

VARIABILITY, CORRELATION, PATH ANALYSIS AND STEPWISE REGRESSION FOR YIELD COMPONENTS OF DIFFERENT WHEAT GENOTYPES

Mirela MATKOVIC STOJSIN^{1*}, Veselinka ZECEVIC¹, Sofija PETROVIC²,
Miodrag DIMITRIJEVIC², Danica MICANOVIC³, Borislav BANJAC², Desimir KNEZEVIC⁴

¹Megatrend University, Faculty of Biofarming, Backa Topola, Serbia,

²University of Novi Sad, Faculty of Agriculture, Novi Sad, Serbia,

³Chamber of Commerce and Industry of Serbia, Belgrade, Serbia

⁴University of Pristina, Faculty of Agriculture, Kosovska Mitrovica, Lešak,
Kosovo and Metohia, Serbia.

Matković Stojšin, M., V. Zečević, S. Petrović, M. Dimitrijević, D. Mićanović, B. Banjac, D. Knežević (2018): *Variability, correlation, path analysis and stepwise regression for yield components of different wheat genotypes.*- Genetika, Vol 50, No.3, 817-828.

In order to evaluate the variability and relationship between different wheat yield components, a randomized complete block design experiment with ten genotypes of wheat had been carried out during three growing seasons (2010-2012). The number of spikelet per spike and grain weight per spike had low genotypic and phenotypic variability, while plant height had the highest one. High heritability was observed for plant height ($h^2=93.1\%$), spike length ($h^2=92.3\%$) and spike density ($h^2=92.9\%$). The low heritability was found for grain weight per spike ($h^2=35.6\%$). Grain weight per spike was in significant positive genotypic and phenotypic correlation with all the traits (plant height, spike height, number of spikelet per spike, number of grain per spike and spike weight) except spike density. The spike weight had the highest phenotypic ($r_p=0.988$), while number of spikelet per spike had the highest genotypic correlation with grain weight per spike ($r_g=0.981$). Path coefficient analysis revealed that all the traits had highly significant direct effect on grain weight per spike, except spike length. The stepwise regression revealed that 87.1% of the grain weight per spike variation was explained by model which excludes spike length. Spike weight and plant height had the highest shared and unique contribution to grain weight per spike.

Keywords: yield components, correlation, heritability, variability, wheat.

Corresponding author: Mirela Matković Stojšin, Megatrend University, Faculty of Biofarming, Marsala Tita 39, Backa Topola, Serbia, Phone +381 24 712 209, e-mail: mirelam89@gmail.com

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the one of major crops in the World. In the form of bread, wheat provides more nutrients than any other single food source (PENA, 2002). It has been estimated that the global demand for wheat would be increased with the growth of World population by a further 60% by 2050 (LICKER *et al.*, 2010). One of the main goals in wheat breeding is increasing grain yield. An important strategy for sustaining yield production is breeding high yielding wheat cultivars phenotypically suitable for the industrial agricultural food production (GARCIA DEL MORAL *et al.*, 2003). Studying the genetic variability and association of morpho-agronomic traits with grain yield provides the necessary information for successful selection (ALI *et al.*, 2008). Improving of grain yield in breeding programs is very difficult because grain yield, as a quantitative trait, is controlled by a number of genes with weak individual effect (minor genes) and it is significantly influenced by the environment (DENG *et al.*, 2011). Thus, apart from direct selection for grain yield, it is more effectively applying indirect selection through traits related to grain yield (ASHFAQ *et al.*, 2003; ROHANI and MARKER, 2016a). The study of the correlation between traits that determine yield can help in the indirect selection of components of yield (GARCIA DEL MORAL *et al.*, 2003; ZECEVIC *et al.*, 2004; HRISTOV *et al.*, 2011). Genotypic and phenotypic correlation between grain weight per spike and other yield components has been studied by a number of researchers. NUKASANI *et al.* (2013) and DESHEVA (2016) reported significant positive genotypic and phenotypic correlation of grain weight per spike with number of spikelet per spike and number of grain per spike. In the studies conducted by ROHANI and MARKER (2016a) grain weight per spike was in significant positive correlation with plant weight and spike length, both at genotypic and phenotypic levels. Grain weight per spike, together with numerous traits, contributes to the formation of total grain yield (KNEZEVIC *et al.*, 2015). Therefore, this trait can be included in the indirect indicators of grain yield (PETROVIC *et al.*, 2009). According to ROHANI and MARKER (2016b) correlation between yield and its components presents a confusing picture due to interrelationships between component characteristics by themselves. Correlations by themselves express only the degree of traits interrelationships, while path analysis quantifies and separates the interrelationships between yield components to their direct and indirect effects on grain yield (ASHFAQ *et al.*, 2003). In terms of bread wheat yielding capacity increment in breeding programs, the investigation of direct and indirect impact of various characteristics on yield is of major importance (MOHAMMADI *et al.*, 2012). SHIMELIS *et al.* (2006) reported that grain weight per spike and number of spikelet per spike had the most direct and positive effect on grain yield. ZECEVIC *et al.* (2004) obtained by path analysis that the spike length through number of spikelet per spike had the highest positive indirect effect on grain weight per plant. According to ABDERRAHMANE *et al.* (2013), a stepwise regression can reduce the effect of significantly non-important traits in the regression model. SOLEYMANIFARD *et al.* (2012), NASRI *et al.* (2014), MIRTAHERI *et al.* (2015) have used stepwise regression on wheat. The main objectives of this study were to determine the genetic and phenotypic variability, heritability, inter-relationship and direct and indirect effects of some wheat traits among themselves and with grain weight per spike. Also, the goal is to determine which traits could be used as a yield phenotypic selection marker in a breeding process.

