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Evaluation of the productivity and resistance to net blotch of some barley genotypes

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ABSTRACT

Ten barley genotypes with different responses to net blotch disease were evaluated at Sakha Agricultural Research Station during two growing seasons (2020/2021 and 2021/2022) to determine the high potential yield of the promising elite barley genotypes and resistance to net blotch disease. Earliness traits, grain yield and its attributes in addition to reaction to net blotch disease infection were studied. The analysis of variance showed significant or highly significant differences for the studied traits. Results revealed that Line 2 and Line 6 exhibited the highest values of grain yield (ton fed^{-1}) in both seasons under all experimental conditions. Moreover, Giza134, Line 2, Line 5 and Line 6 were the most resistant genotypes with low values for net blotch (NB) disease reaction. The correlation coefficient between the studied traits indicated that positive significant correlation between plant height with net blotch resistance (R=0.68). On the other hand, there was a significant negative correlation between the heading date and maturity date with net blotch (R=-0.73 and R=-0.67, respectively) in the second season. Concerning molecular analysis seven SSR primers including GBM1078, EBMAC0695, 5SCSSR104770, GBM1405, GBM1419, GBM1461 and GBM1516 were used to study the polymorphic among net blotch resistance and sensitive of barley selected genotypes. All primers generated clear patterns with height polymorphism. So, genotypes (Giza 134, Line 2, Line 5 and Line 6) would be useful in breeding programs for evolving better barley yield and more resistance against (NB) disease.

Keywords: *Hordeum vulgare*, Productivity, Net blotch, Resistance, SSR, Correlation.

INTRODUCTION

Barley (*Hordeum vulgare* L.) is classified as a self-pollinated crop with 2n = 2x =14. Barley is among the oldest domesticated crops. In the 2020/2021 season world barley production was ranked fourth among cereals with 160.23 million tons, behind maize, rice and wheat behind maize, rice and wheat (FAO STAT, 2022). It is considered one of the highest nutrient cereal crops having high protein contents, many chemical compounds, elements, and dietary fibers which are important for intestinal function and reducing blood cholesterol.

Barley grains are mainly used malt industry as a traditional and early method of preparation and human food in different regions around the world. It is used in soups, stews, and baby food (Poehlman, 1994). Until the sixteenth-century barley flour was used instead of wheat to make bread (Bukantis and Goodman, 1980).

Barley is grown in Egypt mainly for animal feed (grain and straw), the brewery industry, and bread-making by Bedouins. It is a good tolerant crop to biotic and abiotic stresses as well as climate change. Net blotch is considered a significant and common problem in barley production worldwide (Shipton *et al*., 1973), caused by phytopathogen *Pyrenophora teres*. It can cause losses in productivity from 10% to 40% with a reduction in grain weight (Mathre, D.E., 1997, Michael and Cooke 2008, Liu, Z. *et al*., 2011 and Petta and Lavilla 2023), but it could reach to 100% when the host is susceptible, and the environment is favorable to fungus (Steffenson *et al*., 1996). While Hollaway *et al*., (2020) revealed a 20% grain yield reduction due to net blotch whereas scald symptoms covering between 20-60 % of leaf areas of the top three leaves could affect the photosynthesis rate. Studying the net blotch resistance and its genetic mechanism is essential in developing new resistance of barley cultivars (Dora *et al.,* 2017).

Moreover, the evaluation of the physiological and morphological variances of quantitative traits is usually used in genetic diversity studies between genotypes. Contrarily specified genetic differences at the DNA level are

abundant and distinct from environmental events (Garland *et al*., 1999). Microsatellite (SSR) markers are common tools for studying genetic diversity and in plant breeding studies. This method is based on polymerase chain reaction (PCR) requires small amounts of DNA, co-dominantly, multi-allelic, highly illuminating, and dominant in plant genomes (Powell *et al*., 1994).

Thus, the main goal of this investigation is to identify the high-yield potential of promising cultivars and more resistance to net blotch disease using field evaluation and molecular methods.

MATERIALS AND METHODS

In this study, ten barley genotypes were used containing two local varieties, and eight promising Egyptian lines. The genotypes were used to evaluate the productivity and the behavior of the Net Blotch disease (resistant or sensitive). The names of the ten genotypes and the pedigree of the barley genotypes are presented in **Table (1).**

This study was conducted during the two successful growing seasons; 2020/2021 and 2021/2022. The barley genotypes were evaluated under the field conditions at Sakha Agricultural Research Station ARC, Kafr el-Sheikh Governorate, Egypt.

