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Original scientific paper

EVALUATION OF RECIPROCAL CROSS POPULATIONS FOR SPIKE-RELATED TRAITS IN EARLY CONSECUTIVE GENERATIONS OF BREAD WHEAT (*Triticum aestivum* L.)

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Breeding effort on increasing grain yield of wheat will incessantly continue because it is indispensable product. Obtaining the genetic information such as genotypic variation, heritability, genetic advance is the fundamental components of these studies. It is important that the maternal effects are put forward throughout successive generations because of genotypic and/or environmental effects as far as variation. This research was conducted to investigate changes of reciprocal crosses throughout successive generations and determine selection criteria for high yield in early generations. For this purpose, the populations were analyzed with regard to genotypic and phenotypic variation coefficient, heritability, genetic advance and Unweighted Pair Group Method (UPGMA) cluster analysis for real crosses, reciprocals and all genotypes separately. According to the results, heritability and genetic advance values of traits investigated were highly varied throughout successive generations among real crosses, reciprocals and all genotypes. This finding indicated that non-additive gen effects or epitasis played a role in inheritance of all traits. Dissimilarity of crosses than their reciprocals indicated variation of successive generation. Dissimilarity value of each parent differed as generation progresses according to combination created. This condition suggested that there were maternal effects in this population throughout successive generations. Grain weight per spike, spike harvest index and spike density had high direct and indirect effects on the grain yield at all of three generations, it proved that these traits can be a selection criterion for early generations.

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Sana was the best parent and ‘Bezostaja x Krasunia’ and ‘Krasunia x Pehlivan’ were best performance in most of traits at all generations.

*Keywords:*cluster analyses, early generation, genotypic effects, reciprocal crosses, spike traits

INTRODUCTION

Wheat has been defined as the king of cereals because it occupies large area in the world, has high productivity and keeps an important place in the international grain trade (SHASHIKALA, 2006). Since wheat is an indispensable crop, breeding studies about it remains important and these studies are still needed due to changing climate conditions and consumer demands. The main purpose of the wheat breeding is to develop high-yielding varieties. For development of high-yielding cultivars, complete information of the available genetic variation about yield and its components is a prerequisite. Knowledge of genetic variation could be obtained from classic variance analysis and some statistical parameters such as phenotypic and genotypic variance coefficients, heritability and genetic advance (CHEEMA *et al*., 2006).

Heritability is a significant parameter for achieving selection and predicting trait transferability to the next generations. However, it alone not adequate for acquire an idea about the expected gain in the next generation. Therefore, it is necessary combining with genetic advance estimates, the variation in mean value among consecutive generations (SHUKLA *et al*., 2006). Heritability and genetic advance offers opportunities for measuring the genetic differences, genetic potential and stability of each genotype (FIROUZIAN, 2003; IJAZ *et al*., 2013). Hence, the presence of actual genetic differences between genotypes in early generations and on their persistence following selection increases the chances of effective selection (ISLAM *et al*., 1985). Throughout the early generations, it is considerable to know whether there is adequate genetic variation in the population created and the traits that can be developed with especially selection intensity (KHAN *et al*., 2011).

For a successful and efficiency selection, there is great importance to analyses of variability among the traits and association of a particular character in relationship with other traits contributing to grain yield (MARY and GOPALAN, 2006). It has been considered that direct selection for grain yield should be applied instead of the indirect selection based one or more yield components (SMITH, 1976; CHANDRA *et al*., 2004). POEHLMAN (1987) reported that three main components are effective on grain yield as called from the spike number of plant, grain number of spike and grain weight of spike. Furthermore, spike characters such as spike length, number of grains and weight per spike and spikelet, spike index, spike density and plant yield influence of grain yield (BILGIN *et al*., 2011). Thus, it is possible to increase of grain yield via improving of these characters.

The effects of genotype and environment on the formation of phenotype should be compiled with information of maternal effects for the successful breeding program. Maternal effects which are based on the phenotypic performance can have a vigorous influence on the selection. Developing more effective breeding strategies and enhancing genetic gain can be provided by understanding the influence of maternal effects on selection (WOLF and WADE, 2009). Maternal effects are categorized as cytoplasmic genetic, endosperm nuclear and maternal phenotypic. Maternal effects might be occurred by any one or a combination of these stated. Different cytoplasmic effects might be masked each other however reappear in later generations (GILSINGER *et al*., 2010; FERFUIA and VANNOZZI, 2015). Although there were very research about genetic variations, heritability and genetic gain in later generations, no information was found about variation of reciprocal differences throughout successive generation. This research was conducted to find answers to the following questions:

i) How changed the potentials of the real crosses compared with their reciprocals and parents as generations progresses? ii) Which cultivars/crosses showed better performance during all generations? iii) Which traits can be selection criteria for high yield in early generations?

MATERIALS AND METHODS

Five bread wheat genotypes (Flamura 85, Sana, Krasunia, Bezostaja-1, Pehlivan) and their twenty crosses (ten real crosses and ten their reciprocals) were used as experimental material in this study. They were crosses grown in the form of population without any selection.

The experiment was performed in Namık Kemal University, Agricultural Faculty, Field Crops Department experimental area at 2009, 2010 and 2011 growing seasons. A randomized complete block design with four replicates was arranged for each trial. Genotypes were sown into plots which were adjusted 4 rows, 2 m long, spaced 20 cm apart and using a seeding rate of 500 seeds per m^2 at the mid-October each year by hand. The plots were fertilized with 80 kg P_2O_5 ha^{-1} at sowing and a total of 130 kg N ha^{-1} at sowing, tillering and pre-anthesis stages. Weeds were chemically controlled to avoid a confounding effect. Grain yield per plot, plant height and spike traits such as spike length, number of grain per spike, grain weight per spike, number of grain per spikelet, spike density and spike index were evaluated in three consecutive segregating populations (F_2, F_3 and F_4) in this study.

Variance analyse was calculated using randomized complete block design for all the examined traits. Genotypic and phenotypic variances were estimated using the mean squares according to JOHNSON *et al.* (1955). Heritability in broad sense was calculated according to FALCONER (1989). Phenotypic coefficient of variation and genotypic coefficient of variation were determined using the mean values for genetic analyses to according to SINGH and CHAUDHURY (1985). Genetic advance was calculated with the method suggested by SINGH and CHAUDHURY (1985) assuming K constant = 2.06 at 5% selection intensity. Phenotypic and genotypic correlations were estimated using the standard procedure suggested by MILLER *et al.* (1958) and KASHIANI and SALEH (2010) from the corresponding variance and covariance components. Path-coefficients were determined according to DEWEY and LU (1959) and LI (1986).

Above-mentioned all statistical analysis was performed writing necessary source code in R statistical package program, version 3.2.3. A dendrogram based on the genetic distance matrix was constructed using the Unweighted Pair Group Method (UPGMA). The groups were determined by the Euclidean dissimilarity method with IBM SPSS 20 software program.

