Original Research Article

Estimation of inheritance leaf rust, powdery mildew, yield and yield components in barley through generation means analysis

of :[1WU]Comment

:[2WU]Comment

ABSTRACT

The success breeding program for improvement any crop depends mainly on the available background of the inheritance of the studied traits to be selected. This study was carried out during 2018/2019, 2019/2020 and 2020/2021 grown seasons at the experimental farm of Sakha Agricultural Research Station, Agricultural Research Center, Egypt to estimate the effect of genetic parameters controlling yield and yield component traits in addition leaf rust and powdery mildew disease infection. Six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) model was used. Results indicated that, mean effect (m) was highly significant in all evaluated crosses for all studied traits. The relative importance of additive and dominance effects differed from trait to another in each cross. For epistatic components, dominance × dominance interaction effects were more effective than other components in most studied traits. Significant or/and highly significant values in desirable direction of heterosis compared to mid and better parent were obtained from most studied crosses in yield and its attribute traits, but it found over mid parents only for cross no.1 in leaf rust and crosses no. 1 and 2 in powdery mildew infection. The estimation of broad-sense heritability showed high values for studied traits and crosses, while narrow-sense heritability and genetic advance from selection ranged from low to medium in most crosses for the agronomic traits, while it ranged from low to high for leaf rust and powdery mildew infection. Finally, the results of this study recommended the barley crosses no. 4 for improve yield potential and resistant to leaf rust and cross no. 5 to improve resistant to powdery mildew, where it had high genetic advance associated with high heritability.

of :[3WU]Comment

ce :[4WU]Comment

Key words: Barley, improvement, Genetic components, disease resistance, yield.

1. INTRODUCTION

Barley (*Hordeum vulgare* L.) considered as one of the great important crop species grown in the world **[1]**, ranking fourth important crop after wheat, rice and maize **[2]** with a great adaptation potential. Barley used for different purposes such as human food in few countries, animal feeding in wide areas around the world and malt industry. Enhancement of yield potential considered as an important goal in barley breeding program **[3].** Barley considered as dry, cold, salt-tolerant and well adapted crop to low-input environmental conditions and climatic change **[4]**. Breeding cereal crops for high productivity, good quality and resistant to common disease are important to satisfy food demand of this world. Powdery mildew and leaf rust diseases caused a loss on yield in barley. The loss of productivity due to powdery mildew can reach up to 30%, at an average of 5–10% **[5].** Yield losses due to barley leaf rust may be up to 60% in susceptible varieties **[6].** However, the mean yield losses of barley caused by barley leaf or stem rust often reach 10–25% **[7].** Due to the great problems that result from the use of fungicides and their negative effects on the environment and health, the use of resistance cultivars is considered an environmentally benign and effective way to control these diseases **[8]**. Generation mean analysis considered as important method for genetic analysis of quantitative traits **[1].** The present study was conducted to estimate the effect of genetic parameters controlling yield and its attribute traits in addition the infection of leaf rust and powdery mildew diseases in six barley cross combinations.

is :[5WU]Comment

2. PLANT MATERIALS AND METHODOLOGY

2.1. Genetic materials and experimental design:

The current study was carried out during 2018/2019, 2019/2020 and 2020/2021 growing seasons at the experimental farm of Sakha Agricultural Research Station, Agricultural Research Center, Egypt. Experimental material was the six generations *viz.*, P_1, P_2, F_1, F_2 and two backcrosses (BC_1 and BC_2) relating to six crosses involving three sensitive local cultivars (Giza 123, Giza 126 and Giza 125) and two resistant exotic lines (Line-1 and Line-2) (Table 1).

Table (1): Name, pedigree and disease reaction of the five barley genotypes.

No.	Genotype	Pedigree	Origin	Disease reaction	
				LR	PM
1	Giza 123	Giza $_{117}$//FAO$_{86}$	Egypt	S	S
2	Giza 126	Baladi Bahteem/S D729-Por12762-BC	Egypt	S	S
3	Giza 125	Giza117/Bahteem52//Giza118/FAO86	Egypt	S	S
4	Line-1	LAMOLINA96/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1	ICARDA	R	R
5	Line-2	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1/6/BRS180	ICARDA	R	R

Resistant (R), Sensitive (S), Leaf rust (LR), Powdery mildew (PM)

The selected parents were crossed in 2018/2019 growing season to produce F_1 hybrids of six barley crosses; 1 (Giza 123 × Line-1), 2 (Giza 126 × Line-1), 3 (Giza 125 × Line-1), 4 (Giza 123 × Line-2), 5 (Giza 126 × Line-2) and 6 (Giza 125 × Line-2). In the second season (2019/2020) the hybrid seeds were sown and F_1 plants of each cross were backcrossed to their respective parents to produce the two backcrosses (BC_1 and BC_2) seeds. At the same time, some of the F_1 plants were selfed to produce F_2 seeds. In the third season (2020/2021), the obtained seeds of these populations, i.e. P_1's, P_2's, F_1's, F_2's, BC_1's and BC_2's for the six studied crosses were sown in the field using a randomized complete blocks design (RCBD) with three replications. Each plot was about one row for each P_1, P_2, F_1, six rows for F_2 and two rows for each of BC_1, BC_2 in each replicate, rows were 2.5m long, 25cm width and the space from plant to plant in a row was 10cm. All agricultural practices were followed according to the growing barley recommendations. The experiment was grown under natural infection in the field and the experiment was surrounded with highly sensitive cultivars for both diseases as spread disease cultivars.

2.2. Data recording and measurements:

Data were recorded on 30 individual guarded plants in each P_1, P_2 and F_1, 90 plants in each BC_1 and BC_2 and 300 plants in each F_2. Plant height (cm), spike length (cm), number of grains/spike, number of spikes/plant, 100 grain weight (g), grain yield/plant (g) in addition to the reaction of leaf rust and powdery mildew disease. Leaf rust severity was recorded as stated by **Peterson et al. [9].** While powdery mildew severity was measured as stated by **Sarri and Prescott [10]**. Heterosis percentage (%) calculated as the increase of F_1 over the mid- and better parent values.

