

RESEARCH ARTICLE

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Inheritance of Spike Traits in F1 Generation in Wheat Depending on Parents' Genetic Diversity

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Abstract

The aim of research was to assess the inheritance of wheat spike length (SL), based on the parents diversity as genes donors, identification and determination the best cross combinations in the F1 generation, as well estimation of heterosis indicators as relation: parents/offspring (P1/F1 and P2/F1). Field trials were conducted during the years 2016/17 and 2017/18, at the Experimental Didactic Farm of the Faculty of Agriculture and Veterinary in Prishtina. Experimental design was a RCBD, with plot size 1m² in three replications. The experimental formula was: Parents (20-P) + F1-genotypes (10-GF1) x Replications (3-R) x Plants (10P) = 900 results. The mean genes value effect (μ) and genotype variation (gv) for (SL) were: for female parents set (P1) μ = 8.99cm spike⁻¹ and gv = ± 38.93 %, for the male parents set (P2) μ = 8.40cm spike⁻¹ and gv = ± 39.66 %, for mid-parent (MP), the μ value was 8.69cm spike⁻¹ and gv = ± 30.67 %; while for better parent (BP) μ = 9.31cm spike⁻¹ and gv = ± 37.61 %, and for F1 generation μ = 10.07cm spike⁻¹ and gv = ± 22.74 %. Magnitude of variation for heterosis (Ht) was 3.47 to 35.30% and for Hb was -11.39 to 28.57%. Through, cross combination of parents, it was possible to identify the superior genotypes in F1 generation: G5; G13 and G24 for SL (11.0cm spike⁻¹). The obtained results were with wide range variability and highly significant differences between parents and genotypes of the F1 generation, on the level of LSDp=0.05 and LSDp=0.01.

Keywords: Wheat, inheritance, parents, spike, F1-generation, heterosis.

1. Introduction

In principle wheat production is important in both terms: for grain and seed, due to the fact of its use for food and as reproduction material (Fetahu et al., 2017; 2019). Food production, in sufficient and high quality, healthy and economically reasonable, today is a challenge for mankind, but this challenge will be even greater in the future (Fetahu et al., 2013a; 2015a).

The precondition for developing of new genotypes with high production capacity, requires genetic distance among parents that participating in the breeding program (Martin et al. 1995; Morgan, 1998; Dedaniya et al., 2018). Parental impact in the development of new cultivars and the efficient identification of superior combinations is a fundamental issue in plant breeding programs (Morgan, 1998; Gowda et al., 2010). Therefore, it was suggested that the heterosis in relation to the better

parent could be useful to optimize heterozygous combination (Kant et al., 2011; Fetahu et al., 2015a). The crop cultivation and realized yield per unit area depends on the influence of factors such as: genotype, environment and applied agrotechnique from the moment of sowing until harvest, including the economic cost (Fetahu et al., 2014b). Information on genotype variability to environmental changes helps to predict the yield of cereals (Yong et al 2004; Fetahu et al., 2014a). Cultivar selection for a specific location is one of the essential challenges for improving yield for grain or seed, without increasing the cost of wheat production (Fetahu et al., 2013b; 2014b; 2019). The goal of each breeding program is to obtain high yielding cultivars and excellent quality, which meets market requirements (Williams et al. 2008). Hybridization is the crossing of two cultivars differing from each other in one or more characters to generate offspring with new desirable characters, as a result of genetic recombination. The hybrid of F1 generation is

superior over either parent for one or more characters, and it is known as hybrid vigor or heterosis (Fetahu et al., 2015a). From the perspective of the breeder, heterosis of superiority over BP, is more effective than heterosis of MP, particularly in the breeding of self-pollinating crops, when the objective is identification of superior genotypes in F1 generation (Fetahu et al., 2015a). The variability, heritability, and components of phenotypic variation for spike length are important for the cultivar creation, as it is recommended by Kraljevic-Balalic et al. (1995). Selection of parents with genetic diversity is the crucial stage from the standpoint of breeding programs in order to develop new genotypes having desirable characters. Therefore, the aim of the research was to assess the inheritance of wheat SL, based on the diversity of parents as genes donors, identification and determination of the best cross combinations in F1 generation, as well estimation of heterosis indicators as relation parents/offspring (F1/MP and F1/BP).

2. Material and Methods

2.1. Plant material and experimental design

Twenty parents with genotype diversity and variability were included in the combination and crossing program in order to obtain the hybrid generation in F1. Diversity of crossing parents, both with genotypes of F1 generation were: Jagger x Brea/F1-G5; Lira x Brea/F1-G7; Lorena x Brea/ F1-G12; Gabi/Boema x Gabi/F1-G13; Marina/Dora x Marina/F1-G14; Soys248 x Apach/F1-G16; Victoria/Mambo x Victoria/F1- G18; Lorena x Euclid/ F1- G19; Anica x Srpanjka/F1- G22 and Boema x Lutescens/F1-G24.