RESULTS AND DISCUSSION

Descriptive Statistic, Variance Analyses and Genetic-Statistical Evaluation

Maximum and minimum values, mean values, variance analysis and genetic-statistical evaluation results of the traits examined in F_2 generations are presented in Table 1a and b. According to observation values, the best parents were Bezostaja-1 for plant height and spikelet number per spike; Krasunia for spike length and grain weight per spike; Sana for grain number per spikelet/spike, spike density and grain yield per plot. Among the real crosses, 'Bezostaja x Krasunia' and 'Krasunia x F85' had the best performance for many of traits (Table 1a).

Table 1a. Performance of 25 bread wheat genotypes in F_2 generations.

		PH	SL	SpNS	GNSp	GNS	GWS	SHI	SD	GY
Range	Parents	85.80-121.57	9.26-11.29	19.33-21.63	2.06-2.65	42.73-55.97	1.90-2.13	71.33-75.92	1.84-2.25	3.55-5.23
	Real Cross	92.40-119.13	9.76-11.54	19.20-22.07	2.11-2.64	43.57-56.23	1.87-2.65	70.83-78.43	1.80-2.14	3.51-5.21
	Reciprocal	85.97-119.43	9.93-11.84	19.83-21.73	2.18-2.81	42.30-55.70	1.93-2.53	72.78-76.48	1.74-2.18	3.90-5.43
Mean	Parents	104.58±5.79	10.37±0.37	20.45±0.42	2.30±0.10	47.50±2.43	2.04±0.05	73.79±0.78	1.99±0.07	4.71±0.30
	Real Cross	100.70±2.53	10.63±0.17	20.48±0.33	2.31±0.05	48.85±1.31	2.23±0.07	74.64±0.72	1.94±0.04	4.41±0.18
	Reciprocal	101.03±3.24	10.81±0.18	20.69±0.20	2.47±0.07	50.32±1.54	2.22±0.06	74.45±0.40	1.92±0.04	4.64±0.20
	All Genot.	101.61±1.94	10.65±0.12	20.56±0.17	2.37±0.04	49.17±0.92	2.19±0.04	74.40±0.35	1.94±0.03	4.56±0.12
Best Genotype	Parents	Bezostaja	Krasunia	Bezostaja	Sana	Sana	Krasunia	F85	Sana	Sana
	Real Cross	Bezostaja x Krasunia	Bezostaja x Krasunia	Bezostaja x Krasunia	Krasunia x F85	Krasunia x F85	Krasunia x F85	Krasunia x F85	Pehlivan x Sana	Sana x F85
	Reciprocal	Krasunia x Bezostaja	Krasunia x Pehlivan	Sana x Bezostaja	F85 x Sana	F85 x Sana	F85 x Pehlivan	F85 x Pehlivan	Sana x Pehlivan	Sana x Krasunia

PH: plant height, SL: spike length, SpNS: Spikelet number per spike, GNSp: Grain number per spikelet, GNS: Grain number per spike, GWS: grain weight per spike, SHI: Spike harvest index, SD: Spike density, GY: grain yield per parcel.

Performance of the reciprocal crosses varied greatly for the traits. ‘Krasunia x Bezostaja-1’, ‘Krasunia x Pehlivan’, ‘Sana x Bezostaja-1’, ‘F85 x Sana’, ‘F85 x Pehlivan’, ‘Sana x Pehlivan’ and ‘Sana x Krasunia’ combinations came into prominence with their performance (Table 1a). The result of variance analysis showed that all the traits examined were highly significant except for grain weight per spike and spike harvest index indicating the presence of sufficient variability for effective selection to identify potential genotypes. In addition, no significant variation was found for spike length among real crosses, and for spikelet number per spike among reciprocal crosses (Table 1b).

The progress of a breeding program is conditioned by the degree and the nature of the genotypic and phenotypic variation in the different traits (DEGEWIONE *et al.*, 2013). The genotypic variances for plant height and grain number per spike were high. Therefore, it can be said that the phenotype reflected the genotype and the selection based on the phenotypic performance for these traits would be effective. Because there were low genotypic variance both real crosses and reciprocals in other traits, it would be unsuccessful the selection depend on phenotype in the F_2 generation. To provide better information than each parameter should be evaluated not only high heritability and genetic advance but also high genotypic coefficients of variation (SINGH *et al.*, 2015). PRAMODA and GANGAPRASAD (2007), classified broad sense heritability values as low (<0.40), medium (0.40-0.59), moderately high (0.60-0.79), and very high (≥0.80). In addition, DESHMUKH *et al.* (1986), defined PCV and GCV values as high (>20%), medium (10-20%) and low (<10%). According to Table 1b, low broad sense heritability values were found in spike length, spikelet number per spike, grain weight per spike and spike harvest index for all genotypes.

When the real crosses and their reciprocals were evaluated separately, it was seen that plant height, grain number per spike and spike harvest index had low heritability. At the same time, genetic advance values were found low for all traits. On the other hand, high phenotypic coefficient of variation and genotypic coefficient of variation values were found both real crosses and their reciprocals for grain number per spikelet, grain weight per spike, spike density and grain yield per plot, although these values were low for evaluation of all genotype. The genotypic coefficient of variation for the all traits examined was less than the phenotypic coefficient of variation (Table 1b). The reason of this result was role of environment is dominant in the expression of these traits. KHAN *et al.* (2013) and HAKIM *et al.* (2014) determined to low heritability, genetic advance and genotypic coefficient of variance for these traits while KHAN *et al.* (2003), HUSSAIN *et al.* (2013), WAQAS *et al.* (2014), VERMA *et al.* (2013) attained to high values unlike our results.

Table 1b. Genetic variability of 25 bread wheat genotypes in F_2 generations

		PH	SL	SpNS	GNSp	GNS	GWS	SHI	SD	GY
F values	Parents	31,83**	4,54**	3,09*	4,21**	6,25**	0,36ns	0,94ns	5,87**	7,60**
	Real Cross	12,14**	1,90ns	3,86**	2,23*	3,64**	1,57ns	1,62ns	2,64*	5,30**
	Reciprocal	20,00**	2,12*	1,41ns	3,74**	5,02**	1,09ns	0,51ns	3,93**	6,51**
	All Genot,	17,80**	2,43**	2,53**	3,45**	4,54**	1,26ns	0,99ns	3,60**	5,97**
σ^2G	Real Cross	4,05	0,63	1,29	0,74	1,21	0,52	0,54	0,88	1,77
	Reciprocal	6,67	0,71	0,47	1,25	1,67	0,36	0,17	1,31	2,17
	All Genot,	88,48	0,22	0,44	0,03	16,64	0,01	0,05	0,01	0,3
σ^2P	Real Cross	19,85	1,09	2,14	0,78	15,33	0,61	10,12	0,89	1,95
	Reciprocal	22,47	1,16	1,32	1,28	15,79	0,45	9,75	1,32	2,35
	All Genot,	104,28	0,67	1,29	0,07	30,76	0,09	9,63	0,03	0,48
$H^2_{b,s}$	Real Cross	0,2	0,58	0,6	0,95	0,08	0,86	0,05	0,98	0,91
	Reciprocal	0,3	0,61	0,36	0,97	0,11	0,81	0,02	0,99	0,92
	All Genot,	0,85	0,32	0,34	0,45	0,54	0,08	0,01	0,46	0,62
EGA	Real Cross	1,87	1,25	1,82	1,73	0,64	1,38	0,35	1,92	2,61
	Reciprocal	2,9	1,35	0,84	2,26	0,87	1,12	0,11	2,35	2,92
	All Genot,	17,85	0,55	0,79	0,25	6,18	0,05	0,03	0,15	0,89
GCV	Real Cross	4,42	9,82	7,14	38,31	8,01	35,01	4,26	48,83	31,64
	Reciprocal	2	7,48	5,55	37,33	2,25	32,43	0,98	48,45	30,13
	All Genot,	9,26	4,39	3,21	7,57	8,3	3,98	0,3	5,64	12,04
PCV	Real Cross	4,69	9,99	5,56	45,89	7,9	30,31	4,19	59,9	33,06
	Reciprocal	2,56	7,79	3,32	45,18	2,57	27,25	0,55	59,59	31,76
	All Genot,	10,05	7,71	5,52	11,3	11,28	14,02	4,17	8,27	15,25