MATERIALS AND METHODS

Field experiment was conducted during three different vegetation seasons (2010-2012) at the experimental field of the Center for Small Grains in Kragujevac, Serbia (20°55'12" E, 44°01'12" N, 185 m alt.). The field experiment was performed on the soil of the smonitza (*Vertisol*) type, with a relatively high clay content and the unfavorable physical properties. The experimental material consisted of ten wheat genotypes: Arsenal, KG-56, Gruza, Mironovskaya 808, Norin 10, Rana Niska, Spartanka, Sterna, Osjecanka, and Szegedi 765, which were planted in the field according to a randomized complete block design with three replications. Sparse sowing was performed in 1 m long rows, with 20 cm space between the rows and 10 cm distance between each seed in a row. Because of the sparse sowing method, genotypes have been able to express their maximal genetic potential for tillering, and the lush vegetative mass, as well as spike characteristics. The main sample consisted of 10 plants per replication (30 plants per genotype). In this study, plant height (of the main tiller, measured from the base of the stem up to the apex excluding spike [cm]), primary spike traits (spike length [cm], number of spikelet per spike, number of grain per spike, spike density (number of spikelet per spike/spike length), spike weight [g] and grain weight per spike [g]), were evaluated. Analyses of variance and covariance, correlation, multiple linear regression and stepwise regression for all collected data, were conducted, using the IBM SPSS Statistics Trial Version 22.0 (<https://www.ibm.com/>). The mean squares (MS) from analysis of variance were used to estimate components of the variance (genotypic variance σ_g^2 , phenotypic variance σ_p^2 , genotype \times year variance $\sigma_{g \times y}^2$, and ecological variance σ_e^2) (COMSTOCK and ROBINSON, 1952), as follows:

$$\sigma_e^2 = \frac{MS1 - MS2}{r \cdot y}$$

$$\sigma_e^2 = MS3$$

$$\sigma_{g \times y}^2 = \frac{MS2 - MS3}{y}$$

$$\sigma_p^2 = \sigma_g^2 + \frac{\sigma_{g \times y}^2}{y} + \frac{\sigma_e^2}{r \cdot y}$$

Where: MS1 = mean square for genotype, MS2 = mean square for genotype \times year, MS3 = mean square for error, r = replications, y = years

The mean values (\bar{X}) were used for genetic analyses to determine genotypic coefficient of variation (CV_g) and phenotypic coefficient of variation (CV_p), according to SINGH and CHAUDHURY (1985), using equation:

$$CV_g(\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

$$CV_p(\%) = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

Heritability in broad sense (h^2) for all traits was computed using the formula given by FALCONER (1989), as:

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

The genotypic and phenotypic correlation coefficients were calculated by the method described by FALCONER (1989), using equations:

$$r_{g\ xy} = \frac{cov_{g\ xy}}{\sqrt{\sigma_{gx}^2 \cdot \sigma_{gy}^2}}$$

$$r_{p\ xy} = \frac{cov_{p\ xy}}{\sqrt{\sigma_{fx}^2 \cdot \sigma_{fy}^2}}$$

Where: cov_g = genotypic covariance, cov_p = phenotypic covariance, x and y = mean values of traits.

