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GENETIC AND PHENOTYPIC VARIABILITY OF GRAIN MASS PER SPIKE OF WINTER WHEAT GENOTYPES (*Triticum aestivum* L.)

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ABSTRACT. Variability of grain mass per spike were studied in 10 wheat genotypes. Wheat genotypes were grown during three years on the experimental field in three replications. Samples of 60 wheat plants (20 plants/replication at each year) were analyzed in full maturity stage. The differences in average values for all the studied traits among investigated cultivars were determined. The expressed variability of grain mass per spike estimated by coefficient of variation (CV) which value was CV=5.60%.

Key words: wheat, variability, grain mass, spike, yield.

INTRODUCTION

Wheat yield is the complex trait, depending from genetic and environmental factors and their interaction. Actually yield is a result of value of yield components as well: plant of height, number of productive tillers, number of spikelets spike^{-1}, number of grain spike^{-1}, grain mass spike^{-1}, number of spikes m^{-2}, thousand grain mass and other. Environmental factors as well levels of water, fertilizer, pesticide application play important role in wheat yield increasing (JOLÁNKAI *et al.*, 2006). Expression of genetic yields potential also, depending from genotype/environmental interaction. Environmental conditions (precipitation, drought, temperature) have influence to efficiency of fertility, grain filling, capacity of assimilation acceptors and translocation of assimilates from stalk and leaves to the grain (UŽIK & ŽOFAJOVÁ, 2006; KNEZEVIC *et al.*, 2007a). The main task of wheat breeding is to obtain genotypes possesing high genetically potential for yield. The genetic yield potential of a wheat cultivar may be dependent on favorable conditions and good agronomy for its expression (DREZNER *et al.*, 2006). The ideal cultivar for high grain yield

or for any other desirable traits needs to express genetic potential in different environment with low value of variance in different environmental factors of growing (ŠURLAN and KNEŽEVIĆ, 1993; JOSHI *et al.*, 2002). The grain yield of wheat is variable traits, which depends on numerous yield components and environmental factors (KRALJEVIC-BALALIC *et al.*, 2001). The characters as height of plants, length of spike, number of spikelets per spike are in positive correlation with grain yield (ZEČEVIĆ & KNEŽEVIĆ, 1998). Also positive correlation were established between spike lenght and number of fertile spikelets spike^{-1}, number of kernels spike^{-1}, grain mass spike^{-1}, and one thousand grain mass, while negative correaltion between lenght of spike and number of sterile spikelets (STOJANOVIĆ *et. al.*, 1998). Similar results were found in investigation of barley cultivars (MADIC *et al.*, 2006). Breeders permanently looking for efficient method of developing cultivars with improved yield. For that reason they should be include new genotypes in various cross combination in order to produce recombination of desirable genes. For breeder is very important to estimate genotype/environmental interactions through phenotypic variability. Also, important is estimate how efficiently a genotype can withstand the limiting environmental factors as well how efficiently genotype can utilize the favourable environmental factors (IVEZIĆ, 1994, KOVAČEVIĆ, 2007).

The aim of this paper is study of variability and components of phenotypic variance of grain mass spike^{-1}, in genetically divergent wheat genotypes.

MATERIALS AND METHODS

The variability of grain mass spike^{-1} and some yield components were studied in 10 Serbian wheat genopypes. For this investigation used cultivars KG-35265-1/94, KG-52, KG-3625/97, KG-3089/97, KG-3062/1-93, KG-4, KG-3617/98, KG-35171/94, KG-3419-3/97 and Pobeda. The seeds of cultivars were sown in basic plot 5 m^2. For analysis of grain mass spike^{-1} were used 60 plants in full maturity stage (20 plants/replication). The folowing parameters were computed: the average value (x); the variance (σ^2); the coefficient of variation (V) as an index of relative variability of the trait. The analysis of variance was performed and significant differences between the average value were estimated by F-test values.

RESULTS AND DISCUSSION

Analyzed wheat genotypes expressed differences of grain mass spike^{-1} values (Tab. 1). Grain mass spike^{-1}, i.e. grain productivity spike^{-1} has the highest impact in expression of genetic yield potential. The values of grain mass spike^{-1} ranged from $\bar{x}$= 2.23g for cultivar KG-3419-3/97 to $\bar{x}$= 2.92g, for KG-3625/97 cultivar (Table 1). Variability expressed by coefficient of variability (CV=4.67).

