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VARIABILITY AND PATH ANALYSIS FOR YIELD COMPONENTS OF DIFFERENT WHEAT GENOTYPES

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Abstract

The study was carried out to investigate the genotypic and phenotypic variability, heritability and relationship between wheat yield components. A randomized complete block design experiment was conducted, with sixteen wheat genotypes (Dukat, Dunavka, Fundulea 4, Iskra, Jedina, Jugoslavija, Kavkaz, Mačvanka 1, Marija, NS-5804, Pitoma, Poljana, Skopjanka, Tamiš, Vali PKA-7114 and Zvezda), in Novi Bečej (Vojvodina, Serbia), during 2016 and 2017 growing seasons. Grain weight per plant had the highest genotypic and phenotypic variability (15.45 and 20.58%, respectively), while spike length had the lowest ones (5.68 and 6.78%, respectively). High broad sense heritability was observed for plant height (H^2=86.19%) and spike length (H^2=71.73%). Heritability was low in the case of spike weight (H^2=38.82%) and grain weight per spike (H^2=26.56%), which indicates that environmental factors had higher impact on expression of these traits in relation to genetic factors. Path analysis revealed that spike weight and spike length had the highest significant direct positive effect on the grain weight per plant, while thousand grain weight had the highest significant negative effect. The grain weight per spike, number of grains per spike and spike length had a significant indirect effect, through spike weight, on grain weight per spike.

Key words: *Heritability, variability, direct effect, indirect effect*

Introduction

Bread wheat (*Triticum aestivum* L.) is one of the most widely planted crops worldwide and provide about 20% of total food calories for the people of the world (Nukasani *et al*., 2013).
The study of genetic variability and correlation of morpho-agronomic traits with grain yield provides information necessary for successful selection (Ali *et al.*, 2008). It is particularly important to examine the genetic variability of varieties in different agroecological conditions and different soil categories to determine the degree of phenotypic variation and identify the sources of this variability (Petrović *et al*., 2007). Thus, an ideal variety, characterized by high yield or a high value of another desired trait, should exhibit a genetic potential with a low variance value in different environmental conditions (Zečević *et al*., 2008).
It is necessary to separate the total variation into heritable and non-heritable components with the help of genetic parameters, i.e. the genotypic and phenotypic coefficient of variation, and heritability (Paul *et al.*, 2006). Higher heritability values make the selection process more effective, by helping breeders in predicting the interactions of genes in the succeeding generation (Waquas *et al.*, 2014; Saleem *et al.*, 2016). Higher heritabilities indicate that the given trait is under relatively minor influence of the environment (Zerga *et al.*, 2016).
Many researchers have investigated the relationship between yield components and found that knowledge of correlations between traits which determine yield can help in the indirect selection of yield components (Zečević *et al*., 2004a, Hristov *et al*., 2011). In accordance with Rohani and Marker (2016), correlations between yield and its components give a confusing picture due to the mutual relations between the yield components themselves. Thus, mutual

correlations represent only the degree of interaction between given characteristics, while Path analysis quantifies and separates the relationships between yield components into their direct and indirect effects on grain yield (Ashfaq *et al*., 2003).
Path analysis is widely used in plant breeding to determine the nature of the relationship between grain yield and its components, and to determine which yield components with a significant yield effect can be potentially used as selection criteria (Naghavi *et al*., 2014).
The aim of this investigation was to analyze the variability, heritability and direct and indirect effects of yield components on the grain weight per plant. A secondary goal was to determine which traits could be used as yield phenotypic selection markers in a breeding process.

Material and Methods

The experimental material consisting of sixteen diverse wheat genotypes: Yugoslavia, Jedina, Fundulea 4, Iskra, Dunavka, Tamis, Caucasus, Skopjanka, Dukat, Pitoma, Poljana, Marija, NS 58-04, Mačvanka 1, Vali PKA 7114 and Zvezda. Selected genotypes are genetically divergent, which could be used for the development of germplasm in the future plant breeding. The experiment was carried out in a randomized block design with three replications, during two growing seasons (2015/2016 and 2016/2017) in Novi Bečej (Vojvodina, Serbia). The plot size was 2 m^2, where sowing density was 650 grains per m^2. Normal agronomic practices were applied to the experiment throughout the growing season. Ten plants per replication were used for recording plant height (cm), spike length (cm), spike weight (g), number of grain per spike, grain weight per spike (g), grain weight per plant (g) and thousand grain weight (g).
The genetic parameters of variability, estimation of heritability and parameters of variance were computed according to the method suggested by Falconer (1981). The direct and indirect effects of yield components on grain weight per plant were measured by Path analysis as described by Dewey and Lu (1959).