Field trials were conducted in randomized complete block design with three replications (RCBD) at Experimental Didactic Farm (EDF), Faculty of Agriculture and Veterinary (FAV) in Prishtina, located in geographical position: 42°38'97"N and 21°08'45"E, altitude of 570 m.a.s.l.

In the autumn of 2015, the seed of the parents were sown in plastic pots, under greenhouse conditions, while in May 2016, emasculation of female parents was done, and then crossings were realized. Then, hybrid genotypes obtained in F1, both with parents, were sown in micro-plots with 500 seeds per 1m² in autumn of 2016. During the growth period, normal agronomic and plant protection care was applied, except irrigation. Plant harvest was done during the summer of 2017 at full maturity stage, with maximum of 14% grain moisture.

2.2. Measurements

After harvesting, the spike length (SL) was determined in 10 plants, for parents P1, P2 and F1. After that, the spike length of the mid-parents (MP) and the better-parents (BP) is determined.

The experimental formula was: EF = 20-Parents + 10-GF1-Genotypes x 3-Replications x 10-Plants = 900 spikes. Heterosis indicators (Ht) and (Hb) are defined as percent increase or decrease of F1 genotype over MP as well as BP. The possible heterotic effects, was estimated according to formula of Fonseca and Patterson (1968):

$$Ht(\%) = \frac{F1 - MP}{MP} \times 100$$

$$Hb(\%) = \frac{F1 - BP}{BP} \times 100 \quad \text{(Fetahu et al., 2015b)}$$

$$gv(\%) = \frac{Xg - \mu}{\mu} \times 100$$

Where, *gv*-genotype variability; *Xg*-average genotype value, *μ*-mean value population; *Ht*-heterosis and *Hb*-heterosis for better parents.

2.2. Statistical analysis

The research data were subject of ANOVA, according to the program MINITAB-18©, while the significance is determined for the level of probability *P*₀₀₅ and *P*₀₀₁. The parent's variation P1; P2 and F1, as well as the effect of the parents and the interaction of P1/F1 and P2/F1 were calculated.

3. Results and Discussion

Spike length (SL), has been considered one of the most important contributing factors associated with increases of wheat yield that have occurred in the

modern plant breeding. Average results of our research and comparisons for general and genotype variation (gv) for P1; P2; F1; MP and BP are presented in (Table 1), while heterosis indicators for F1/Ht and F1/BP in Figure 1. The variance analysis for spike length shows differences among parental genotypes P1; P2 and F1; Parents x F1 interaction was also highly significant (Table 2). The significant difference indicates the existence of genetic variability among the parents that is precondition for cross breeding, as objective to obtain F1 genotypes with high heterosis (Ht) over MP and BP.

The average spike length for the parent's set P1 was $\mu P1 = 8.99\text{cm spike}^{-1}$. Among the parents with the maximal and minimal values, were cultivars: Lira with 10.5cm spike^{-1} and Victoria with 7.0cm spike^{-1} , the differences between them were 3.5cm spike^{-1} , and the interval of general variation was $gv = \pm 38.93\%$.

Cultivar Lira, compared with the $\mu P1$ value, had a longer spike for 1.51cm or $gv = +16.78\%$, while Victoria cultivar, had shorter spike for -1.99cm or $gv = -22.14\%$. The P2 parent set had average spike length of $\mu P2 = 8.40\text{cm spike}^{-1}$. While, the genotype Gabi / Brea had maximal length ($10.33\text{cm spike}^{-1}$), whereas cultivars: Victoria and Srpanjka, had minimal length or 7.0cm spike^{-1} , and the difference was 3.33cm or the

general variability of $gv = \pm 39.66\%$. The genotype Gabi/Brea compared to the $\mu P2$ value, had longer spikes $+1.93\text{cm}$ or $gv = 22.98\%$, while the cultivars Victoria and Srpanjka differed for -1.4cm spike^{-1} or $gv = -16.67\%$.

Average spike length for mid parent (MP) was $\mu MP = 8.69\text{cm spike}^{-1}$. Genotypes with maximal and minimal values were: G-16 with 9.67cm spike^{-1} , respectively G-7 with 7.0cm spike^{-1} , with a difference 2.67cm spike^{-1} or with general variability $gv = \pm 30.67\%$.

The combination, Soys248 x Apach/G-16, had longer spike for 0.97cm or $gv = 11.22\%$, respectively the combination Victoria/Mambo x Victoria/G18, was shorter for $-1.69\text{cm spike}^{-1}$ or $gv = -19.48\%$.