2.3. Statistical and genetic analysis:

- Scaling test was performed as stated by Mather **[11]** to identify the presence of non- allelic interactions.
- Generation mean analysis was performed as stated by Mather and Jinks **[12]**.
- Types of gene effects were culculated as stated by Gamble **[13].**
- Broad (h^2b) and narrow senses (h^2n) heritability were estimated as stated by Allard **[14]** and Mather **[11].**
- Expected genetic advance from selection (GA) was estimated as stated by Johnson et al. **[15]** formulae.
- Predicted genetic advance from selection was expressed as percentage of F_2 mean (GA%) was estimated as stated by Miller et al. **[16]**.

3. RESULTS

3.1. Mean performance

The calculated means and variances of the measured traits in the evaluated crosses for the tested populations P_1, P_2, F_1, F_2, BC_1 and BC_2 are presented in Table (2). Results indicated that, F_1 mean values were higher than average of the two parents and favorable parent for yield and related traits in the all evaluated crosses except for plant height in cross no. 4 in the comparison to mid and high parents, spike length in cross no. 6, grains number/spike in cross no. 2 and 100 grain weight in crosses no. 2 and 5 in comparison to better parent.

For the two-barley disease, F_1 mean values showed desirable values in negative direction in cross no. 1 for leaf rust and in crosses no. 1 and 2 for powdery mildew, where it showed values less than average of the two parents. The data of F_1 performance reflected the presence of heterotic effect in most studied crosses and traits. Mean values of the F_2 population were in-between the two barley parents and smaller than F_1 mean values in most barley crosses for and traits reflecting the importance of non-additive components of genetic variance for the calculated traits. However, the two populations (BC_1 and BC_2) mean values varied in each trait tended towards the mean of its recurrent parent.

Table (2-a): Mean ($\bar{X}$) and variance (S^2) of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of the six barley crosses for plant height, spike length, number of grains/spike and number of spikes/plant.

Traits	Cross	Statistical Parameter	P_1	P_2	F_1	F_2	BC_1	BC_2
Plant height	1	$\bar{X}$	108.26	114.14	122.96	112.39	110.33	116.30
		S^2	7.05	3.29	4.21	109.11	102.44	94.90
	2	$\bar{X}$	114.45	113.30	129.68	114.07	121.34	117.64
		S^2	5.26	4.13	3.93	114.46	92.22	100.10
	3	$\bar{X}$	106.05	115.01	125.79	113.35	116.47	117.64
		S^2	4.69	3.56	7.03	102.49	90.79	91.74
	4	$\bar{X}$	108.12	111.37	108.05	100.72	104.33	105.25
		S^2	6.96	7.26	6.63	95.77	86.31	80.61
	5	$\bar{X}$	115.15	113.05	121.80	107.56	111.72	111.93
		S^2	5.28	7.10	5.26	107.54	98.43	88.65
	6	$\bar{X}$	107.03	112.53	115.82	103.71	111.05	112.27
		S^2	4.90	7.00	6.82	102.62	79.89	86.19
Spike length	1	$\bar{X}$	7.58	7.50	8.60	7.08	7.32	7.20
		S^2	0.11	0.06	0.05	1.34	1.03	1.05
	2	$\bar{X}$	6.88	7.48	7.77	7.30	7.36	7.64
		S^2	0.08	0.05	0.09	1.65	1.37	1.21
	3	$\bar{X}$	7.82	7.53	8.13	6.98	7.36	7.08
		S^2	0.10	0.06	0.10	1.14	0.96	0.80
	4	$\bar{X}$	7.67	7.35	8.09	7.59	7.39	7.77
		S^2	0.11	0.08	0.07	1.52	0.97	1.29
	5	$\bar{X}$	6.93	7.25	8.61	6.64	6.80	6.64
		S^2	0.07	0.09	0.08	1.71	1.51	1.39
	6	$\bar{X}$	7.88	7.14	7.70	7.22	7.69	7.31
		S^2	0.11	0.08	0.08	1.23	1.05	0.85
Number of grains/ spike	1	$\bar{X}$	58.02	61.32	66.15	59.09	60.48	59.72
		S^2	3.17	2.77	2.48	45.50	38.96	36.13
	2	$\bar{X}$	52.52	60.48	61.11	60.48	59.22	60.73
		S^2	3.21	2.80	2.62	60.93	51.84	53.63
	3	$\bar{X}$	56.16	60.11	61.74	59.22	57.20	55.19
		S^2	2.98	2.36	3.57	49.38	41.58	43.46
	4	$\bar{X}$	58.78	60.80	63.84	62.24	59.98	59.98
		S^2	3.55	2.31	2.83	53.32	42.57	46.88
	5	$\bar{X}$	52.00	60.06	68.46	56.07	55.95	57.68
		S^2	3.60	2.38	3.31	67.30	58.91	53.12
	6	$\bar{X}$	56.36	59.85	64.89	57.96	60.98	58.46

		S^2	2.41	2.21	3.62	58.67	48.41	50.64
Number of spikes/ plant	1	$\bar{X}$	13.25	13.97	14.81	11.60	14.37	13.69
		S^2	0.99	0.94	0.83	20.11	17.33	17.65
	2	$\bar{X}$	13.97	14.00	17.01	16.40	14.13	15.35
		S^2	1.00	0.95	0.79	27.84	21.02	24.17
	3	$\bar{X}$	13.23	13.65	16.07	13.11	14.29	13.95
		S^2	0.90	0.93	0.87	19.68	16.90	15.82
	4	$\bar{X}$	13.13	12.50	14.39	12.27	13.37	13.25
		S^2	0.99	0.86	0.87	28.76	24.58	26.42
	5	$\bar{X}$	14.00	12.60	16.80	12.38	13.59	11.52
		S^2	0.96	0.88	0.76	23.65	18.81	19.14
	6	$\bar{X}$	13.03	12.45	14.81	12.36	13.98	13.85
		S^2	0.90	0.93	0.86	25.99	22.43	21.18

Table (2-b): Mean ($\bar{X}$) and variance (S^2) of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of the six barley crosses for 100-grain weight, grain yield/plant, leaf rust and powdery mildew.