σ^2G: Genotypic variance, σ^2P: Phenotypic variance, $H^2_{b.s}$: Broad sense heritability, EGA: Expected genetic gain, GCV: Genotypic variability coefficient, PCV: Phenotypic variability coefficient, PH: plant height, SL: spike length, SpNS: Spikelet number per spike, GNSp: Grain number per spikelet, GNS: Grain number per spike, GWS: grain weight per spike, SHI: Spike harvest index, SD: Spike density, GY: grain yield per parcel.

When Table 2a examined, the highest mean values were observed in reciprocal crosses for plant height, spike length, spikelet number per spike, spike harvest index and in parents for grain number per spikelet, grain number per spike, grain weight per spike, spike density, grain yield per plot in F_3 generations. Krasunia and Sana; 'Bezostaja-1 x Krasunia' and 'Sana x F85'; 'Sana x Krasunia' and 'Krasunia x Pehlivan' were the best genotype among parents, real crosses and reciprocals respectively (Table 2a). According to variance analyses, there was adequate variation among genotypes to evaluate genetic differences. However, differences of parents were not significant for grain number per spikelet and spike harvest index. There were not significant differences among crosses for spike length, grain number per spikelet and grain weight per spike (Table 2b). Genotypic and phenotypic variances were high only for plant height and grain number per spike. High broad sense heritability was found in plant height, spikelet number per spike, spike density and grain yield per plot. When real crosses and reciprocals were evaluated separately, higher heritability was obtained from spike length, spikelet number per spike, grain number per spikelet, grain weight per spike, spike density and grain yield per plot. Genotypic coefficient of variance was smaller than phenotypic coefficient of variance for all traits examined. Nevertheless, genotypic coefficient of variance was bigger than phenotypic coefficient of variance for plant height, spikelet number per spike, grain number per spikelet and grain weight per spike in the assessment separately (Table 2b). For these traits, this variation observed among the crosses and their reciprocals may be caused from 'cytoplasm and nucleus' interaction. Because, their heritability and genetic advance were higher than all genotype evaluation, especially for reciprocal crosses.

Table 2a. Performance of 25 bread wheat genotypes in F_3 generations.

		PH	SL	SpNS	GNSp	GNS	GWS	SHI	SD	GY
Range	Parents	79.17-113.73	8.33-10.46	19.50-22.30	2.17-2.91	44.23-57.90	1.87-2.77	68.95-74.73	1.93-2.45	3.30-5.29
	Real Cross	91.37-113.33	9.11-10.62	18.40-22.83	2.33-2.81	43.33-55.93	1.75-2.27	67.23-76.32	1.82-2.37	3.87-5.18
	Reciprocal	83.40-114.07	9.15-10.35	18.63-23.40	2.16-2.78	46.07-59.43	1.97-2.68	69.26-80.57	1.85-2.35	3.39-5.37
Mean	Parents	91.18±6.09	9.65±0.36	20.56±0.51	2.54±0.12	52.11±2.71	2.22±0.16	72.62±1.09	2.13±0.09	4.63±0.36
	Real Cross	98.24±2.08	9.71±0.16	20.33±0.44	2.45±0.05	46.91±1.12	2.04±0.05	72.15±0.85	2.09±0.06	4.56±0.15
	Reciprocal.	100.69±2.98	9.71±0.13	20.59±0.49	2.49±0.07	50.44±1.53	2.21±0.07	73.96±1.11	2.12±0.05	4.48±0.20
	All Genot.	97.81±1.93	9.69±0.10	20.48±0.27	2.48±0.04	49.36±0.98	2.14±0.05	72.97±0.60	2.11±0.03	4.54±0.12
Best Genotype	Parents	Bezostaja	Krasunia	Krasunia	Sana	Sana	Krasunia	Sana	Sana	Sana
	Real Cross	Bezostaja x Krasunia	Bezostaja x Krasunia	Bezostaja x Krasunia	Sana x F85	Sana x F85	Krasunia x F85	Sana x F85	Sana x F85	Pehlivan x Krasunia
	Reciprocal	Krasunia x Bezostaja	Krasunia x Pehlivan	Krasunia x Pehlivan	Sana x Krasunia	Sana x Krasunia	Sana x Krasunia	F85 x Krasunia	Sana x Krasunia	Sana x Pehlivan

PH: plant height, SL: spike length, SpNS: Spikelet number per spike, GNSp: Grain number per spikelet, GNS: Grain number per spike, GWS: grain weight per spike, SHI: Spike harvest index, SD: Spike density, GY: grain yield per parcel.