Results and Discussion

The high broad sense heritability of plant height (H^2 = 86.19%) indicates that the analyzed traits had been mostly conditioned by genetic factors, which can help breeders to more easily predict phenotypes of the progeny, based on the genotypes of the parents. This is in agreement with results obtained by Zečević *et al*. (2004a), Petrović *et al*. (2007), Ali *et al*. (2008) and Bhushan *et al*. (2013). The low genotypic and phenotypic coefficients of variation for plant height (GCV = 8.18% and PCV = 8.81%) indicate low variability of this trait, which could be related to the fact that the variation in plant height in European wheat varieties is controlled by the presence or absence of major dwarfing genes (Rht-D1 and Rht-B1) (Würschum *et al*., 2015) (Table 1).
Heritability of spike length was high (H^2 = 71.73%), which is in accordance with results obtained by Ali *et al*. (2008) (76.2%) who noted that the high heritability was contributed by additive gene effects. Thus, selection for this trait can be effective in the early generations. Kotal *et al*. (2010), Rahman *et al*. (2016), Sabbit *et al*. (2017) also found high heritability for spike length. Genotypic and phenotypic variation of spike length was not statistically significant (GCV = 5.68%, PCV = 6.71%), which was confirmed by its small proportion of ecological variance (Table 1).
The low broad sense heritability for spike weight (H^2 = 38.82%) showed that this trait would make the selection process more difficult. Also, Sabbit *et al*. (2017) found low heritability for spike weight. Due to the significant influence of ecological variation, a very significant difference was observed between genotypic and phenotypic variabilities, (GCV = 7.96% and PCV = 11.3%) (Table 1).

Grain weight per spike was a trait with very low broad sense heritability (H^2 = 26.56%). Thus, it would be very difficult to perform effective selection for this trait. This finding is in agreement with results obtained by Zečević *et al*. (2010). The PCV was 12.84%, which was almost twice the GCV (6.67%) (Table 1).

Table 1. Genotypic and phenotypic variance and broad sense heritability of wheat yield components

Yield components[1]	Mean values	Estimates of variance components[2]				CV (%)	GCV (%)	PCV (%)	H^2 (%)
		σ^2_g	σ^2_{ph}	$\sigma^2_{g\times y}$	σ^2_E				
PH	89.26	53.37	61.92	15.86	8.549	6.37	8.18	8.81	86.19
SL	10.18	0.335	0.467	0.228	0.133	10.22	5.68	6.71	71.73
SW	2.58	0.033	0.085	0.093	0.052	22.50	7.96	11.3	38.82
GWS	1.97	0.017	0.064	0.085	0.047	26.10	6.67	12.84	26.56
NGS	47.41	22.93	35.93	22.89	12.992	19.99	10.1	12.64	63.82
GWP	13.86	4.67	8.14	6.098	3.47	34.99	15.45	20.58	57.37
TGW	41.26	5.543	9.65	6.002	4.107	4.39	5.69	7.528	57.44

[1]PH – plant height, SL – spike length, SW – spike weight, GWS – grain weight per spike, NGS – number of grains per spike, GWP – grain weight per plant, TGW – thousand grain weight; [2] σ^2_g – genetic variance, σ^2_{ph} – phenotypic variance, $\sigma^2_{g\times y}$ – genptype and phenotype variance, σ^2_E – environmental variance

Heritability in the broad sense for grain number per spike was moderate (63.82%) (Table 1), which is in accordance with results obtained by Zečević *et al*. (2010). Significant GCV and PCV were found for number of grains per spike (10.1 and 12.64%, respectively) (Table 1). Also, Knežević *et al*. (2012) showed a significant phenotypic variability for number of grains per spike, and concluded that it is very advantageous to perform selection for this yield component.

Moderate heritability was recorded for grain weight per plant (H^2 = 57.37%), which confirms a significant proportion of ecological variance within the total phenotypic variance (Table 1). This is in accordance with results obtained by Ali *et al*. (2008), Kotal *et al*. (2010) and Sabbit *et al*. (2017). GCV and PCV for the trait were 15.45 and 20.58%, respectively, showing high variability for grain weight per plant, which, with moderate heritability, could facilitate the selection of parents. The large difference between GCV and PCV indicates a significant contribution of ecological variance to total phenotypic variance (Table 1).