Traits	Crosses	Statistical Parameter	P_1	P_2	F_1	F_2	BC_1	BC_2
100-grain weight	1	$\bar{X}$	5.15	5.20	5.47	5.34	5.41	5.37
		S^2	0.04	0.06	0.02	0.41	0.37	0.39
	2	$\bar{X}$	4.68	5.14	5.08	4.50	4.62	5.07
		S^2	0.07	0.04	0.04	0.55	0.54	0.50
	3	$\bar{X}$	5.84	5.18	5.88	5.32	5.80	5.36
		S^2	0.02	0.02	0.04	0.44	0.40	0.38
	4	$\bar{X}$	5.10	5.18	5.64	5.39	5.48	5.34
		S^2	0.05	0.02	0.05	0.46	0.39	0.43
	5	$\bar{X}$	4.70	5.17	5.02	4.87	4.31	4.97
		S^2	0.06	0.02	0.04	0.42	0.37	0.33
	6	$\bar{X}$	5.81	5.15	5.94	5.55	5.81	5.67
		S^2	0.02	0.02	0.03	0.43	0.36	0.39
Grain yield / plant	1	$\bar{X}$	16.69	18.43	22.17	15.95	18.42	22.65
		S^2	1.10	2.96	2.39	47.02	37.21	42.35
	2	$\bar{X}$	19.42	18.91	23.96	14.17	16.14	15.70
		S^2	2.71	2.96	1.77	35.69	32.33	33.71
	3	$\bar{X}$	20.92	18.32	21.61	18.89	20.25	19.81
		S^2	2.13	2.89	2.31	55.52	43.34	47.85
	4	$\bar{X}$	16.68	17.13	20.27	20.02	19.82	18.50
		S^2	1.15	2.18	2.10	44.41	36.87	40.16
	5	$\bar{X}$	19.45	17.00	21.07	17.92	20.96	18.11
		S^2	2.74	1.83	1.76	88.26	74.73	69.89
	6	$\bar{X}$	20.39	16.99	22.43	17.65	20.41	19.65
		S^2	2.17	1.78	2.02	61.66	52.36	51.71
Leaf rust	1	$\bar{X}$	35.95	7.66	20.80	34.57	31.28	14.53
		S^2	1.12	0.93	2.13	764.06	650.45	682.63
	2	$\bar{X}$	45.08	7.63	28.00	46.64	43.24	16.32
		S^2	1.95	0.99	1.55	913.84	802.48	821.73
	3	$\bar{X}$	55.48	7.56	36.00	45.76	55.00	13.52
		S^2	1.83	0.96	1.24	651.55	600.27	517.39
	4	$\bar{X}$	35.77	3.12	28.00	20.19	25.46	9.30
		S^2	11.75	1.12	1.17	529.23	490.58	483.87
	5	$\bar{X}$	45.15	3.74	32.80	31.27	36.67	11.48
		S^2	1.65	0.92	2.96	658.13	476.77	421.99
	6	$\bar{X}$	55.65	3.54	36.53	43.48	49.49	16.14
		S^2	1.57	0.94	2.33	808.04	627.28	613.79

Powdery mildew	**1**	$\bar{X}$	**3.77**	**2.25**	**2.55**	**3.49**	**3.60**	**2.93**
		S^2	**0.13**	**0.12**	**0.16**	**2.80**	**0.82**	**2.69**
	2	$\bar{X}$	**5.13**	**2.26**	**3.37**	**4.94**	**4.89**	**3.49**
		S^2	**0.19**	**0.14**	**0.18**	**6.70**	**3.45**	**4.39**
	3	$\bar{X}$	**6.70**	**2.37**	**5.41**	**4.45**	**5.13**	**3.90**
		S^2	**0.16**	**0.13**	**0.14**	**5.63**	**3.82**	**2.53**
	4	$\bar{X}$	**3.88**	**1.46**	**3.03**	**2.91**	**2.53**	**1.75**
		S^2	**0.12**	**0.16**	**0.10**	**2.57**	**2.12**	**0.72**
	5	$\bar{X}$	**5.20**	**1.43**	**4.28**	**3.48**	**3.47**	**2.98**
		S^2	**0.18**	**0.17**	**0.19**	**3.59**	**1.94**	**4.63**
	6	$\bar{X}$	**6.63**	**1.43**	**5.20**	**4.37**	**4.90**	**3.06**
		S^2	**0.17**	**0.16**	**0.12**	**6.89**	**3.71**	**3.49**

3.2. Heterosis, inbreeding depression and potence ratio

Heterosis over both mid and favorable parent values are presented in Table (3). For the agronomic traits (yield and its related traits), results reflected significant heterosis over both mid and better parents in favorable direction that were found for all traits and crosses except for cross no. 4 over mid and better parents for plant height, cross no. 6 for spike length, cross no. 2 for number of grains/spike and crosses no. 2 and 5 for 100 grain weight where it showed negative or insignificant values. Concerning barley diseases, highly significant and negative heterosis over mid parents in desirable direction were found for cross no. 1 for leaf rust and cross no. 1 and cross no. 2 for powdery mildew.

Results presented in Table 3 reflected significant and positive values of inbreeding depression for spike length, spikes number/plant and 100 grain weight in all evaluated crosses except of cross no. 2 for spikes number/plant, number of grains/spike in cross no. 5 and for grain yield/plant in crosses no. 1, 2 and 6. For barley disease infection, significant and favorable values for inbreeding depression were noted for studied disease in barley crosses no. 1 and 2, while the other barley crosses of powdery mildew showed significant and positive values. On the other hand, the rest crosses reflected insignificant values which considered as a desirable value for these traits.