Yield is very important agroeconomics trait which will in the focus of investigation in the future. All the genotypes in study belonged to semi-dwarf wheat which have advantages in efficient utilization mineral elements for the head development and should be include in breeding programs (ZEČEVIĆ *et al.*, 2004). Also, translocation of mineral elements is more efficient in semidwarf cultivars from the vegetative organs to grain (DIMITRIJEVIĆ *et al*., 2000). Genotype reaction for grain mass spike^{-1} in interaction making phenotypic expression for this trait is difficult predictable.

Table 1. Average values of grain mass spike^{-1} (g) in winter wheat genotypes

	Cultivar	Grain mass per spike	Rank	Yield (kg ha^{-1})
1	KG-35265-1/94	2.76	3	5122.22
2	KG-52	2.84	2	5436.56
3	KG-3625/97	2.92	1	5615.60
4	KG-3089/97	2.57	6	5015.62
5	KG-3062/1-93	2.43	8	4365.56
6	KG-4	2.60	5	5167.78
7	KG-3617/98	2.38	9	4263.31
8	KG-35171/94	2.44	7	4302.24
9	KG-3419-3/97	2.23	10	3777.84
10	Pobeda	2.61	4	5154.42
	CV %	4.67		5.60

In this study wheat lines showed connection between grain mas spike^{-1} and grain yield, but it is not rule. So, lines with the highest grain yield ha^{-1} (KNEZEVIC *et al.*, 2007b) KG-3625/97 (5615.60 kg ha^{-1}) in this study expressed the highest value of grain mass spike^{-1} (2.92 g). Also, lines with the lowest grain yield ha^{-1} (KNEZEVIC *et al.*, 2007b) KG-3419-3/97 (3777.84 kg ha^{-1}) in this study expressed the lowest value of grain mass spike^{-1} (2.23 g). Yield is in negative correlation with quality, what represents main dificulties in efficient wheat breeding and developing enhanced cultivars with increased and stable grain yield (KNEZEVIC *et al.*, 2006). Investigation of biomass plant^{-1} and grain yield showed that both traits strongly influenced by genotype/environment interaction (GEI) i.e. by different sensitivity to soil moisture and maximum soil and air temperatures during different growth stages (DODIG *et al*., 2007).

The genotypes with the best values indicated possibility to select wheat genotypes which combine the desirable values for other yield components. On the base of phenotypic variability and stability is possible to identify which one could be involve in future wheat breeding. However, for successiful breeding and developing improved cultivars is necessary conduct investigation of big number of cultivars for better knowledge of interdependance genotypes and environment as well heritability of traits.

Table 2. Components of phenotipic variance for grain mass spike^{-1} in wheat (g)

Source of variance	Degree of freedom	Mean squere	Mean square	F-test	Comp. of variance		LSD	
					δ^2	%	0.01	0.05
Repeticions–R	2	0.27	0.136	9.39				
Cultivar – C	9	3.78	0.421	29.10	0.0442	71.53	1.72	1.29
Years – Y	2	0.01	0.005	0.32	0.0006	0.97	2.44	1.83
C x Y	18	0.42	0.023	1.60	0.0030	4.85	1.41	1.05
Error	58	0.84	0.014		0.0140	22.65		
					0.0618	100.00		

For analyzed genotypes grain mas spike^{-1} influenced by genetic components 51.53% while environmet (0.97%) and interaction genotype/environment (4.85%) had less influence (Tab. 2). The sensitivity of grain mass spike^{-1} under environmental variation noticed KRALJEVIĆ-BALALIĆ *et al.* (1982). The high impact of the genotype on the entire

phenotypic variance of grain mass spike^{-1} expression were found for cultivars from different countries (ZECEVIC & KNEZEVIC, 1998).

Phenotypic distance and similarity of studied genotypes were computed by cluster analysis. Average values of grain mass spike^{-1} were used for computing coeficient of similarity. Similarity presented in UPGMA (unweighted pair group of mathematics averages) dendogram. By analysis of dendogram we can find three group of wheat genotypes with the smallest distance 70.76%. Each gorup consists three genotypes. The most similar genotypes are KG-3061/1-93 and KG-3617/98. The genotypes KG 3419-3/97 is the most similar to previous two and those three genotypes represents first cluster of genotypes. Within second group there are also 3 genotypes KG/3089/97, KG-4 and Pobeda. Third group consists three very similar genotypes. Within this group more similar are lines KG-3625/97 and KG-53 and than with KG-35265-1/94. Among those group the most similar are first and second and those two group are less similar with third group. Genotype KG-3419-3/97 expressed the highest distance in relation to reamin 9 wheat genotypes (Fig. 1).