Test of significance (at 5 and 1% probability levels) of correlation was done using t-test at n-2 degree of freedom. Path analysis was carried out according to method described by DEWEY and LU (1959).

RESULTS AND DISCUSSION

Highly significant differences ($p < 0.01$) were observed among the genotypes for all the traits, indicating that the genetic variation was present. (Table 1). The phenotypic coefficient of variation (CV_p) was higher than the genotypic coefficient of variation (CV_g) for all analyzed traits. This indicates that the present variation was not only due to genotypes but also due to influence of environment. The higher value of CV_p for all characters have also reported by PETROVIĆ *et al.* (2007), ALI *et al.* (2008) and BHUSHAN *et al.* (2013). Plant height had the highest CV_g and CV_p (22.62 and 23.51%), while the number of spikelet per spike had the lowest values (4.98 and 5.8%). Similar results were reported by BHUSHAN *et al.* (2013), where they found the lowest CV_p for number of spikelet per spike. Grain weight per spike had low CV_g and CV_p (5.63 and 9.45%, respectively), but high difference between phenotypic and genotypic coefficient of variation indicating the greater influence of the environment. Moderate values of CV_g and CV_p were observed for spike length, number of grains per spike, spike density and spike weight (Table 1). The selection success largely depends on the extent to which the desired traits are heritable (ROHANI and MARKER, 2016a). The estimates of broad sense heritability were from low to high in various traits. Highest heritability of 93.1% was exhibited by plant height, which is in agreement with results reported by KASHIF and KHALIQ (2004) and ALI *et al.* (2008). Also, heritability was high in case of spike length (92.3%) and spike density (92.9%). The traits such as number of spikelets per spike, number of grains per spike and spike weight showed moderately high heritability values of 73.3, 75.9 and 72.2%, respectively. KASHIF and KHALIQ (2004) reported similar results for number of spikelets per spike (70.61%) and number of grains per spike (78.41%). Also, ERKUL *et al.* (2010) observed similar heritability for number of spikelet per spike (62%). The low heritability (35.6%) was observed for grain weight per spike

because genetic variance was lower in magnitude (0.021) than environmental variance (0.038) (Table 1). This is in agreement with results reported by KNEZEVIC *et al.* (2014), who emphasizes that environmental factors had higher impact on grain weight per spike expression in relation to genetic ones.

Table 1. The mean value, variance and heritability of analyzed yield components

Traits ^a	Mean values	Estimates of variance components ^b				MS of genotypes	CV (%)	CVg (%)	CVp (%)	h ² (%)
		σ_g^2	σ_p^2	σ_{g*y}^2	σ_E^2					
PH	58.15	174.17	187.05	37.72	12.87	16834.2**	14.22	22.69	23.51	93.1
SL	9.93	3.174	3.438	0.144	0.264	290.52**	9.82	17.94	18.09	92.3
NSS	22.28	1.23	1.678	1.214	0.447	151.012**	11.61	4.98	5.80	73.3
NGS	63.92	60.621	79.876	53.48	19.255	7188.87**	22.41	12.18	13.98	75.9
SD	2.24	0.079	0.085	0.016	0.006	121.411**	11.09	12.54	13.01	92.9
SW	3.46	0.112	0.155	0.115	0.043	13.992**	21.11	9.67	11.37	72.2
GWS	2.57	0.021	0.059	0.105	0.038	5.304**	24.43	5.63	9.45	35.6

^aPH – plant height; SL – spike length; NSS – number of spikelet per spike; NGS – number of grains per spike; SD – spike density; SW – spike weight, GWS – grain weight per spike; ^b σ_g^2 , σ_{ph}^2 , σ_{g*y}^2 and σ_E^2 indicate the genetic, phenotypic, genotype and phenotype interaction and environment variance, respectively; **p<0.01