For the agronomic traits, potence ratio exhibited over dominance (values mor than unity) for all evaluated crosses and traits except for spike length in cross no. 6 and 100 grain weight in crosses no. 2 and 5. For barley disease traits, the values of potence ratio were smaller than the unit reflecting partial dominance for all evaluated crosses for the two barley disease.

Table (3): Heterosis, inbreeding depression and potence ratio in the evaluated barley crosses for all studied traits.

Traits	Cross	Heterosis		ID	PR%
		MP	BP		
Plant height	1	10.58**	7.73**	8.59	4.00
	2	13.88**	13.30**	12.03	27.36
	3	13.81**	9.37**	9.89	3.41
	4	-1.55**	-2.99**	6.78	-1.04
	5	6.75**	5.78**	11.69	7.33
	6	5.50**	2.92**	10.45	2.20
Spike length	1	14.10**	13.53**	17.67**	28.33
	2	8.12**	3.79**	6.01**	1.94
	3	5.94**	3.98**	14.18**	3.16
	4	7.69**	5.48**	6.10**	3.67
	5	21.48**	18.84**	22.94**	9.67
	6	2.56**	-2.22**	6.26**	0.52
Number of grains/ spike	1	10.86**	7.88**	10.67	3.93
	2	8.16**	1.04	1.03	1.16
	3	6.20**	2.71**	4.08	1.82
	4	6.78**	5.01**	2.50	4.03
	5	22.18**	13.99**	18.10*	3.08
	6	11.68**	8.42**	10.68	3.89
Number of spikes/ plant	1	8.80**	6.02**	21.66**	3.35
	2	21.67**	21.54**	3.60	20.00
	3	19.53**	17.69**	18.40**	12.50
	4	12.30**	9.60**	14.70**	5.00
	5	26.34**	20.04**	26.31**	5.02
	6	16.21**	13.62**	16.54**	7.12
100-grain weight	1	5.80**	5.27**	2.50**	11.63
	2	3.42**	-1.25**	11.25**	0.72
	3	6.74**	0.69**	9.56**	1.12
	4	9.69**	8.77**	4.37**	11.47
	5	1.80**	-2.89**	3.11**	0.37
	6	8.42**	2.26**	6.54**	1.40
Grain yield / plant	1	26.26**	20.31**	28.05**	5.31
	2	25.02**	23.40**	40.87**	19.02
	3	10.15**	3.29**	12.59	1.53
	4	19.91**	18.32**	1.23	14.86
	5	15.62**	8.32**	14.98	2.32
	6	20.04**	10.01**	21.35**	2.20
Leaf rust	1	-4.60**	171.49**	-66.22*	-0.07
	2	6.25**	267.13**	-66.57*	0.09
	3	14.23**	376.36**	-27.11	0.19
	4	44.00**	797.44**	27.90	0.52
	5	34.17**	776.07**	4.68	0.40
	6	23.45**	933.18**	-19.00	0.27
Powdery mildew	1	-15.28**	13.54**	-36.80**	-0.60
	2	-8.98**	48.81**	-46.67**	-0.23
	3	19.29**	128.49**	17.74**	0.40
	4	13.38**	106.98**	3.93*	0.30
	5	29.23**	200.00**	18.65**	0.51
	6	29.11**	264.29**	16.01**	0.45

(*) and (**) significant at 0.05 and 0.01 levels of probability, respectively.

3.3. Scaling test and type of gene action estimates

Scaling test and six parameters were culculated using the collected data as stated by **Gamble procedure (1962)**. At least, one of the scales (A, B and C) should be significant. However, the significance of any one of the scales reveals the presence of non- allelic interaction. Data of all evaluated crosses for all measured traits exhibited the presence of non-allelic interaction (table-4).

The six parameter estimates, i.e. means (m), additive (a), dominance (d), additive × additive (aa), additive × dominance (ad) and dominance × dominance (dd) are presented in Table 4. From finding of six-parameter model it was found that, mean effects for all studied traits in the all evaluated crosses were highly significant, indicating that these traits are quantitatively inherited.

Additive gene effects (a) were quite small in effects compared to the dominance gene (Table 4). Positive (favorable direction) and significant results of the effects of additive gene were found in cross no. 2 for plant height, cross no. 6 for spike length and grains number/spike, cross no. 5 for spikes number/plant and grain yield/plant and cross no. 3 for 100 grain weight.

Dominance (d) gene effect estimates reflected significant values and positive for the evaluated agronomic traits and crosses except in cross no. 4 for spike length and grain yield/plant, crosses no. 2, 3 and 4 for grains number/spike, cross no. 2 for spikes number/plant and cross no. 5 for 100-grain weight. For disease traits, effects of dominance gene were significant and negative for leaf rust in all evaluated crosses except in cross no. 4 and for powdery mildew in crosses no. 1, 2 and 4 (Table 4).

For additive × additive (aa) types of epistasis, significant and positive values (desirable direction) for the agronomic traits were found for plant height in all evaluated crosses except in barley cross no.1, spike length in crosses no. 3 and 6, grains number/spike in crosses no. 1 and 6, spikes number/plant in crosses no. 1, 3, 4 and 6, 100-grain weight in all evaluated crosses except in cross no.5 and grain yield/plant in crosses no. 1, 2 and 6. For disease traits, the effects of additive × additive gene reflected desirable values for powdery mildew in crosses no. 2 and 4 (Table 4), indicating that these traits had accumulating genes and selection for its development could be effective.

Concerning additive × dominance (ad) types of epistasis, desirable data (significant and positive) were detected for plant height in cross no. 3, grains number/spike in crosses no. 1, 2, 3 and 6, while significant and negative finding were recorded for powdery mildew in crosses no. 4, 5 and 6 (Table 4).