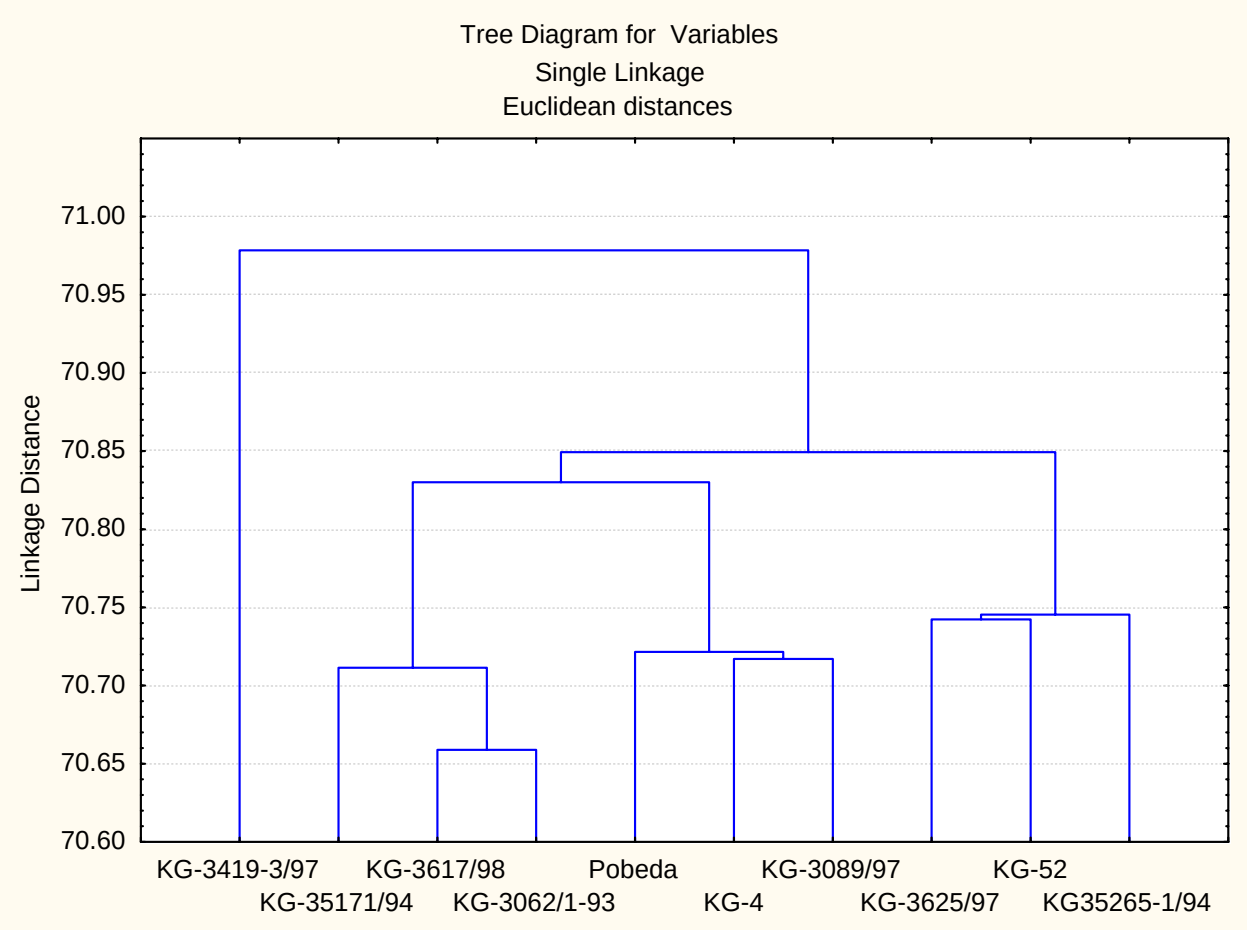

Figure 1. UPGMA Dendogram of analyzed wheat lines developed in Kragujevac obtained on the base coefficient of similarity of average grain mass spike^{-1} values

CONCLUSIONS

The analyzed wheat genotypes showed differences in average values for grain mass spike^{-1}. Generally speaking, analyzed genotypes reacted similarly to environmental variation for grain mass spike^{-1}. Phenotypic analysis of variance indicated that genetic factors had a higher influence (71.53%) to expression grain mass spike^{-1} in wheat than environmental factors. For prediction of yield is very important determination of genetic control grain mass spike^{-1} and other yield components as well investigation of influence of environmental factors and effects of genotype/environment interaction. Increasing of genetic potential of grain yield is possible achieve through increasing of size and capacity of spike. The long and fertile spike is one of the most important and promising direction in improvement of grain yield of wheat. For increasing grain mass spike^{-1} the important role have morphological and anatomical structure of plants and their organs.

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