Table 1. Name of the ten barley genotypes used in this study.

No.	Name
1	Giza 121 /4/Arar//Hr/Nopal/3/ Alanda -01/ Alanda-01
2	ACSAD 1182/4/ Arr/ ESP // Alger/ Ceres 362-1-1/3/ WI /5/ Alanda/Hamra// Alanda-01
3	Rihane-03// Lignee527NK1272/5/ Arizona5908/ Aths// Avt/attiki /3/s.t/ Barley/4/Aths/ Lignee 640/6/Giza 126
4	Giza 121/4/ Arar//Hr/Nopal/3/ Alanda -01/ Alanda-01
5	Lignee527/ NK1272/6/Cita'S'/4/ Apm/Rl//Manker/3/Maswi/ Bon/5/ Copal'S'+Aths/ Lignee 686/5/ Apm/RL/4/Api/ EB489-8-2-15-4// por/ U.Sask1766/3/ Cel/CI
6	Alanda/ Hamra/3/ AwBlack/Aths// Rhn-08/4/Giza 126
7	Panniy/ Salmas/5/ Baca"s"/3/AC253// CI08887/ CI05761/4/ JLB70-01
8	Giza 2000/4/ CalMr/3/ Alanda// Lignee527/Arar
9	GIZA 126
10	GIZA 134

Barley grains were sown at the seeding rate of 50 kg fed^{-1} for barley irrigated land of Egypt (hand drilled). Each barley genotype was sown in a plot size of 10.5 m^2 (15 rows of 3.5 m long and 20 cm apart rows). Sowing was performed on the first of December for the two seasons. This experiment was laid out in a randomized complete block design (RCBD) and was replicated three times. The experiment was surrounded by a powder mixture containing highly pathogenic genotypes.

Data were recorded from each plot on traits: days to heading (days), days to maturity (days), plant height (cm), spike length (cm), number of spikes m^{-2}, number of grains spike^{-1}, biological yield (ton fed^{-1}), grain yield (ton fed^{-1}), 1000 kernel weight (g) and net blotch disease.

According to Kearsey and Pooni (1996), the variance analysis was performed for each season's experiment. The mean performance for traits studied was measured and statistically significant level was compared using LSD at 0.05 and 0.01 levels of probability. Simple correlation(r) coefficients were performed according to Kearsey and Pooni (1996). All statistical analyses were performed using the computer software Costas Computer Program (Snedecor and Cochran, 1969).

Molecular studies:

DNA extraction and PCR amplification:

DNA was extracted from a fine powder of leaf tissues (100 -150 mg). The sequences of SSRs were revealed from the Grain Genes database according to Elakhdar *et al*., (2016). The markers were designated based on their identical distribution in the barley genome and their responsiveness to biotic stress (Varshney et al., 2007). DNA was extracted using the CTAB method (Doyle and Doyle 1990). A total volume of 10 µL of the PCR reaction was performed and the band size was observed using Ethidium Bromide staining and then visualized under UV light according to Elakhdar *et al*., (2016).

Genotypic data analysis and data scoring:

DNA was isolated by the CTAB method (Doyle and Doyle 1990) the polymorphic SSR markers were illustrated based on the amplification of the DNA. The molecular weight of each band was detected using Gel Analyzer 2010 (www.gelanalyzer.com). The number of allele frequency availability and polymorphic information content (PIC) were calculated according to Elakhdar *et al*., (2016). PIC was estimated using the subsequent formula: PIC = 1 − ∑ $xk2$.

PIC Values were analyzed for each of SSR loci Nei, (1978). Where xk is the allele frequency. The principal components analysis (PCA) was calculated according to Nei's genetic distance (Jaccard, 1912), between genotypes using the SSR markers. Correlation coefficients and *P* values were calculated using "Hmisc" packages in R, and the "Performance Analytics" package was used for drawing scatter plots.

Table 2. List of SSR markers used in the current study.