Thousand grain weight exhibited a moderate heritability (57.44%), which is consistent with results reported by Eid *et al*. (2009), who analyzed heritability in arid conditions, while at favorable environmental conditions, they established a higher heritability. Thousand grain weight had low variability (GCV = 5.69%, PCV = 7.53%) (Table 1).

Spike length had a very significant ($p<0.01$) and positive direct effect (0.156**) on grain weight per plant (Table 2). The results obtained are consistent with those reported by Baranwal *et al*. (2012), where they found that spike length had a significant direct and positive effect on grain yield. Path analysis showed that spike length had a significant positive indirect effect (0.229), through spike weight, on grain weight per plant (Table 2). Zečević *et al*. (2004b) found that spike length had the highest positive indirect effect on grain weight per plant through number of spikelets per spike. Spike weight had the strongest direct and positive effect (0.674**) on grain weight per plant, while the indirect effect, through other traits, was not significant (Table 2). These results indicate that spike weight can be a good selection criterion in wheat breeding. Grain weight per spike had a very high positive effect on grain weight per plant, though the greatest influence was contributed by the indirect effect that this property had through spike weight (0.665). These findings suggest that indirect selection can be made for higher grain weight per spike by selecting plants with a higher average spike weight.

Table 2. Direct and indirect effects of yield components on grain weight per plant

Yield components[1]	**Direct effect**	**Indirect effect**						**Total indirect effect**	**Total effect**
		PH	SL	SW	GWS	NGS	TGW		
PH	0.021	-	0.026	0.032	0.001	-0.023	0.005	0.041	0.062
SL	0.156**	0.004	-	0.229	0.010	0.024	0.012	0.280	0.435
SW	0.674**	0.001	0.053	-	0.010	0.073	0.012	0.172	0.846
GWS	0.034	0.001	0.048	0.665	-	0.075	-0.013	0.777	0.810
NGS	0.090	-0.005	0.042	0.545	0.028	-	-0.001	0.609	0.699
TGW	-0.156**	0.000	-0.010	-0.042	0.002	0.000	-	-0.050	-0.246
R^2=0.745								1.828	2.607
Dependent variable: grain weight per plant									

**p<0.01

[1]PH – plant height, SL – spike length, SW – spike weight, GWS – grain weight per spike, NGS – number of grains per spike, TGW – thousand grain weight

The positive influence of number of grains per spike was reflected through the indirect positive effect that this trait had through spike weight (0.545). Therefore, selection for more grains per spike would not necessarily guarantee a higher grain weight per plant. In this case, the selection of plants with a higher number of grains per spike could be done indirectly by selecting for spike weight, all to increase grain weight per plant. Khaliq *et al*. (2004) found that number of grains per spike had a very high and positive indirect effect on grain yield, through spike length. Thousand grain weight had a highly significant and negative direct effect on grain weight per plant (-0.156 **). Kashif and Khaliq (2004) established that thousand grain weight had a significant negative direct and indirect effect on grain yield. Similarly, Nukasani *et al*. (2013) found that thousand grain weight had a negative direct effect on yield, though without statistical significance.

Path analysis showed that plant height had no significant direct or indirect effect on grain weight per plant (Table 2). Nukasani *et al*. (2013) established a positive, but non-significant, direct effect of plant height on grain yield.

Conclusion

High heritability was observed for plant height and spike length. In these traits, ecological variance and genotype × environment interaction made minor contributions to the total phenotypic variance, which could help breeders to predict phenotypes of the progeny based on the genotypes of the parents. Very low heritability was recorded for spike weight and grain weight per spike, which could complicate the process of breeding. Also, significant genotypic and phenotypic variability was observed, especially in grain weight per spike. Spike weight and spike length had the highest significant direct positive effects on grain weight per plant, while thousand grain weight had the highest significant negative effect. Thus, the grain weight per plant could be increased by direct selection for spike weight and spike length. Grain weight per spike, number of grains per spike and spike length had significant indirect effects, through spike weight, on grain weight per spike. Thus, it could be concluded that spike weight was the trait which contributed most to the increase in grain weight per plant amongst these diverse wheat genotypes.

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