All the values of genotypic correlations were generally higher comparing to phenotypic ones, showing the existence of inherent association among the traits. This is in line with findings of MUNIR *et al.* (2007) and AJMAL *et al.* (2009). Plant height had highly significant and positive genotypic and phenotypic correlation to the spike length ($r_g=0,844$, $r_{ph}=0,819$) and the number of spikelet per spike ($r_g=0,766$, $r_p=0,671$) which corresponds to the results obtained by RAHMAN *et al.* (2016). The genotypic and phenotypic correlation of spike length was statistically significant and positive with number of spikelet per spike ($r_g=0,980$, $r_p=0,906$). Similar results were observed by ZECEVIC *et al.* (2004), KHALIQ *et al.* (2004) and DESHEVA (2016). Also, spike length correlated positively and significantly to the grain weight per spike ($r_g=0,708$, $r_p=0,395$), which is in agreement with previous reports of MUNIR *et al.* (2007) and ROHANI and MARKER (2016a). DESHEVA (2016), also, noticed that spike length was in positive and significant correlation, at phenotypic level, to the grain weight per spike. The grain weight per spike had the highly significant and positive genotypic and phenotypic correlation to the number of spikelet per spike ($r_g=0,981$, $r_p=0,560$), confirmed by NUKASANI *et al.* (2013) and DESHEVA (2016). Also, grain weight per spike had highly significant and positive correlation to the number of grains per spike ($r_g=0,861$, $r_h=0,615$), which was confirmed by findings of ZECEVIC *et al.* (2004), MUNIR *et al.* (2007) and DESHEVA (2016). The spike weight had significant to highly significant positive

correlation to all the characteristics except plant height and spike density (Table 2). Significant to highly significant negative genotypic and phenotypic correlations were exhibited by spike density to all of the characteristics in study. The strongest negative genotypic and phenotypic correlation was observed between spike density and spike length ($r_g=-0,992$, $r_p=-0,970$), which means that the spike length increment decreases spike density. Similar result was obtained by KHALIQ *et al.* (2004).

Table 2. Genotypic – r_g (above diagonal) and phenotypic – r_p (below diagonal) correlation coefficients of analyzed traits

Traits ^a	PH	SL	NSS	NGS	SD	SW	GWS
PH	-	0.844**	0.766**	-0.226	-0.830**	0,216	0.488*
SL	0.819**	-	0.980**	0.038	-0.992**	0.496*	0.708**
NSS	0.671**	0.906**	-	0.331	-0.989**	0.787**	0.981**
NGS	-0.251	0.032	0.267	-	-0.022	0.767**	0.861**
SD	-0.788**	-0.970**	-0.847**	-0.024	-	-0.578*	-0.801**
SW	0.153	0.402*	0.584**	0.731**	-0.465*	-	0.961**
GWS	0.259	0.395*	0.560**	0.615**	-0.443*	0.988**	-

^aPH – plant height; SL – spike length; NSS – number of spikelet per spike; NGS – number of grains per spike; SD – spike density; SW – spike weight; GWS – grain weight per spike; * $p<0.05$; ** $p<0.01$

In order to obtain more accurate results of the interrelationship between different traits, the direct and indirect effects of the different traits on grain weight per spike were calculated (Table 3). The spike weight had the highly significant ($p<0.01$) and the highest positive direct effect (0.908) on grain weight per spike. The direct effect of plant height on grain weight per spike was highly significant ($p<0.01$) and positive (0.157). Highly significant and positive direct effect of plant height on grain weight per plant was established by ZECEVIC *et al.* (2004). MOHAMMADY *et al.* (2012) reported that the plant height had positive direct effect on grain yield. Plant height had positive indirect effect on grain weight per spike, via spike weight (0.145), only. According to ZECEVIC *et al.* (2010), as well as, SREENIVASULU and SCHNURBUSCH (2012) grain number per spike plays an important role in wheat grain yield improvement. Number of grains per spike had highly significant ($p<0.01$) and positive direct effect (0.087) on grain weight per spike, which is in accordance to the results obtained by ASHFAQ *et al.* (2003) and KHAN and DAR (2010). The positive indirect effect of number of grains per spike on grain weight per spike was via spike weight (0.652), only. The path coefficient analysis gave somewhat different results comparing to the genotypic and phenotypic correlation analysis. The genotypic and phenotypic correlation analysis indicated that number of spikelet per spike had highly significant and positive effect on grain weight per spike, but path analysis suggested that this trait had direct