Table 2b. Genetic variability of 25 bread wheat genotypes in F_3 generations

		PH	SL	SpNS	GNSp	GNS	GWS	SHI	SD	GY
F values	Parents	43,22**	5,40**	5,75**	2,52ns	3,83**	3,39*	1,66ns	6,61**	14,97**
	Real Cross	10,11**	2,04ns	8,31**	0,84ns	1,31ns	0,78ns	2,01ns	5,81**	5,27**
	Reciprocal	20,61**	1,50ns	10,29**	1,52ns	2,42*	1,40ns	3,44**	4,80**	9,36**
	All Genot,	21,67**	2,23**	8,00**	1,34ns	2,51**	1,60ns	2,52**	5,14**	8,06**
σ^2G	Real Cross	3,37	0,68	2,77	0,28	0,44	0,26	0,67	1,94	1,76
	Reciprocal	6,87	0,5	3,43	0,51	0,81	0,47	1,15	1,6	3,12
	All Genot,	88,84	0,15	1,6	0,01	14,53	0,02	0,05	0,02	0,31
σ^2P	Real Cross	16,26	1,04	3,46	0,37	29,29	0,37	11,44	1,95	1,89
	Reciprocal	19,76	0,86	4,12	0,6	29,67	0,57	11,91	1,62	3,25
	All Genot,	101,73	0,51	2,29	0,1	43,39	0,13	10,82	0,04	0,44
H^2 b,s	Real Cross	0,21	0,65	0,8	0,75	0,01	0,71	0,06	0,99	0,93
	Reciprocal	0,35	0,58	0,83	0,85	0,03	0,81	0,1	0,99	0,96
	All Genot,	0,87	0,29	0,7	0,1	0,33	0,17	0	0,58	0,7
EGA	Real Cross	1,72	1,37	3,07	0,95	0,17	0,89	0,41	2,85	2,63
	Reciprocal	3,18	1,11	3,48	1,35	0,31	1,27	0,68	2,59	3,56
	All Genot,	18,14	0,43	2,18	0,07	4,55	0,12	0,03	0,24	0,96
GCV	Real Cross	4,42	9,57	9,85	31,11	10,8	34,25	4,67	59,81	40,26
	Reciprocal	2,6	7,3	8,99	28,61	1,78	30,87	1,45	59,49	39,45
	All Genot,	9,64	3,97	6,18	4,14	7,72	6,84	0,31	7,29	12,19
PCV	Real Cross	4,1	10,5	9,14	24,9	11,54	29,82	4,69	66,84	30,11
	Reciprocal	1,87	8,48	8,18	21,6	1,41	25,09	1,14	66,54	29,05
	All Genot,	10,31	7,36	7,39	12,9	13,34	16,77	4,51	9,57	14,55

σ^2G: Genotypic variance, σ^2P: Phenotypic variance, $H^2_{b,s}$: Broad sense heritability, EGA: Expected genetic gain, GCV: Genotypic variability coefficient, PCV: Phenotypic variability coefficient, PH: plant height, SL: spike length, SpNS: Spikelet number per spike, GNSp: Grain number per spikelet, GNS: Grain number per spike, GWS: grain weight per spike, SHI: Spike harvest index, SD: Spike density, GY: grain yield per parcel.

Mean values of crosses and reciprocals were found higher than their parents for plant height, spike length and spikelet number per spike in F_4 generation (Table 3a). Among all genotypes, the highest values were gained from 'Bezostaja-1 x Krasunia' for plant height, spike length, spikelet number per spike; 'Krasunia x Pehlivan' for grain number per spikelet and spike; Sana for grain weight per spike, spike harvest index, spike density and grain yield per plot (Table 3a). Differences were not significant among parents for grain number per spikelet and spike; among real crosses for spike harvest index and spike density; among reciprocals for grain number per spikelet, grain weight per spike, spike harvest index, spike density and grain yield per plot.

Nonetheless, there was adequate variation among all genotypes to calculate genetic-statistical parameters (Table 3b). Genotypic and phenotypic variance was very low for all traits except plant height, grain number per spike and spike harvest index. Medium heritability was observed in spike length, spikelet number per spike and grain yield per plot at F_4 generation. The heritability of plant height was moderately high (Table 3b). Genetic advance values were found low for all traits. Phenotypic coefficient of variation was higher than genotypic coefficient of variation. These results indicated that environmental effects predominated for all traits in F_4 generations.

Table 3a. Performance of 25 bread wheat genotypes in F_4 generations.

		PH	SL	SpNS	GNSp	GNS	GWS	SHI	SD	GY
Range	Parents	76,83-108,97	8,43-9,70	20,23-22,63	1,77-2,26	36,53-48,50	1,72-2,34	66,87-78,67	2,09-2,58	3,92-5,92
	Real Cross	89,40-115,47	8,59-10,67	20,57-23,43	1,65-2,28	34,30-48,60	1,71-2,34	68,41-75,56	2,11-2,45	3,96-5,63
	Reciprocal	81,63-112,77	8,32-10,45	19,07-23,33	1,72-2,32	28,36-53,87	1,86-2,24	66,35-75,89	2,00-2,35	4,44-5,55
Mean	Parents	93,90±5,80	9,27±0,23	20,98±0,42	2,00±0,08	42,79±2,23	2,06±0,11	72,89±1,89	2,25±0,09	5,24±0,37
	Real Cross	97,53±2,42	9,29±0,22	21,39±0,26	1,88±0,06	40,72±1,84	2,01±0,06	71,63±0,93	2,30±0,04	4,91±0,18
	Reciprocal	96,09±3,33	9,53±0,18	21,14±0,39	2,01±0,06	41,34±2,19	2,05±0,04	71,53±1,00	2,22±0,04	5,11±0,11
	All Genot,	96,23±1,93	9,38±0,12	21,21±0,20	1,95±0,04	41,38±1,19	2,04±0,03	71,84±0,64	2,26±0,03	5,06±0,11
Best Genotype	Parents	Bezostaja	Krasunia	Sana	F85	F85	Sana	Sana	Sana	Sana
	Real Cross	Bezostaja x Krasunia	Bezostaja x Krasunia	Bezostaja x Krasunia	Krasunia x F85	Krasunia x F85	Krasunia x F85	Bezostaja x Pehlivan	Bezostaja x Sana	Pehlivan x F85
	Reciprocal	Krasunia x Bezostaja	Krasunia x Pehlivan	Krasunia x Pehlivan	Krasunia x Pehlivan	Krasunia x Pehlivan	Krasunia x Pehlivan	Sana x Krasunia	Sana x Bezostaja	Sana x Krasunia

PH: plant height, SL: spike length, SpNS: Spikelet number per spike, GNSp: Grain number per spikelet, GNS: Grain number per spike, GWS: grain weight per spike, SHI: Spike harvest index, SD: Spike density, GY: grain yield per parcel.

If Table 1, 2 and 3 were evaluated together, it seemed clearly that all traits examined had variation according to generations. Sana was the best parent in all of three generations, and 'Bezostaja x Krasunia' and 'Krasunia x Pehlivan' were best performance in most of traits at all generations. Heritability and genetic advance values either remained the same degree or increased in plant height, grain weight per spike and spike harvest index throughout successive generations. However, they showed differences among real crosses, reciprocals and all genotypes evaluations. So, it may be said that additive and maternal gen effects were prominent for these traits. Heritability and genetic advance of other traits investigated were decreased or undulated throughout successive generations**.** This condition was suggested that non-additive gen effects or epitasis played a role in inheritance of these traits. These results signified that leaving of selection in later generations would be sagacious. AHMED *et al.* (2007), KOTAL *et al*. (2010) and LALIC *et al*. (2010) stated that the selection should be leaved to later generations for spike length, spikelet number per spike, grain number per spikelet and spike, spike density traits.

Maternal effects are heritable and are normally detected in each successive generation of inbreeding in self-pollinated generations. However, if there were cytoplasmic x nuclear genetic effects, these effects might be disappeared and reappeared later generations. In the present of cytoplasmic effects, among reciprocal crosses occur significant differences in each successive self-pollinated generation (FERFUIA and VANNOZZI, 2015**)**. This information was supported that differences among real crosses and reciprocals for mean observation values, genotypic/phenotypic variance, degree of heritability and genetic advance values. Moreover, these differences were varied each successive generation and indicated significant differences among reciprocal crosses.