For dominance × dominance (dd) epistasis gene effects, significant or highly significant and positive valued were detected for spike length in crosses no. 1, 3 and 5, grains number/spike in crosses no. 3, 4 and 5, spikes number/plant in crosses no. 2 and 5, 100-grain weight in cross no. 5 and grain yield/plant in cross no. 2. While the other crosses showed insignificant and/or significant undesirable values (Table 4). These results confirm the important role of dd gene action in the genetic system.

Table (4): Scaling test parameter A, B and C and estimated type of gene action in the evaluated barley crosses for all studied traits.

Traits	Cross	Scaling test			Type of gene action					
		A	B	C	(m)	(a)	(d)	(aa)	(ad)	(dd)
Plant height	1	-10.54**	-4.49	-18.73**	112.39**	-5.96**	15.46**	3.70	-3.02	11.34
	2	-1.45	-7.69**	-30.81**	114.07**	3.70*	37.47**	21.67**	3.12	-12.54
	3	1.09	-5.52*	-19.22**	113.35**	-1.18	30.06**	14.80**	3.30*	-10.38
	4	-7.50**	-8.91**	-32.71**	100.72**	-0.92	14.60**	16.30**	0.70	0.12
	5	-13.51**	-10.99**	-41.56**	107.56**	-0.21	24.76**	17.06**	-1.26	7.44
	6	-0.75	-3.81	-36.34**	103.71**	-1.22	37.82**	31.78**	1.53	-27.22**
Spike	1	-1.54**	-1.70**	-3.96**	7.08**	0.12	1.78**	0.72	0.08	2.52**

length	2	0.07	0.03	-0.70*	7.30**	-0.28	1.38**	0.80	0.02	-0.90
	3	-1.24**	-1.51**	-3.70**	6.98**	0.28	1.42**	0.96*	0.14	1.78**
	4	-0.97**	0.11	-0.82**	7.59**	-0.38*	0.53	-0.04	-0.54**	0.90
	5	-1.93**	-2.58**	-4.85**	6.64**	0.17	1.86**	0.34	0.33	4.18**
	6	-0.20	-0.22	-1.54**	7.22**	0.38*	1.31**	1.12**	0.01	-0.69
Number of grains/ spike	1	-3.21*	-8.02**	-15.26**	59.09**	0.76	10.51**	4.03**	2.41*	7.20
	2	4.81**	-0.13	6.70**	60.48**	-1.51	2.59	-2.02	2.47*	-2.67
	3	-3.49*	-11.47**	-2.87	59.22**	2.02	-8.49**	-12.10**	3.99**	27.06**
	4	-2.67	-4.68**	1.72	62.24**	0.01	-5.02	-9.07**	1.01	16.43**
	5	-8.56**	-13.15**	-24.70**	56.07**	-1.73	15.42**	2.99	2.30	18.72**
	6	0.72	-7.81**	-14.15**	57.96**	2.52*	13.84**	7.06*	4.27**	0.04
Number of spikes/ plant	1	0.69	-1.39	-10.43**	11.60**	0.68	10.93**	9.74**	1.04	-9.04**
	2	-2.72*	-0.30	3.61**	16.40**	-1.23	-3.60	-6.63**	-1.21	9.64**
	3	-0.72	-1.81	-6.57**	13.11**	0.33	6.67**	4.05*	0.54	-1.52
	4	-0.77	-0.39	-5.31**	12.27**	0.13	5.73**	4.16*	-0.19	-3.00
	5	-3.61**	-6.35**	-10.67**	12.38**	2.07**	4.21*	0.71	1.37	9.25**
	6	0.12	0.45	-5.66**	12.36**	0.12	8.30**	6.23**	-0.17	-6.80*
100-grain weight	1	0.20	0.08	-1.15**	5.04**	0.04	1.73**	1.43**	0.06	-1.71**
	2	-0.52**	-0.07	-1.95**	4.50**	-0.46**	1.53**	1.36**	-0.23	-0.78
	3	-0.12	-0.33*	-1.51**	5.32**	0.44**	1.42**	1.05**	0.11	-0.59
	4	0.22	-0.15	-1.19**	5.09**	0.14	1.75**	1.26**	0.18	-1.32**
	5	-1.10**	-0.25	-0.45**	4.87**	-0.66**	-0.82**	-0.91**	-0.42**	2.27**
	6	-0.13	0.24	-1.83**	5.25**	0.15	2.41**	1.94**	-0.18	-2.06**
Grain yield / plant	1	-2.02	4.71**	-15.65**	15.95**	-4.23**	22.95**	18.34**	-3.36**	-21.03**
	2	-11.09**	-11.48**	-29.58**	14.17**	0.45	11.81**	7.02**	0.19	15.54**
	3	-2.03	-0.32	-6.90**	18.89**	0.45	6.54*	4.55	-0.86	-2.20
	4	2.68	-0.39	5.74**	20.02**	1.31	-0.08	-3.45	1.54	1.16
	5	1.39	-1.86	-6.93**	17.92**	2.85*	9.31**	6.46	1.62	-5.99
	6	-2.01	-0.13	-11.67**	17.65**	0.76	13.27**	9.52**	-0.94	-7.38
Leaf rust	1	5.81	0.61	53.09**	34.57**	16.75**	-47.67**	-46.67**	2.60	40.25*
	2	13.40*	-2.99	77.85**	46.64**	26.92**	-65.79**	-67.44**	8.19	57.03**
	3	18.53**	-16.52**	48.01**	45.76**	41.48**	-41.52**	-46.00**	17.52**	43.99**
	4	-12.86*	-12.52*	-14.14**	20.19**	16.15**	-2.68	-11.24	-0.17	36.61*
	5	-4.60	-13.58**	10.57	31.27**	25.19**	-20.40*	-28.75**	4.49	46.93**
	6	6.79	-7.79	41.65**	43.48**	33.34**	-35.70**	-42.64**	7.29	43.64*
Powdery mildew	1	0.87**	1.06**	2.83**	3.49**	0.67**	-1.36*	-0.90	-0.09	-1.03
	2	1.28**	1.35**	5.62**	4.94**	1.40**	-3.32**	-2.99**	-0.03	0.36
	3	-1.85**	0.02	-2.09**	4.45**	1.23**	1.13	0.26	-0.93**	1.57
	4	-1.84**	-0.98**	0.24	2.91**	0.78**	-2.70**	-3.06**	-0.43*	5.88**
	5	-2.55**	0.24	-1.26**	3.48**	0.49	-0.08	-1.05	-1.40**	3.35**
	6	-2.04**	-0.51	-0.99	4.37**	1.84**	-0.39	-1.56	-0.76*	4.11**

(*) and (**) significant at 0.05 and 0.01 levels of probability, respectively.