negative influence on grain weight per spike (-0.110**). The direct negative effect of number of spikelet per spike was masked from the positive indirect effect of this trait through the spike weight (0.429) and plant height (0.073). The path analysis showed that spike length had non-significant ($p>0.05$) direct effect on grain weight per spike (-0.028). Highly significant and positive genotypic and phenotypic correlation coefficients between spike length and grain weight per spike were mainly because of indirect effect through spike weight (0.287) and plant height (0.111). Therefore, selection for longer spike cannot guarantee a high grain weight per spike. Although genotypic and phenotypic correlation showed that spike density had highly significant and negative effect on grain weight per spike, path coefficient indicated that this trait had highly significant ($p<0.01$) and positive direct effect (0.073). Similar results were obtained by KHALIQ *et al.* (2004) and ATA *et al.* (2014). Path analysis also showed that spike density had negative indirect effect on grain weight per spike through spike weight (-0.113) and plant height (-0.071). This negative indirect effect covered direct positive effect. The highest positive total indirect effect belonged to a number of grains per spike (0.595), followed by the number of spikelet per spike, and that was controlled through spike weight (0.652 and 0.429), while only spike density had negative total indirect effect (0.162) on grain weight per spike also via spike weight. KHALIQ *et al.* (2004) reported that number of grains per spike had the highest positive indirect effect on grain yield, but via spike length. Spike weight had the highest total effect on grain weight per spike (0.926), followed by number of grains per spike (0.681) and number of spikelet per spike (0.412) (Table 3).

Table 3. Direct and indirect effect of different traits to grain weight per spike calculated by Path analysis

Traits ^a	Direct effect	Indirect effects						Total indirect effect	Total effect
		PH	SL	NSS	NGS	SD	SW		
PH	0.157**	-	-0.020	-0.051	-0.001	-0.033	0.145	0.040	0.197
SL	-0.028	0.111	-	-0.067	0.017	-0.052	0.287	0.297	0.269
NSS	-0.110**	0.073	-0.017	-	0.039	-0.001	0.429	0.522	0.412
NGS	0.087**	-0.002	-0.006	-0.049	-	0.000	0.652	0.595	0.681
SD	0.073**	-0.071	0.020	0.002	0.000	-	-0.113	-0.162	-0.089
SW	0.908**	0.025	-0.009	-0.052	0.062	-0.009	-	0.018	0.926
$R^2=0.871$								1.309	2.396

^aPH – plant height; SL – spike length; NSS – number of spikelet per spike; NGS – number of grains per spike; SD – spike density; SW – spike weight; GWS – grain weight per spike; ** $p<0.01$

A stepwise regression analysis was computed in order to remove effect of non-effective traits in regression model on grain weight per spike (Table 4). The stepwise regression analysis

revealed that 87.1% ($R^2=0,871$) of the grain weight per spike variation was explained by a model which excludes spike length. In order to all independent variables that are included in a model, the spike weight had the strongest variation in grain weight per spike ($\beta=0.909$), confirming the results reported by the genotypic and phenotypic correlation and path analysis. The spike weight had the highest shared (73.8%) and unique (68.1%) contribution to grain weight per spike, which indicates that spike weight explains the most part of grain weight per spike variation as well. NASRI *et al.* (2014) reported the importance of spike weight per unit area to grain yield. It was observed that 82.3% of variation in grain weight per spike was explained by spike weight and plant height. This shows that these two traits had the most effect on the increasing of grain weight per spike. SOLEYMANIFARD *et al.* (2012) found that plant height significantly explained variation in grain yield, also. Although, grain number per spike was in stronger association with grain weight per spike in relation to other traits, except spike weight, ($r=0.682$), this trait had the lowest shared and unique contribution to grain weight per spike (2.4 and 0.3%). Number of spikelet per spike was in positive correlation to grain weight per spike ($r=0.412$), but this trait had the negative impact on variation in grain weight per spike ($\beta=-0.124$). In the other hand, spike density was in negative association with grain weight per spike ($r=-0.089$), but it had positive effect on variation in grain weight per spike ($\beta=0.091$), Table 4.