Table 3b. Genetic variability of 25 bread wheat genotypes in F_4 *generations*

		PH	SL	SpNS	GNSp	GNS	GWS	SHI	SD	GY
F values	Parents	20,15**	2,85*	3,06*	2,04ns	2,01ns	5,30**	3,13*	5,08**	7,89**
	Real Cross	6,98**	5,12**	2,31*	2,72*	2,73*	2,62*	1,52ns	1,76ns	3,71**
	Reciprocal	13,27**	3,37**	5,13**	2,04ns	3,90**	1,13ns	1,74ns	2,05ns	1,39ns
	All Genot,	11,17**	3,82**	3,38**	2,36**	2,87**	2,33**	1,79*	2,41**	3,45**
σ^2G	Real Cross	4,42	1,12	1,72	0,68	1,3	0,38	0,58	0,68	0,46
	Reciprocal	1,35	0,25	0,36	0,24	0,34	0,12	0,4	0,005	0,87
	All Genot,	84,99	0,27	0,7	0,02	23,1	0,02	4,52	0,01	0,21
σ^2P	Real Cross	29,49	1,41	2,6	0,73	38,32	0,41	17,7	0,71	0,72
	Reciprocal	26,42	0,54	1,24	0,28	37,35	0,15	17,52	0,03	1,13
	All Genot,	110,06	0,55	1,58	0,07	60,11	0,05	21,65	0,03	0,47
$H^2{}_{b,s}$	Real Cross	0,15	0,8	0,66	0,94	0,03	0,91	0,03	0,97	0,64
	Reciprocal	0,05	0,47	0,29	0,84	0,01	0,76	0,02	0,17	0,77
	All Genot,	0,77	0,48	0,44	0,31	0,38	0,31	0,21	0,32	0,45
EGA	Real Cross	1,68	1,95	2,19	1,64	0,43	1,21	0,28	1,67	1,13
	Reciprocal	0,54	0,71	0,66	0,92	0,11	0,61	0,2	0,06	1,69
	All Genot,	16,69	0,74	1,15	0,17	6,14	0,15	2	0,12	0,63
GCV	Real Cross	5,35	7,71	5,26	26,63	14,78	19,08	5,85	7,49	20,77
	Reciprocal	1,21	5,29	2,82	24,34	1,4	16,59	0,88	3,05	18,25
	All Genot,	9,58	5,52	3,96	7,47	11,61	6,31	2,96	4,63	9,04
PCV	Real Cross	5,57	12,78	7,53	45,34	15,2	31,99	5,87	36,58	17,31
	Reciprocal	2,16	11,41	6,13	43,85	2,8	30,52	1,06	35,98	13,89
	All Genot,	10,9	7,93	5,93	13,37	18,74	11,39	6,48	8,17	13,49

σ^2G: Genotypic variance, σ^2P: Phenotypic variance, $H^2{}_{b,s}$: Broad sense heritability, EGA: Expected genetic gain, GCV: Genotypic variability coefficient, PCV: Phenotypic variability coefficient, PH: plant height, SL: spike length, SpNS: Spikelet number per spike, GNSp: Grain number per spikelet, GNS: Grain number per spike, GWS: grain weight per spike, SHI: Spike harvest index, SD: Spike density, GY: grain yield per parcel.

Cluster Analyse

Dissimilarity values for reciprocals presented in Table 4. 'Pehlivan x Krasunia' showed the most dissimilarity than its reciprocals as a mean all generations. 'Krasunia x F85' followed it. Dissimilarity values increased for ‘Krasunia x F85’ and ‘Pehlivan x Sana’ crosses, while decreased ‘Pehlivan x F85’, ‘Bezostaja-1 x F85’ and ‘Bezostaja-1 x Krasunia’ crosses. Declining dissimilarity value in F_3 increased in F_4 for 'Pehlivan x Krasunia' cross. The others dissimilarity values decreased in F_3 generation, and then increased in F_4 generation unlike of this cross (Table 4).

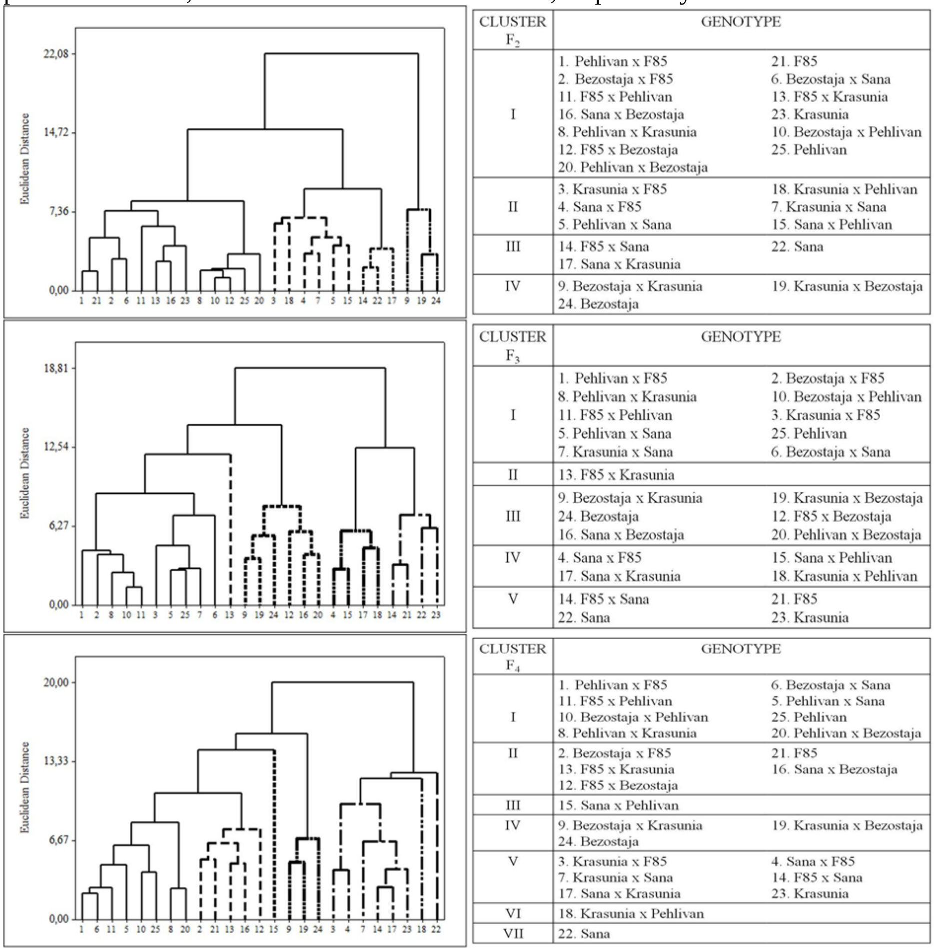
Table 4. Dissimilarity values for reciprocals.

