa, pri čemu je jedino sa visinom biljke ispoljen negativan predznak. Path analizom utvrđeni su visokoznačajni direktni efekti broja zrna i mase zrna primarnog klasa, kao i mase 1000 zrna na prinos zrna po biljci. Analiza parametara stabilnosti pokazala je da stabilnost mase zrna po biljci u najvećoj meri zavisi od stabilnosti broja zrna i mase zrna primarnog klasa, kao i žetvenog indeksa. Klaster analizom grupisani su genotipovi visokih performansi za prinos zrna po biljci i parametre stabilnosti, ukazujući na mogućnost stvaranja sorti sa visokim potencijalom i dobrom stabilnošću za određeno svojstvo.

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