Table 4. Stepwise regression showing the relative contribution of some traits in predicting grain weight per spike

Traits included in model ^a	R ²	B coefficient	β coefficient	Correlations			Contribution (%)		Probability
				zero-order	partial	part	shared	unique	
SW		0.745	0.909	0.926	0.859	0.603	73.8	36.4	p<0.01
PH		0.007	0.151	0.196	0.292	0.110	8.5	1.2	p<0.01
NGS	0.871	0.003	0.087	0.682	0.156	0.057	2.4	0.3	p<0.01
NSS		-0.029	-0.124	0.412	-0.242	-0.089	5.8	0.8	p<0.01
SD		0.155	0.091	-0.089	0.209	0.077	4.4	0.6	p<0.01
Final equation	GWS = 0.745SW + 0.007PH + 0.003NGS - 0.029NSS + 0.155SD - 0.327 ϵ								

^aSW – spike weight; PH – plant height; NGS – number of grains per spike; NSS – number of spikelet per spike; SD – spike density GWS – grain weight per spike

CONCLUSION

Grain weight per spike was in high and positive genotypic and phenotypic correlation with number of spikelet per spike, number of grains per spike and spike length. However, path analysis showed that the highest part of these correlations belongs to the indirect positive effects of mentioned traits through the spike weight and plant height. These results confirmed that path

analyzes quantifies the interrelationships between traits in detail, which makes it more useful for breeders compared to correlation analysis. Path coefficient analysis indicated that spike weight had the strongest positive and direct effect on grain weight per spike. A great number of traits had high indirect effect on grain weight per spike via spike weight and plant height, only. The stepwise model included all the traits except spike length. Spike weight and plant height had the highest shared and unique contribution to grain weight per spike. Based on path coefficient analysis and stepwise regression, we concluded that spike weight and plant height can be used as a selection criteria to increase grain weight per spike. Respectively, the assimilative translocation from vegetative to generative plant parts is at its best, giving the increment of the grain weight per spike.

ACKNOWLEDGEMENTS

This investigation was supported by Ministry of Education, Science and Technology Development of Republic of Serbia, Project TR 31092.

Received, October 15nd, 2017

Accepted April 18th, 2018

REFERENCES

- ABDERRAHMANE, H., F. ABIDINE, B. HAMENNA, B. AMMAR (2013): Correlation, path analysis and stepwise regression in durum wheat (*Triticum durum* Desf.) under rainfed conditions. *J. Agric. Sustain.*, 3:122-131.
- AJMAL, S.U., N. ZAKIR, M.Y. MUJAHID (2009): Estimation of genetic parameters and character association in wheat. *J. Agric. Biol. Sci.*, 1(1): 15-18.
- ALI, Y., B.M. ATTA, J. AKHTER, P. MONNEVEUX, Z. LATEEF (2008): Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. *Pak. J. Bot.*, 40(5): 2087-2097.
- ASHFAQ, M., A.S. KHAN, Z. ALI (2003): Association of morphological traits with grain yield in wheat (*Triticum aestivum* L.). *Int. J. Agric. Biol.*, 5(3): 262-264.
- ATA, A., B. YOUSAF, A.S. KHAN, G.M. SUBHANI, H.M. ASADULLAH, A. YOUSAF (2014): Correlation and path coefficient analysis for important plant attributes of spring wheat under normal and drought stress conditions. *J. Biol. Agric. Healthc.*, 4(8): 66-74.
- BHUSHAN, B., S.S. GAURAY, R. KUMAR, R. PAL, M. PANDAY, A. KUMAR, S. BHARATI, S.S. NAGAR, V.P. RAHUL (2013): Genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.). *Environ. Ecol.*, 31(2): 405-407.
- COMSTOCK, R.R. and H.F. ROBINSON (1952): Genetic parameters, their estimation and significance. *Proceedings of the 6th international Grassland Congress, 1*, Nat. publ. Co. Wash., DC, USA: 248-291.
- DENG, S., X. WU, Y. WU, R. ZHOU, H. WANG, J. JIA, S. LIU (2011): Characterization and precise mapping of a QTL increasing spike number with pleiotropic effects in wheat. *TAG*, 122: 281-289.
- DESHEVA, G. (2016): Correlation and path coefficient analysis of quantitative characters in winter bread wheat varieties. *Trakia J. Sci.*, 1: 24-29.
- DEWEY, D.R. and K.H. LU (1959): A correlation and path coefficient analysis of components of crested wheatgrass seed production. *Agron. J.*, 51: 515-518.
- ERKUL, A., A. UNAY, C. KONAK (2010): Inheritance of yield and yield components in a bread wheat (*Triticum aestivum* L.) cross. *Turk. J. Field Crops.*, 15(2): 137-140.
- FALCONER, D.S. (1989): *Introduction to quantitative genetics*, 3rd Edition. Burnt Mill, Harlow, Essex, England: Longman, Scientific and Technical, New York: Wiley, 438.