Genotype	F_2	F_3	F_4
Pehlivan x F85	8.676	4.234	2.620
Bezostaja x F85	8.306	8.189	7.321
Krasunia x F85	10.800	12.368	12.883
Sana x F85	8.369	13.311	10.888
Pehlivan x Sana	4.239	10.706	11.674
Bezostaja x Sana	7.341	13.134	7.172
Krasunia x Sana	6.179	12.337	6.612
Pehlivan x Krasunia	18.110	13.651	27.736
Bezostaja x Krasunia	6.529	3.695	4.835
Bezostaja x Pehlivan	4.101	6.398	5.857

Table 5. Dissimilarity values of each cross from its parents.

Genotype	F_2		F_3		F_4	
	♀	♂	♀	♂	♀	♂
Pehlivan x F85	7.641	1.819	7.325	17.949	4.668	13.674
F85 x Pehlivan	7.606	12.366	18.556	8.575	11.805	4.315
Bezostaja x F85	22.278	4.872	14.385	16.679	12.465	5.057
F85 x Bezostaja	6.515	15.223	22.514	9.847	7.474	7.565
Krasunia x F85	15.210	11.551	14.980	11.418	10.988	8.105
F85 x Krasunia	5.618	4.864	20.394	22.250	7.190	18.607
Sana x F85	9.229	10.586	16.100	10.917	14.591	9.769
F85 x Sana	17.923	2.200	3.266	8.516	19.232	8.123
Pehlivan x Sana	13.146	12.773	2.754	16.357	6.886	21.873
Sana x Pehlivan	13.108	12.896	18.698	9.574	25.638	11.098
Bezostaja x Sana	22.481	16.540	18.937	22.645	14.722	24.392
Sana x Bezostaja	20.661	17.776	30.193	7.955	24.778	11.067
Krasunia x Sana	15.748	9.853	12.739	16.997	5.366	14.591
Sana x Krasunia	4.748	20.676	12.421	7.321	8.195	4.501
Pehlivan x Krasunia	1.994	6.140	6.842	19.669	6.152	20.898
Krasunia x Pehlivan	16.440	19.321	9.268	10.870	13.540	23.350
Bezostaja x Krasunia	8.722	12.290	6.475	31.103	8.660	31.789
Krasunia x Bezostaja	12.445	3.427	31.664	4.550	28.812	5.090
Bezostaja x Pehlivan	16.165	2.159	11.493	9.857	12.963	3.955
Pehlivan x Bezostaja	2.819	12.929	15.865	5.597	5.729	8.402

Increasing dissimilarity values among parents indicate that there were a great number of contrasting alleles at the desired loci. In a cross of distantly related parents, these loci recombine in the subsequent F_2 and F_3 generations and wide range of variability in these segregating populations reveal (HAILEGIORGIS *et al*., 2011). If dissimilarity of a cross is more than its parents, it means that there is an adequate variability in the populations. Dissimilarity of each cross from its parents is presented in Table 5. Dissimilarity of crosses than that of their parents indicated that variation both among reciprocal crosses and successive generations. Each parent had different dissimilarity value according to combination created and this value differed as generation progresses (Table 5). This condition may be due to the changes in the distribution of alleles from parents. Moreover, the parents contributed differently on their crosses as male or female. This finding indicated that there were maternal effects in this population throughout successive generations. It might be considered that the parents which have lower dissimilarity value have the ability of transfer to offspring its property. According to combinations created, Bezostaja-1, Krasunia and Pehlivan were a best parents as a male, female and either male or female, respectively.



CLUSTER F_2	GENOTYPE	
I	1. Pehlivan x F85 2. Bezostaja x F85 11. F85 x Pehlivan 16. Sana x Bezostaja 8. Pehlivan x Krasunia 12. F85 x Bezostaja 20. Pehlivan x Bezostaja	21. F85 6. Bezostaja x Sana 13. F85 x Krasunia 23. Krasunia 10. Bezostaja x Pehlivan 25. Pehlivan
II	3. Krasunia x F85 4. Sana x F85 5. Pehlivan x Sana	18. Krasunia x Pehlivan 7. Krasunia x Sana 15. Sana x Pehlivan
III	14. F85 x Sana 17. Sana x Krasunia	22. Sana
IV	9. Bezostaja x Krasunia 24. Bezostaja	19. Krasunia x Bezostaja

CLUSTER F_3	GENOTYPE	
I	1. Pehlivan x F85 8. Pehlivan x Krasunia 11. F85 x Pehlivan 5. Pehlivan x Sana 7. Krasunia x Sana	2. Bezostaja x F85 10. Bezostaja x Pehlivan 3. Krasunia x F85 25. Pehlivan 6. Bezostaja x Sana
II	13. F85 x Krasunia	
III	9. Bezostaja x Krasunia 24. Bezostaja 16. Sana x Bezostaja	19. Krasunia x Bezostaja 12. F85 x Bezostaja 20. Pehlivan x Bezostaja
IV	4. Sana x F85 17. Sana x Krasunia	15. Sana x Pehlivan 18. Krasunia x Pehlivan
V	14. F85 x Sana 22. Sana	21. F85 23. Krasunia

CLUSTER F_4	GENOTYPE	
I	1. Pehlivan x F85 11. F85 x Pehlivan 10. Bezostaja x Pehlivan 8. Pehlivan x Krasunia	6. Bezostaja x Sana 5. Pehlivan x Sana 25. Pehlivan 20. Pehlivan x Bezostaja
II	2. Bezostaja x F85 13. F85 x Krasunia 12. F85 x Bezostaja	21. F85 16. Sana x Bezostaja
III	15. Sana x Pehlivan	
IV	9. Bezostaja x Krasunia 24. Bezostaja	19. Krasunia x Bezostaja
V	3. Krasunia x F85 7. Krasunia x Sana 17. Sana x Krasunia	4. Sana x F85 14. F85 x Sana 23. Krasunia
VI	18. Krasunia x Pehlivan	
VII	22. Sana	

Figure 1. Dendorgram of 25 bread wheat genotypes based on nine traits and their distribution into different clusters

Cluster diagram based on Euclidean dissimilarity using average linkage method clearly demonstrated the wide diversity changed throughout generations. The cluster analysis showed clear separation in variable groups between the F_2, F_3 and F_4 genotypes in the studied traits (Figure 1). The F_2 genotypes were categorized into four clusters at 22% linkage distance, cluster I consisted thirteen genotypes, cluster II six and cluster III and IV three genotypes each. Most of crosses located the same cluster with its parent. 'Pehlivan x Krasunia', 'Krasunia x F85', 'Sana x F85' and 'Krasunia x Sana' were presented in divergent groups than their reciprocals (Figure 1). The 25 wheat genotypes were grouped into five clusters in F_3 generations. All crosses except 'Bezostaja x Krasunia' and 'Pehlivan x F85' formed a wide group having divergent distance from their reciprocals and these two crosses with their reciprocals appeared to be nearly identical (Figure 1). In F_4 generations, the cluster I contained eight genotypes, followed by cluster V with six genotypes, cluster II with five genotypes and cluster IV with three genotypes. The cluster III, VI and VII were mono-genotypic. 'Pehlivan x Krasunia', 'Krasunia x F85', 'Bezostaja-1 x Sana' and 'Pehlivan x Sana' were presented in divergent groups than their reciprocals (Figure 1). These changes occurred in the group of genotypes as progressed generations might be based on enhancement the number of loci segregation in the subsequent inbred generations. At the same time, it might be considered that the environmental factors were effective because the parental genotypes were presented different cluster.