No	Marker	forward primer	reverse primer	Chr
1	GBM1078	GGGCCTCCTTTCTCTCTCTC	CCTTCTGCCTCCTCCTCAAT	3H
2	EBmac0695	AGTTGGTGACAGCCAAATA	ATCCTAAGACACATTTGCACT	1H
3	scssr10477	AGAGCAATGAGCTCCTACCC	GCTTACTCGCTCGTTTAGTCG	1H
4	GBM1405	TACACGCACTGAAAAGACGG	CTCGCTGCTGAGTTTGTCTG	3H
5	GBM1419	CGTCACGCCACTCACCTC	CTTGAAGTCGGAACCCATGT	7H
6	GBM1461	AAACCATGCATTCTTCAGAGA	TTTAGACCGACCCGATGAAG	1H
7	GBM1516	CCCTCTCCTTTCCCTATCGT	GTGGGGTTGATGTTCCTGTT	7H

RESULTS

Mean performance and interactions effect:

The differences between genotypes were significant or highly significant for all traits studied except for days to maturity were non-significant **Table (3).**

Effect of years:

Regarding the effect of years on the studied traits for the two seasons, data in Fig (1) showed that the second season had higher mean values of all studied traits compared to the first season except for the days to heading.

Table 3. The analyses of variance over genotypes (G) for studied traits.

SOV	df	Heading Date		Maturity Date		Plant height		Spike length		No. of grains spike^{-1}	
Seasons		**Season1**	**Season2**	**Season1**	**Season2**	**Season1**	**Season2**	**Season1**	**Season2**	**Season1**	**Season1**
Rep	2	2.53	0.13	2.63	1.03	0.23	0.3	0.26	0.13	9.73	3.1
Genotype	9	24.85**	26.06**	22.60^{ns}	31.94**	270.83**	175.20**	3.27**	3.63*	173.64**	77.1**
error	18	3.13	0.61	10.15	1.11	1.53	1.45	0.13	1.24	12.84	7.1
SOV	**df**	**No. of spikes m^{-2}**		**Biological yield**		**Grain yield**		**1000 Kernel weight**		**Net blotch**	
Seasons		**Season1**	**Season2**	**Season1**	**Season2**	**Season1**	**Season2**	**Season1**	**Season2**	**Season1**	**season2**
Rep	2	266.7	86.7	193083.3	748013.33	32250	5890	0.42	0.14	0.4	0.3
Genotype	9	1790.0**	2702.2*	2134453.7**	2863318.52**	381713.0**	357746.7**	47.06**	47.29**	22.4**	24.0**
error	18	322	685.6	60120.4	171465.19	10768.5	11501.1	6.66	0.17	0.3	0.4

The main effect of genotypes:

Concerning the genotypes means over the seasons, data in **Table (4)** clearly showed that Line 6 recorded the low number of days until the heading and exhibited the earliest Line, while Line 4 was the latest. Line 6 was the earliest in maturity; on the contrary Line 4 and Giza134 possessed the reverse trend for the same character. In addition, Giza 126 was the tallest genotype in both seasons with high values of plant height (125.67, and 123cm), in contrast, Line 6 was the shortest genotype (91, and 99cm), respectively.

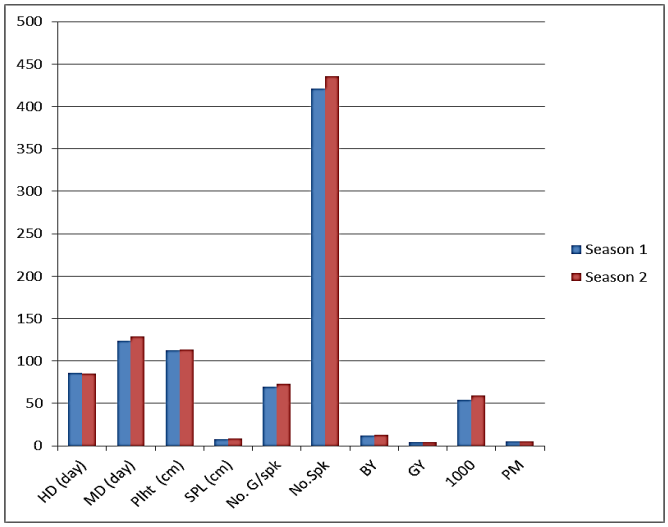

Fig. 1. The average of the different studied traits over the two seasons.