3.4. Heritability estimates and expected genetic advance from selection

The assessment of heritability in both broad (h^2b) and narrow (h^2n) sense and expected genetic advance from selection for barley studied traits are presented in Table (5). Heritability estimates in broad sense were relatively high for all studied traits in all crosses. Broad sense heritability for plant height ranging from 92.83% in cross 4 to 96.23% in cross no. 2, for spike length ranged from 92.31 in cross no. 3 to 95.49% in cross no. 2, for grains number/spike ranged from 93.68% in cross no. 3 to 95.38% in cross no. 2, for spikes number/plant ranged from 95.47% in cross no. 3 to 96.89% in cross no. 4, for 100 grain weight ranged from 93.54% in cross no. 1 to 97.71% in cross no. 5, for grin yield/plant ranged from 91.08% in cross no. 4 to 93.60% in cross no. 6, for leaf rust infection ranged from 98.28% in cross no. 1 to 98.83% in cross no. 2 and for powdery mildew infection ranged from 94.93% in cross no. 1 to 97.93% in cross no. 6.

Table (5): Heritability percentage in broad (h^2b) and narrow (h^2n) senses and expected genetic advance from selection (GA) in the six barley crosses for all studied traits.

Trait	Cross	Heritability	Genetic advance	Trait	Cross	Heritability	Genetic advance

		h^2b	h^2n	GA	GA %			h^2b	h^2n	GA	GA %
Plant height	**1**	**95.70**	**19.15**	**4.12**	**3.67**	**100-grain weight**	**1**	**95.30**	**16.27**	**0.22**	**4.04**
	2	**96.23**	**31.97**	**7.05**	**6.18**		**2**	**93.54**	**12.46**	**0.19**	**4.23**
	3	**94.56**	**21.91**	**4.57**	**4.03**		**3**	**95.65**	**19.63**	**0.27**	**5.02**
	4	**92.83**	**25.70**	**5.18**	**5.14**		**4**	**95.76**	**21.79**	**0.30**	**5.65**
	5	**94.68**	**26.04**	**5.56**	**5.17**		**5**	**97.71**	**31.21**	**0.42**	**8.54**
	6	**93.78**	**38.16**	**7.96**	**7.68**		**6**	**96.76**	**26.73**	**0.36**	**6.53**
Spike length	**1**	**95.13**	**44.37**	**1.06**	**14.95**	**Grain yield / plant**	**1**	**91.08**	**30.78**	**4.35**	**27.26**
	2	**95.49**	**44.14**	**1.17**	**16.01**		**2**	**91.13**	**14.96**	**1.84**	**13.00**
	3	**92.31**	**45.41**	**1.00**	**14.33**		**3**	**92.82**	**35.76**	**5.49**	**29.05**
	4	**94.64**	**51.40**	**1.31**	**17.20**		**4**	**90.82**	**26.54**	**3.64**	**18.19**
	5	**95.24**	**30.99**	**0.84**	**12.60**		**5**	**90.52**	**36.14**	**6.99**	**34.04**
	6	**93.16**	**46.33**	**1.06**	**14.68**		**6**	**93.60**	**31.21**	**5.05**	**28.61**
Number of grains /spike	**1**	**94.02**	**34.95**	**4.86**	**8.22**	**Leaf rust**	**1**	**98.79**	**25.53**	**14.54**	**42.04**
	2	**95.38**	**26.90**	**4.33**	**7.15**		**2**	**98.83**	**22.26**	**13.86**	**29.73**
	3	**93.68**	**27.79**	**4.02**	**6.79**		**3**	**98.80**	**28.46**	**14.97**	**32.71**
	4	**94.59**	**32.25**	**4.85**	**7.79**		**4**	**98.28**	**15.87**	**7.52**	**37.26**
	5	**95.32**	**33.55**	**5.67**	**10.11**		**5**	**98.68**	**63.44**	**33.53**	**107.23**
	6	**94.94**	**31.19**	**4.92**	**8.49**		**6**	**98.78**	**46.41**	**27.18**	**62.51**
Number of spikes /plant	**1**	**95.54**	**26.00**	**2.40**	**20.71**	**Powdery mildew**	**1**	**94.93**	**74.60**	**2.57**	**73.73**
	2	**96.83**	**37.66**	**4.09**	**24.96**		**2**	**97.40**	**82.96**	**4.42**	**89.58**
	3	**95.47**	**33.76**	**3.08**	**23.53**		**3**	**97.47**	**87.08**	**4.26**	**95.68**
	4	**96.89**	**22.68**	**2.51**	**20.42**		**4**	**95.20**	**89.53**	**2.96**	**101.69**
	5	**96.46**	**39.57**	**3.96**	**32.02**		**5**	**94.96**	**17.12**	**0.67**	**19.18**
	6	**96.59**	**32.24**	**3.39**	**27.40**		**6**	**97.93**	**95.57**	**5.17**	**118.30**

Heritability estimates in narrow sense were low to high and ranging from 19.15% in cross no. 1 to 38.16% in cross no. 6 for plant height, from 30.99% in cross no. 5 to 51.40% in cross no. 4 for spike length, from 26.90% in cross no. 2 to 34.95% in cross no. 1 for grains number/spike, from 22.68% in cross no. 4 to 39.57% in cross no. 5 for spikes number/plant, from 12.46% in cross no. 2 to 31.21% in cross no. 5 for 100 grain weight, from 14.96% in cross no. 2 to 36.14% in cross no. 5 for grain yield/plant, from 15.57% in cross no. 4 to 63.44% in cross no. 5 for leaf rust infection and from 17.20% in cross no. 5 to 95.57% in cross no. 6 for powdery mildew infection, which indicate that these traits were greatly affected by additive and non-additive effects.