Correlations

Correlation studies are important in determining the degree of association of various yield contributing parameters with grain yield (KHAN *et al*., 2013). Comprehension of their direct positive and negative effects is vital importance for selection of high yielding genotypes and adopting suitable selection strategy (SALEHI *et al.,* 2013). Genotypic correlation coefficient represents a measure of the genetic relationship between traits and may supply an important criterion of the selection methods (GOLPARVAR *et al.*, 2015). The genotypic and phenotypic correlations at F_2, F_3 and F_4 generations are presented in Table 6, Table 7 and Table 8 respectively. In addition, obtained phenotypic observation coefficients were fragmented direct and indirect effects with path coefficient analyses and direct and indirect contributions of other traits on grain yield were examined. Considering Table 6, 7 and 8 together, grain yield had significant positive genotypic and phenotypic correlation with grain number and weight per spike, spike harvest index and spike density, while plant height and spike length showed strongly negative genotypic and phenotypic correlation with grain yield in successive generations. Significant and positive phenotypic and genotypic correlation were found for spike density with spikelet number per spike and spike harvest index; spike harvest index with grain weight per spike; grain weight per spike with spike length, spikelet number per spike, grain number per spikelet and spike; spikelet number per spike and grain number per spikelet with spike length. Additionally, grain weight per spike, spike harvest index and spike density had high direct effect coefficient on grain yield (Table 6, 7 and 8). Indirect effects of spike harvest index and spike density via plant height were very high in F_4 generations (Table 8). The comparison of the correlation coefficient showed that estimates of genotypic correlation coefficient are generally of smaller magnitude then those of phenotypic correlation coefficient at all generations (Table 6, 7 and 8). This revealed that association among these traits was both genetic controlled and environmental effects. The increased plant height was correlated with decrease in yield albeit plant height is one of the most important traits identifying the yield and a major selection parameter in wheat breeding programs (YAGDI and SOZEN, 2009).

Table 6. Phenotypic and genotypic correlation and direct and indirect path coefficient among traits in F_2 wheat populations

		PH	SL	SpNS	GNSp	GNS	GWS	SHI	SD	GY
PH	r_G		0.294	0.043	-0.499	-0.475	-0.123	0.168	-0.297	-0.466
	r_P		0.298**	0.043ns	-0.505**	-0.481**	-0.124ns	0.170ns	-0.301**	-0.472**
	PC		-0.029	-0.007	-0.101	0.076	-0.036	0.001	-0.138	**-0.239**
SL	r_G			-0.039	0.116	0.135	0.291	-0.080	-0.578	-0.340
	r_P			-0.040ns	0.118ns	0.136ns	0.295**	-0.081ns	-0.586**	-0.345**
	PC	-0.071		0.006	0.023	-0.022	0.085	-0.001	-0.269	**-0.097**
SpNS	r_G				-0.021	0.224	0.076	0.106	0.528	0.060
	r_P				-0.021ns	0.227*	0.077ns	0.107ns	0.535**	0.061ns
	PC	-0.010	0.004		-0.004	-0.036	0.022	0.001	0.246	**-0.161**
GNSp	r_G					0.808	0.390	0.067	-0.077	0.258
	r_P					0.818**	0.395**	0.068ns	-0.078ns	0.261*
	PC	0.121	-0.011	0.003		-0.130	0.114	0.001	-0.036	**0.199**
GNS	r_G						0.374	0.087	0.105	0.226
	r_P						0.379**	0.088ns	0.106ns	0.229*
	PC	0.115	-0.013	-0.036	0.163		0.110	0.001	0.049	**-0.159**
GWS	r_G							0.395	-0.259	0.178
	r_P							0.400**	-0.262*	0.180ns
	PC	0.030	-0.029	-0.012	0.079	-0.060		0.003	-0.120	**0.290**
SHI	r_G								0.016	0.081
	r_P								0.016ns	0.082ns
	PC	-0.041	0.008	-0.017	0.013	-0.014	0.116		0.007	**0.009**
SD	r_G									0.389
	r_P									0.394**
	PC	0.072	0.057	-0.086	-0.015	-0.017	-0.076	0.0001		**0.459**

r_G: Genotypic correlation coefficient, r_P : Phenotypic correlation coefficient, PC: Path coefficient, PH: plant height, SL: spike length, SpNS: Spikelet number per spike, GNSp: Grain number per spikelet, GNS: Grain number per spike, GWS: grain weight per spike, SHI: Spike harvest index, SD: Spike density, GY: grain yield per parcel. ** Residual= 0.784.

These results suggest that selections might be based on grain number and weight per spike, spike harvest index and spike density for developing high yielding wheat varieties. The magnitude of the genotypic and phenotypic correlations and their utilization in the selection had been stated by many earlier researchers (CHANDRA *et al*., 2004; ALI *et al*., 2008; KHAN *et al*., 2011; KADDEM *et al*., 2014; OULMI *et al*., 2014). Although a trait has positive and significant correlation with grain yield, path analysis can be implied that this trait has a direct negative effect on yield and this effect has been masked by indirect contribution of another trait (ILKER, 2006). The fact that grain weight per spike, spike harvest index and spike density had high direct and indirect effects on the grain yield of all three generations, proved that these traits can be a selection criterion for early generations.

Table 7. Phenotypic and genotypic correlation and direct and indirect path coefficient among traits in F_3 *wheat populations*

		PH	SL	SpNS	GNSp	GNS	GWS	SHI	SD	GY
PH	r_G		0.187	-0.185	-0.325	-0.446	-0.228	-0.142	-0.313	-0.500
	r_P		0.190ns	-0.188ns	-0.329**	-0.452**	-0.231*	-0.144ns	-0.318**	-0.507**
	PC		0.021	0.045	-0.026	0.015	0.004	-0.048	-0.055	**-0.463**
SL	r_G			0.351	0.345	0.337	0.465	0.059	-0.609	-0.141
	r_P			0.356**	0.349**	0.341**	0.471**	0.060ns	-0.617**	-0.143ns
	PC	-0.088		-0.086	0.028	-0.011	-0.009	0.020	-0.107	**0.110**
SpNS	r_G				0.161	0.522	0.419	0.325	0.406	0.053
	r_P				0.163ns	0.529**	0.424**	0.329**	0.412**	0.054ns
	PC	0.087	0.039		0.013	-0.017	-0.008	0.110	0.071	**-0.241**
GNSp	r_G					0.749	0.498	0.158	-0.126	0.225
	r_P					0.759**	0.505**	0.160ns	-0.128ns	0.228*
	PC	0.152	0.038	-0.039		-0.025	-0.010	0.053	-0.022	**0.080**
GNS	r_G						0.600	0.302	0.152	0.260
	r_P						0.608**	0.306**	0.154ns	0.264*
	PC	0.209	0.037	-0.127	0.060		-0.012	0.102	0.027	**-0.033**
GWS	r_G							0.574	-0.049	0.239
	r_P							0.581**	-0.050ns	0.242*
	PC	0.107	0.052	-0.102	0.040	-0.020		0.194	-0.009	**-0.019**
SHI	r_G								0.237	0.355
	r_P								0.240*	0.360**
	PC	0.067	0.007	-0.079	0.013	-0.010	-0.011		0.042	**0.333**
SD	r_G									0.216
	r_P									0.219*
	PC	0.147	-0.068	-0.099	-0.010	-0.005	0.001	0.080		**0.173**