- GARCIA DEL MORAL, L.F., Y. RHARRABTI, D. VILLEGAS, C. ROYO (2003): Evaluation of grain yield and its components in durum wheat under Mediterranean conditions. *Agron. J.*, 95: 266-274.
- HRISTOV, N., N. MLADENOV, A. KONDIĆ-ŠPIKA, A. MARJANOVIĆ-JEROMELA, B. JOCKOVIĆ, G. JAČIMOVIĆ (2011): Effect of environmental and genetic factors on the correlation and stability of grain yield components in wheat. *Genetika*, 43(1): 141-152.
- KASHIF, M. and I. KHALIQ (2004): Heritability, correlation and path coefficient analysis for some metric traits in wheat. *Int. J. Agri. Bio.*, 6(1): 138-142.
- KHALIQ, I., N. PARVEEN, M.A. CHOWDHRY (2004): Correlation and path coefficient analyses in bread wheat. *Int. J. Agri. Bio.*, 6(4): 633-635.
- KHAN, M.H. and A.N. DAR (2010): Correlation and path coefficient analysis of some quantitative traits in wheat. *Afr. Crop. Sci. J.*, 18(1): 9-14.
- KNEZEVIC, D., A. RADOSAVAC, M. ZELENKA (2015): Variability of grain weight per spike in wheat grown in different ecological conditions. *Acta Agriculturae Serbica*, 20(39): 85-95.
- KNEZEVIC, D., V. ZECEVIC, D. KONDIC, S. MARKOVIC, A. SEKULARAC (2014): Genetic and phenotypic variability of grain mass per spike in wheat under different dose of nitrogen nutrition. *Turk. J. Agric. Nat. Sci.*, 1: 805-810.
- LICKER, R., M. JOHNSTON, C. BARFORD, J.A. FOLEY, C.J. KUCHARIK, C. MONFREDA, N. RAMANKUTTY (2010): Mind the Gap: How do climate and agricultural management explain the yield gap of croplands around the world? *Glob. Ecol. Biogeogr.*, 19:769-782.
- MIRTAHERI, S.M., F. PAKNEJAD, M. BEHDAD (2015): The application of the multivariate analysis method for some traits in wheat under drought stress. *J. Agri. Sci.*, 60(4): 407-417.
- MOHAMMADI, M., P. SHARIFI, R. KARIMIZADEH, M.K. SHEFAZADEH (2012): Relationships between grain yield and yield components in bread wheat under different water availability (dryland and supplemental irrigation conditions). *Not. Bot. Horti. Agrobi.*, 40(1): 195-200.
- MUNIR, M., M.A. CHOWDHRY, T.A. MALIK (2007): Correlation studies among yield and its components in bread wheat under drought conditions. *Int. J. Agri. Biol.*, 9(2): 287-290.
- NASRI, R., A. KASHANI, F. PAKNEJAD, S. VAZAN, M. BARARY (2014): Correlation, path analysis and stepwise regression in yield and yield component in wheat (*Triticum aestivum* L.) under the temperate climate of Ilam province, Iran. *Iran. Indian J. Fundam. Appl. Life Sci.*, 4(4): 188-198.
- NUKASANI, V., N.R. POTDUKHE, S. BHARAD, S. DESHMUKH, S.M. SHINDE (2013). Genetic variability, correlation and path analysis in wheat. *J. Wheat Res.*, 5(2): 48-51.
- PENA, R.J. (2002): Wheat for bread and other foods. In: Bread wheat: improvement and production, eds. Curtis, B.C., Rajaram, S. and Gomez Macpherson, H., 483-494, Food and Agriculture Organization, Rome, Italy.
- PETROVIC, S., M. DIMITRIJEVIC, B. BELIC, B. BANJAC, M. VUKOSAVLJEV (2009): Spike stability parameters in wheat grown on Solonetz soil. *Genetika*, 41(2): 199-205.
- PETROVIĆ, S., M. DIMITRIJEVIĆ, M. BELIĆ (2007): Stem height and spike parameters heritability in wheat grown on black humic-gley soil. *Letopis naučnih radova Poljoprivrednog fakulteta*, 31(1): 146-152 (in Serbian).
- RAHMAN, M.A., M.L., KABIR, M. HASANUZZAMAN, M.A. RAHMAN, R.H. RUMI, M.T. AFROSE (2016): Study of variability in bread wheat (*Triticum aestivum* L.). *Int. J. of Agron. and Agric. Res.*, 8(5): 66-76.
- ROHANI, S.K. and S. MARKER (2016b). Evaluation of genetic variability for some quantitative traits in wheat (*Triticum aestivum* L.). *I. Int. J. Multidisc. Res. Dev.*, 3(7): 12-14.
- ROHANI, S.K. and S. MARKER (2016b): Correlation and path coefficient analysis of some quantitative traits in wheat (*Triticum aestivum* L.). *Int. J. Multidisc. Res. Dev.*, 3(7): 15-20.
- SHIMELIS, H.A. (2006): Associations of yield and yield components among selected durum wheats (*Triticum turgidum* L.). *S. Afr. J. Plant Soil*, 23(4): 305-309.