The average spike length for the better parent (BP) was $\mu BP = 9.31\text{cm spike}^{-1}$. The genotypes G-7 and G-18 differs between them for 3.5cm spike^{-1} , with a general variation interval of $\pm 37.61\%$. Genotype G-7, had longer spikes than μBP for 1.19cm or $gv = 12.82\%$ and genotype G-18, had shorter for -2.31cm or $gv = -24.79\%$.

Table 1. Spike length (cm) in F1

Nr.	P1	gv (%)	P2	gv (%)	MP	gv (%)	BP	gv (%)	F1	gv (%)
G-5	8.60	-4.34	7.66	-8.81	8.13	-6.44	8.60	-7.63	11.00	9.24
G-7	10.50	16.80	7.66	-8.81	9.08	4.49	10.50	12.78	10.00	-0.70
G-12	7.83	-12.9	7.66	-8.81	7.75	-10.87	7.83	-15.90	10.00	-0.70
G-13	9.83	9.34	8.50	1.19	9.17	5.47	9.83	5.59	11.00	9.24
G-14	9.66	7.45	9.33	11.07	9.50	9.26	9.66	3.76	10.00	-0.70
G-16	9.00	0.11	10.33	22.98	9.67	11.22	10.33	10.96	10.00	-0.70
G-18	7.00	-22.14	7.00	-16.67	7.00	-19.45	7.00	-24.81	9.00	-10.63
G-19	7.83	-12.90	9.66	15.00	8.75	0.63	9.66	3.76	10.00	-0.70
G-22	9.83	9.34	7.00	-16.67	8.42	-3.16	9.83	5.59	8.71	-13.51
G-24	9.83	9.34	9.16	9.05	9.50	9.26	9.83	5.59	11.00	9.24
μ	8.99		8.40		8.69		9.31		10.07	

The spikes of F1 generation were of average length $\mu F1 = 10.07\text{cm spike}^{-1}$, and exceeded the spike length of parents set P1 and P2. F1 genotypes, in relation to the $\mu P1$ values, were longer for 1.08cm spike^{-1} or genotype variation was $gv = 10.72\%$, whereas with $\mu P2$, the difference was 1.67cm spike^{-1}

or $gv = 16.58\%$. Three genotypes: G5/F1; G13/F1 and G24/F1, were 11.0cm long, while the G22/F1 genotype had a length of 8.71cm spike^{-1} , the difference between them was 2.29cm spike^{-1} , with a total variability of $\pm 22.74\%$. Genotype variability for G5/F1; G13/F1 and G24/F1, compared with $\mu F1$, the

difference was $+0.93\text{cm spike}^{-1}$ or $gv = 9.24\%$, while with G22/F1 genotype, the difference was $-1.36\text{cm spike}^{-1}$ and $gv = -13.51\%$.

The results for spike length are in agreement with data of Ullah et al. (2014), who reported results for spike length for the parents from 9.57 to 12.87cm, but not matched the results of Rasul et al. (2002), who reported $SL=15.50\text{cm}$ among parents. The similar results were obtained by Fetahu et al. (2008). In the studies of Bilgin et al. (2011) they obtained different results for SL at different wheat genotypes from 8.2 to 11.0cm. Among the F1 hybrids, the maximal spike length was 10.0cm, while the minimal spike length was 8.6cm. Our results are higher for genotypes of F1 generation. These results are also in accordance with Fetahu et al. (2014a; 2015b; 2016); Kant et al. (2011) and Mirza et al. (2017), but not with the results of Kondi et al. (2017) who reported shorter SL.

Heterosis (Ht and Hb): Results and effects of spike length inheritance for F1 generation, for

heterosis indicators: Ht/F1/MP and Hb/F1/BP are presented in Fig. 1. The magnitude of heterosis provides a basis for genetic diversity and guideline for the selection of desirable parents for the development of superior F1 hybrids in order to exploit the hybrid vigor and for building gene pool to be exploited in population improvement.

All genotypes of F1 generation exceeded MP values, and Ht had positive values with variation intervals of 3.47 to 35.30%, which is realized in genotypes G-16 and G-5. However, such an indicator did not identify all possible differences of MP and F1 values. The heterosis indicator Hb, as a BP/F1 ratio, identified two opposite directions of the inheritance for parents exceed for the spike length. The highest desirable heterosis of F1 generation, over BP, was recorded in cross breeding combination G-5 (Jagger x Brea) with $Hb=35.30\%$, while with negative Hb was the genotype G-22 (Anica x Srpanjka), with $Hb=-13.31\%$.