r_G: Genotypic correlation coefficient, r_P : Phenotypic correlation coefficient, PC: Path coefficient, PH: plant height, SL: spike length, SpNS: Spikelet number per spike, GNSp: Grain number per spikelet, GNS: Grain number per spike, GWS: grain weight per spike, SHI: Spike harvest index, SD: Spike density, GY: grain yield per parcel. ** Residual= 0.794.

Table 8. Phenotypic and genotypic correlation and direct and indirect path coefficient among traits in F_4 wheat populations

		PH	SL	SpNS	GNSp	GNS	GWS	SHI	SD	GY
PH	r_G		0.338	-0.086	-0.069	-0.155	-0.038	-0.454	-0.407	-0.490
	r_P		0.343**	-0.087ns	-0.070ns	-0.157ns	-0.038ns	-0.460**	-0.412**	-0.497**
	PC		0.098	0.023	0.020	-0.008	-0.009	-0.019	-0.065	**-0.537**
SL	r_G			0.400	0.218	0.261	0.215	-0.222	-0.603	-0.107
	r_P			0.406**	0.221*	0.264*	0.218*	-0.225*	-0.611**	-0.109ns
	PC	-0.184		-0.106	-0.062	0.013	0.050	-0.009	-0.096	**0.286**
SpNS	r_G				-0.014	0.337	0.409	0.145	0.364	0.080
	r_P				-0.014ns	0.342**	0.415**	0.147ns	0.369**	0.081ns
	PC	0.047	0.116		0.004	0.017	0.096	0.006	0.058	**-0.262**
GNSp	r_G					0.731	0.571	0.084	-0.287	-0.045
	r_P					0.740**	0.579**	0.085ns	-0.291**	-0.046ns
	PC	0.038	0.063	0.004		0.036	0.134	0.003	-0.046	**-0.278**
GNS	r_G						0.538	0.116	-0.021	0.040
	r_P						0.546**	0.118ns	-0.021ns	0.040ns
	PC	0.084	0.075	-0.090	-0.206		0.126	0.005	-0.003	**0.049**
GWS	r_G							0.277	0.048	0.088
	r_P							0.281*	0.049ns	0.089ns
	PC	0.020	0.062	-0.109	-0.161	0.027		0.011	0.008	**0.231**
SHI	r_G								0.302	0.276
	r_P								0.306**	0.280*
	PC	0.247	-0.064	-0.038	-0.024	0.006	0.065		0.048	**0.041**
SD	r_G									0.208
	r_P									0.211ns
	PC	0.221	-0.175	-0.097	0.081	-0.001	0.011	0.012		**0.157**

r_G: Genotypic correlation coefficient, r_P : Phenotypic correlation coefficient, PC: Path coefficient, PH: plant height, SL: spike length, SpNS: Spikelet number per spike, GNSp: Grain number per spikelet, GNS: Grain number per spike, GWS: grain weight per spike, SHI: Spike harvest index, SD: Spike density, GY: grain yield per parcel. ** Residual= 0.840.

CONCLUSION

The higher values of heritability for some traits such as plant height, grain number per spike and spike density may be attributed to the higher contribution of the additive gene effects on the expression of these traits. On the other hand, because these values changed among real crosses, reciprocals and all genotypes evaluations, it may be said that maternal and epistatic gen effects were prominent for these traits. This may suggest that selection for these traits would be effective in early generations. Based on the mean performance, in all three segregating populations 'Bezostaja x Krasunia' and 'Krasunia x Pehlivan' exhibited better results and hence these populations are recommended for further studies.

Dissimilarity values were found very different among the generations for both their reciprocal and parents of crosses. These results could provide beneficial further knowledge about variation of reciprocal crosses throughout successive generations. Such knowledge could be beneficial in defining ideal breeding strategies for wheat improvement and will be the opportunities for the effective selection for yield factors.

Grain yield exhibited significant correlations with grain number and weight per spike, spike harvest index and spike density. In addition, these traits had the highest direct effect on grain yield. Therefore, these traits are the best indirect selection criteria to improve grain yield in wheat cultivars specifically in early generations.

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PROCENA RECIPROČNIH UKRŠTANJA POPULACIJA ZA OSOBINE KLASA KOD RANIH UZASTOPNIH GENERACIJA HLEBNE PŠENICE (*Triticum aestivum* L.)

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Izvod

Napori oplemenjivača za povećanje prinosa zrna pšenice će se neprekidno nastaviti jer je ona neophodan proizvod. Dobijanje genetskih informacija kao što su genotipska varijacija, heritabilnost, genetička dobit su osnovne komponente ovih istraživanja. Važno je da se materinski efektat koristi u uzastopnim generacijama zbog genotipskih i / ili efekata spoljašnje sredine na varijacije. Ovo istraživanje je sprovedeno radi ispitivanja promena recipročnih ukrštanja u kod uzastopnih generacija i određivanja selekcionog kriterijuma za visokog prinos u ranim generacijama. U tu svrhu, populacije su analizirane u odnosu na genotipski i fenotipski koeficijent varijacije, heritabilnost, genetičku dobit i UPGMA klaster analizu za ukrštanja, recipročna ukrštanja i svih genotipova pojedinačno. Prema rezultatima, vrednosti za heritabilnost i genetičku dobit ispitivanih osobina, bile su veoma raznovrsne kod uzastopnih generacija među ukrštanjima, recipročnim ukrštanjima i svim genotipovima. Ovaj rezultati pokazuju da su neaditivni genski efekti ili epistaza imali ulogu u nasleđivanju svih osobina. Različitost ukrštanja u odnosu na njihova recipročna ukrštanja ukazala je na varijacije kod uzastopnih generacija. Nivo različitosti svakog roditelja se razlikovao sa napretkom generacije i napravljenom kombinacijom ukrštanja. To ukazuje da je postojao materinski efekat u ovoj populaciji kroz uzastopne generacije. Masa zrna po klasu, žetveni indeks klasa i gustina klasa imali su visoke direktne i indirektne efekte na prinos zrna u sve tri generacije, pokazalo se da ove osobine mogu biti selekcioni kriterijum u ranim generacijama. Sana je bila najbolji roditelj, a ukrštanja 'Bezostaja x Krasunia' i 'Krasunia x Pehlivan' su imala najbolje perfomanse u većini osobina u svim generacijama.

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