- SINGH, R.K. and B.D. CHAUDHARY (1985): Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, Ludhiana, India, 39-78.
- SOLEYMANIFARD, A., R. NASERIAND, M. MORADI (2012): The study genetic variation and factor analysis for agronomic traits of durum wheat genotypes using cluster analysis and path analysis under drought stress condition in western of Iran. *Int. Res. J. Appl. Basic Sci.*, 3(3): 479-485.
- SREENIVASULU, N. and T. SCHNURBUSCH (2012): A genetic playground for enhancing grain number in cereals. *Trends Plant Sci.*, 17: 91–101.
- ZECEVIC, V., J. BOSKOVIC, M. DIMITRIJEVIC, S. PETROVIC (2010): Genetic and phenotypic variability of yield components in wheat (*Triticum aestivum* L.). *Bulg. J. Agric. Sci.*, 16(4): 422-428.
- ZECEVIC, V., KNEZEVIC, D., D. MICANOVIC (2004): Genetic correlations and path coefficient analysis of yield and quality components in wheat. *Genetika*, 36(1): 13-21.

VARIJABILNOST, KORELACIJE, PATH ANALIZA I STEPWISE REGRESIJA KOMPONENTI PRINOSA RAZLIČITIH GENOTIPOVA PŠENICE

Mirela MATKOVIC STOJSIN^{1*}, Veselinka ZECEVIC¹, Sofija PETROVIC²,
Miodrag DIMITRIJEVIC², Danica MICANOVIC³, Borislav BANJAC², Desimir KNEZEVIC⁴

¹Univerzitet Megatrend, Fakultet za Biofarming, Bačka Topola, Srbija

²Univerzitet u Novom Sadu, Poljoprivredni fakultet, Novi Sad, Srbija

³Privredna komora Srbije, Beograd, Srbija

⁴Univerzitet u Prištini, Poljoprivredni fakultet, Kosovska Mitrovica, Lešak, Kosovo i Metohija, Srbija

Izvod

Sa ciljem da se pouči varijabilnost i međusobni odnos između različitih komponenti prinosa pšenice, zasnovan je ogled po slučajnom blok sistemu, sa deset genotipova pšenice, u tri vegetacione sezone (2010-2012). Broj klasića po klasu i masa zrna po klasu su imale nisku genotipsku i fenotipsku varijabilnost, dok je najviša varijabilnost zabeležena kod visine biljke. Visoka heritabilnost ustanovljena je kod visine biljke ($h^2=93,1\%$), dužine klasa ($h^2=92,3\%$) i rastresitosti klasa ($h^2=92,9\%$). Najniža heritabilnost je zabeležena kod mase zrna po klasu ($h^2=35,6\%$). Masa zrna po klasu je u značajnoj pozitivnoj genotipskoj i fenotipskoj korelaciji sa svim osobinama (visina biljke, dužina klasa, broj klasića po klasu, broj zrna po klasu i masa klasa), osim sa rastresitošću klasa. Najvišu fenotipsku korelaciju sa masom zrna po klasu je ostvarila masa klasa ($r_f=0,988$), a najvišu genotipsku korelaciju broj klasića po klasu ($r_g=0,981$). Path koeficijent pokazuje da sve osobine, osim dužine klasa, imaju značajan direktni efekat na masu zrna po klasu. Stepwise regresijom je ustanovljeno da je 87,1% varijacije mase zrna po klasu objašnjeno modelom koji isključuje dužinu klasa. Masa klasa i visina biljke imaju najviši opšti i pojedinačni doprinos povećanju mase zrna po klasu.

Primljeno 15.X.2017.

Odobreno 18. IV. 2018.