The expected genetic advance from selection at 5% selection intensity of F_2 mean (GA%) ranged from 3.67% in cross no. 1 to 7.68% in cross no. 6 for plant height, from 12.60% in cross no. 5 to 17.20% in cross no. 4 for spike length, from 6.79% in cross no. 3 to 10.11% in cross no. 5 for grains number/spike, from 20.42% in cross no. 4 to 32.02% in cross no. 5 for spikes number/plant, from 4.04% in cross no. 1 to 8.54% in cross no. 5 for 100 grain weight, from 13.0% in cross no. 2 to 34.04% in cross no. 5 for grain yield/plant, from 29.73% in cross no. 2 to 107.23% in cross no. 5 for leaf rust infection and from 19.18% in cross no. 5 to 118.30% in cross no. 6 for powdery mildew infection.

4. DISCUSSION

Data in Table 2 showed mean and variance of the six studied population (P_1, P_2, F_1, F_2, BC_1 and BC_2) for the measured traits. Results indicated that, the mean values of F_1 were higher than mid and favorable parent for most measured traits in most evaluated crosses which indicate the presence of heterosis. Also, variances of parents and the F_1 generation is much less than the variance of F_2 generation and backcrosses. Andy et al. **[17]** reported that, segregation variance refers to variance due to segregation of alleles in F_2 relative to variance observed in F_1 from different genetic lines or divergent populations. When divergent populations are crossed, the variance of the F_1 is not increased because all F_1 offspring have heterozygous loci, with one allele from each divergent parent. However, an outbreak of variation is due to recombination, the “segregation variance,” can often be shown in the F_2 generation **[18,19]**.

The increase in biomass, fertility, stature and other characters that led to desirable performance of the F_1 progeny compared to parents refers to heterosis **[20]**. For variety evolution as well, selection of better combination heterosis role cannot be ignored. Results in Table 3 show the presence of heterotic effects compared to mid and better parents for most measured traits. This reflect that parental genotypes and F_1 hybrids are genetically diverse and have a wide genetic variability for the studied traits (plant height (cm), spike length, number of grains/spike, number of spikes/plant, 100 grain weight, grain yield/plant, leaf rust ang powdery mildew). Mansour **[21]** and **El-**wakeel and Hassan **[22]** reported significant heterosis compared to mid and better parents for grain yield and its attributes and they also reported considerable genetic variability in barley.

The reduction of the mean phenotypic values which shown by traits associated with the reproductive capacity or physiological efficiency of the plant called inbreeding depression, The evaluation of inbreeding only may not be sufficient for guiding a selection program and advancing plant improvement **[23]**. However, despite a developed understanding of the significance of inbreeding depression, identifying specific alleles underlying the reduction in fitness has remained challenging **[24].**

Potence ratios could be used to set the dominance of inherited traits, with values more than ±1 indicating over-dominance, values between −1 and +1 refer to partial dominance, values of 0 indicating no dominance and values of +1.0 indicating complete dominance. The obtained results presented in Table 3 reflected that, partial to over-dominance were clearly involved in the inheritance of barley yield and disease severity traits. A predominance of non-additive variance components for yield related traits were found by many researchers, suggesting that heterosis could be used for breeding improvement **[25,21,26].**

Gene action refers to the behavior or mode of expression of genes in a genetic population. Gene action is useful to crop breeder in selection of parents for hybridization, choice of breeding methods for quantitative characters improvement and estimation of some other genetic parameters such as heritability and genetic advance from selection. Results in Table 4 reflecting that dominance plays greater role in inheritance of most studied traits, so selection for improvement these traits could be effective in late generations. Additive x additive gene effect was more effective than dominance x dominance and additive x dominance reflecting the important of this type of gene action, similar results were obtained by Mansour **[21]**, Andreia et al. **[23]** and Attiq et al. **[20]**.

Results in Table 5 reflected high values of heritability in broad senses for all the measured traits under study. While heritability estimates in narrow sense and genetic advance from selection varied from low to moderate for the agronomic traits and low to high for disease traits. similar results were obtained by Mansour **[21]** and El-wakeel and Hassan **[22].** The measure of the correlation between breeding values and phenotypic values revers to heritability **[27].** Thus, heritability plays a greet role in crop breeding and considered as a guide to breeding value **[28].** There is a direct relevance between heritability and response to the selection, which is referred to as genetic advance. High values of heritability does not necessarily mean high genetic gain and alone is not sufficient to make improvement through selection. Thus, heritability estimates utility is increased when using in estimating genetic advance **[15]**. High values of genetic advance correlated with high values of heritability estimates offers the most effective condition for selection **[29].** The values of heritability increased when it is used to genetic advance calculating, indicating the degree of gain in a characteristic obtained under a certain selection pressure. Moreover, most agronomical important traits, including grain yield, have complex genetic inheritance and require the use of relatively large populations for studying plant breeding.

5. CONCULUSION

Based on the results obtained from heritability and gene action estimates it could be concluded that, this study recommended selection through the following generation in barley crosses no. 4 to improve yield potential and resistant to leaf rust and cross no. 5 to improve resistant to powdery mildew, where it had high genetic advance correlated with high heritability.