Table 2. The variance analysis for spike length in parents genotypes P1; P2 and F1

S. variation	Parental (P1 and P2)					F1 generation			
	d.f.	MS	F	LSD0.05	Lsd0.01	SS	F	LSD _{0.05}	LSD _{0.01}
Repition	2	0.175	0.41	/	/	0.0121	0.028	/	/
Tretmans	9	3.915	9.419**	1.1061	1.5152	1.717	4.025**	1.1207	1.5352
Error	18	0.415				0.4026			
Total	29								

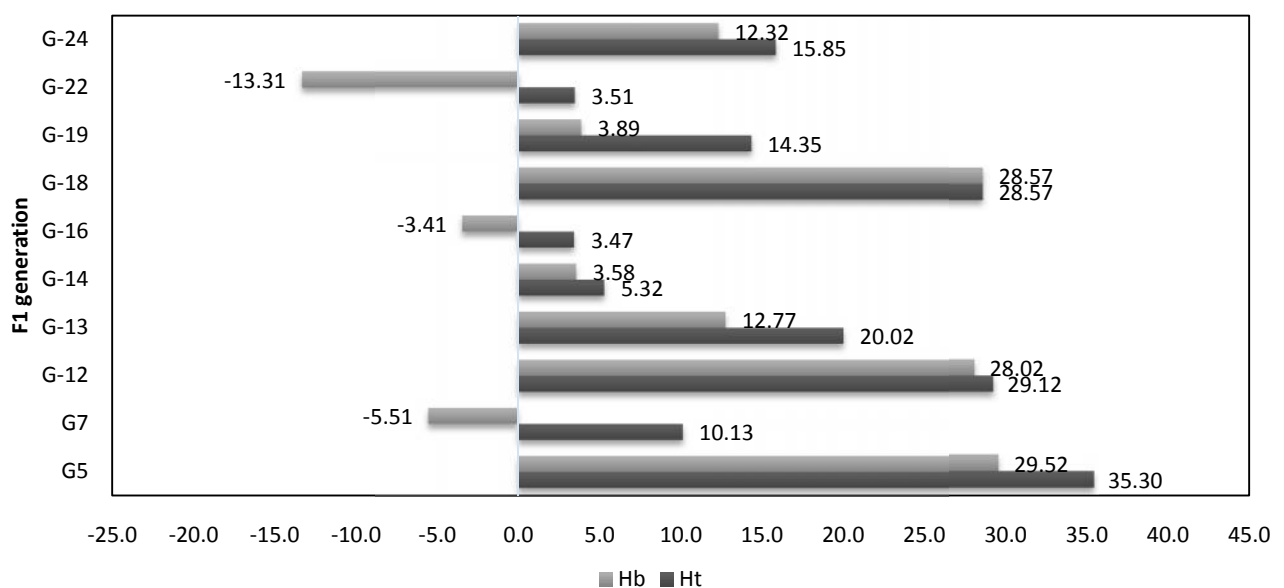


Figure 1. Heterosis inheritance

Table 3. The effect of inheritance from parents to the F1 generation

<i>P1 / F1</i>					
Sources of variation	d. f.	SS	F	LSD0.05	Lsd0.01
Blok	2	0.063	0.15	/	/
Parents (A)	9	3.869	9.54**	0.640	0.876
F1-generation (B)	1	12.97	31.98**	0.388	0.529
Interaction A x B	9	1.764	4.350 **	1.077	1.471
Total	59	0.405	/		
<i>P2/ F1</i>					
Blok	2	0.154	0.210	/	/
Parents (A)	9	4.075	5.54**	1.040	1.425
F1-generation (B)	1	40.671	157.85**	0.273	0.372
Interaction A x B	9	1.511	5.86**	1.205	1.648
Total	59	0.257	/		

Rasul et al. (2002), has reported positive results for heterosis over MP and over BP, with values of Ht = 7.42% and Hb = 6.24%, while our results are significantly higher. The positive heterosis for the spike length is a desirable trait, especially those that exceed BP. In their research Bilgin et al. (2011), reported magnitude of heterosis for SL over MP (8.77 to -18.18%) and BP (8.14 to -25.64%), similar to our research results.

Inamullah et al. (2006), for the Ht and Hb values, also reported different results (+19.11 and +16.2), while Zaazaa, et al. (2012), reported values of MP, Ht (15 to 20.59%) and Hb (13.02 to 19.60%)

4. Conclusions

The identification of the highly significant differences of genotype variation for the spike length and the heterosis indicators for the three sets (P1, P2 and F1), shows the presence of parental diversity, combination abilities through crossing (intraspecific hybridization), to create heterozygous organisms in generation F1, with hybrid vigour.

Research findings identified three superior hybrid genotypes in F1 generation: G-5; G-13 and G-24, obtained from the parents: Jagger x Brea; Gabi/Boema x Gabi and Boema x Lutescens.

Heterosis in relation to mid-parent (Ht/MP) was positive, while the Hb/BP ratio identified the heterosis with two-opposite directions. Therefore, Hb enable to identify parents who have better

combinations ability during crossing and expresses maximal heterosis.

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