REFERENCES

check reference :[6WU]Comment

1. **Eshghi R, Akhundova E.** Inheritance of some important agronomic traits in hulless barley. Inter. J. Agri. Biol. 2010; 12:73-76.
2. **Raikwar RS**. The nature and magnitude of gene effects for yield and its quality traits in barley (Hordeum vulgare L.) under saline sodic soil. Scholarly J. Agri. Sci. 2013; 3: 154-166.
3. **Xue DW, Chen MC, Zhou MX, Chen S, Mao Y and Zhang GP.** QTL analysis of flag leaf in barley (*Hordeum vulgare* L.) for morphological traits and chlorophyll content. J.Zhejiang Univ. Sci. B. 2008; 9: 938-943.
4. **Kumar A, Verma RPS, Singh A, Kumar Sharma H, Devi G.** Barley landraces: Ecological heritage for edaphic stress adaptations and sustainable production. Environ. Sustain. Indic.2020; 6, 100035.
5. **Agostinetto L, Casa RT, Bogo A, Sachs C, Reis EM, Kuhnem PR.** Critical yield-point model to estimate damage caused by brown spot and powdery mildew in barley. Ciência Rural. 2014; 44, 957–963.
6. **Park RF, Golegaonkar PG, Derevnina L, Sandhu KS, Karaoglu H, Elmansour HM, Dracatos PM, Singh D.** Leaf Rust of Cultivated Barley: Pathology and Control. Annu. Rev. Phytopathol. 2015; 53, 565–589.
7. **Çelik Oguz A, Karakaya A.** Genetic Diversity of Barley Foliar Fungal Pathogens. Agronomy. 2021; 11, 434.
8. **Murray GM, Brennan JP.** *The Current and Potential Costs from Diseases of Wheat in Australia*. Barton, KS: Grains Research and Development Corporation, 2009.
9. **Peterson RF, Campbell AB, Hannah AE.** A diagrammatic scale for estimating rust intensity on leaves and stems of cereals. Can. J. Res. Sec. C, 1948; 26: 496-500.
10. **Sarri EE, Prescott M.** A scale for appraising the foliar intensity of wheat disease. Pl. Dis. Rep.,1975; 59: 377-380.
11. **Mather K.** Biometrical genetics. Dover publication, Inc., New York, Ltd., London. 1949.
12. **Mather K, Jinks JL.** Introduction to biometrical genetics. Third edition. Chapman and Hall Ltd., London. 1982; pp 396.
13. **Gamble EE.** Gene effects in corn (*Zea mays L.*). I- Separtion and relative importance of gene effects for yield. Can. J. Plant Sci.1962; 42: 339-348.
14. **Allard AM.** Principles of Plant Breeding. John Wiley and Sons. Inc. NY, USA.1960; p. 92.
15. **Johnson HW, Robinson HF, Comstock RE.** Estimation of genetic and environmental variability in soybeans. Agron. J.1955; 47: 314-318.
16. **Miller PA, Williams JC, Robinson HF, Comstock RE.** Estimates of genotypic and environmental variances and covariance in Upland cotton and their implications in selection. Agron. J. 1958; 50: 126-131.
17. **Andy Benowicz, Michael Stoehr, Andreas Hamann, Alvin D Yanchuk.** Estimation of the F_2 generation segregation variance and relationships among growth, frost damage, and bud break in coastal Douglas-fir (Pseudotsuga menziesii (Mirb.) Franco) wide-crosses. Annals of Forest Science. 2020; 77: 28.
18. **Wright S.** Evolution and the genetics of populations, Vol. I. Biometric foundations. University of Chicago Press, Chicago.1968.
19. **Lande R.** The minimum number of genes contributing to quantitative variation between and within populations. Genetics. 1981; 99: 541-553.
20. **Attiq ur Rehman, Trang Dang, Shanzay Qamar, Amina Ilyas, Reemana Fatema, Madan Kafle, Zawar Hussain, Sara Masood, Shehyar Iqbal, Khurram Shahzad.** Revisiting Plant Heterosis-From Field Scale to Molecules. Genes (Basel). 2021; 12(11): 1688.
21. **Mansour M.** Genetic analysis of earliness and yield component traits in five barley crosses. J. Sus. Agric. Sci. 2017; 43(3):165-173.
22. **El-wakeel Sally E and Badawy R Hassan.** Estimation of genetic parameters for some desirable barley traits using generation means analysis. Egypt. J. Plant Breeding. 2019; 22(2):373-384.
23. **Andreia Somera, Angelita LSL Ragagnin, Maraiza L Costa, Willame dos S Candido, Edésio F dos Reis.** Inbreeding depression and performance of partially self-fertilized maize progenies in a top cross. Chilean J. of Agric. Res. 2018; 78(3):318-326.

24. **Hedrick PW, Garcia-Dorado A.** Understanding inbreeding depression, purging, and genetic rescue. Trends Ecol Evol. 2016; 31(12):940–952.
25. **Mansour M.** Genetical analysis of some quantitative traits in barley under saline soil conditions. Proceeding, the Sixth Field Crops Conference, FCRI, ARC, Giza, Egypt 22-23 Nov. 2016, 99-107.
26. **El-Refaey R A, El-Seidy EH, El-Gammal AA, Mansour M, Ashry HM.** Estimation of genetic parameters through generation mean analysis in barley under normal and drought stress conditions. Egypt. J. Plant Breed.2017; 21(5):416-429.
27. **Falconer DS, Mackay TFC.** Introduction to Quantitative Genetics, Ed 4. Longmans Green, Harlow, Essex, UK.1996.
28. **Addisu A, Shumet T.** Variability, heritability and gene-tic advance for some yield and yield related traits in barley (Hordeum vulgare L.) landraces in Ethiopia. Int. J. Plant. Breed. Genet. 2015; 9:68-76.
29. **Yadav SK, Singh AK, Pandey P, Singh S.** Genetic Variability and Direct Selection Criterion for Seed Yield in Segregating Generations of Barley (Hordeum vulgare L.). American Journal of Plant Sciences. 2015; 9, 1543-1549.

please make uniformity **:[7WU]Comment**

italics **:[8WU]Comment**

make uniformity **:[9WU]Comment**