Also, data in Table (5) indicated that the highest mean values for spike length in both seasons were recorded for Giza 134 (9.67 and 9.67 cm) and line 4 (9.67, and 10.33 cm). On the other hand, line 8 was recorded as the lowest means (6.33, and 7.00 cm). Regarding the response of grains number spike^{-1}, the differences among genotypes were significant in both seasons. Line 6 and Line 2 displayed the highest values for number of grains spike^{-1} in the two seasons, respectively (78.00 and 79.67 grains) (76.00 and 77.67 grains). On the other hand, line 8 (55.33 and 66.00 grains) was the lowest value. The genotypes Giza134 (468.00 and 476.00) and Line 2 (439.00 and 470.00) recorded the highest number of spikes m^{-2} in both growing seasons. While the genotype Line 7 (386.00 and 376.00) was the lowest value.

Table 4. Means of the days to heading (HD), days to maturity (MD) and plant height (PLH cm) for the studied genotypes during the 2020/2021 and 2021/2022 seasons.

Genotypes	HD (day)		MD (day)		PLH (cm)	
	Season1	Season2	Season1	Season2	Season1	Season2
Line 1	84.33	80.00	122.00	126.33	117.00	121.00
Line 2	89.67	88.00	126.67	133.67	117.00	120.67
Line 3	84.67	84.00	122.33	127.67	106.33	111.33
Line 4	89.00	89.33	127.00	133.67	116.67	118.67
Line 5	84.67	85.33	122.67	130.00	114.67	112.00
Line 6	80.33	82.67	119.00	124.67	91.00	99.00
Line 7	87.00	83.00	125.00	127.33	105.00	115.00
Line 8	87.67	85.67	121.00	128.00	115.67	108.00
Giza 126	84.33	84.00	123.00	127.00	125.67	123.00
Giza 134	88.67	88.67	127.00	133.00	115.67	106.33
G LSD 0.05	3.03	1.35	5.47	1.81	2.12	2.06

Results in **Table (6)** indicated that genotypes showed significant differences in biological yield **(ton fed^{-1})**. Line 2 (6.733 and 5.966 **ton fed^{-1}** in the first and second seasons respectively**)** and Line 6 (6.333 and 6.400 **ton fed^{-1}** in the first and second seasons respectively**)** gave the highest mean values in both seasons. While, Line 7 had the lowest performance during the two seasons. The scored data in the same Table showed that the genotypes demonstrated highly significant differences in grain yield **(ton fed^{-1})**. Line 2 (2.433 and 2.200 **ton fed^{-1}** in the first and second season respectively) and Line 6 (2.166 and 2.286 **ton fed^{-1}** in the first and second season respectively) gave the highest mean values. Where Line 7 scored the lowest mean values in both growing seasons.

Table 5. Means of spike length (cm), no. of grains spike^{-1} and no. of spikes m^{-2} for the studied genotypes during the 2020/2021 and 2021/2022 seasons.

Genotypes	spike length (cm)		No. of grains spike^{-1}		No. of spikes m^{-2}	
	Season1	Season2	Season1	Season2	Season1	Season2
Line 1	8.00	9.67	76.00	77.33	428.00	438.00
Line 2	8.00	9.00	76.00	77.67	439.00	470.00
Line 3	7.33	7.00	68.00	74.00	400.00	417.00
Line 4	9.67	10.33	70.00	66.33	391.00	432.00
Line 5	7.83	7.67	72.00	72.67	434.00	440.00
Line 6	8.00	7.33	78.00	79.67	428.00	442.00
Line 7	8.00	9.33	68.00	77.33	386.00	366.00
Line 8	6.33	7.00	55.33	66.00	420.00	434.00
Giza 126	7.00	8.67	58.00	72.00	419.00	440.00
Giza 134	9.67	9.67	74.00	72.00	468.00	476.00
G LSD 0.05	0.62	1.15	**1.77**	4.57	30.78	44.92

For the **1000 kernel weight (g)** mean of the genotypes, Line 2 exhibited the highest mean performance these data are presented in **Table (7).** Moreover, data in the same table showed that genotypes Giza 134 (1.33 and 1.67), Line 2 (2.67, and 1.67), Line 5 (1.67 and 2.33), and Line 6 (2.67 and 3.33) had the lowest mean values for net blotch in the two seasons (Resistant). On the other hand, Line 8 (8.67 and 9.00) was the highest mean value (Susceptible). While Giza 126, Line 1, Line 3, Line 4 and Line 7 were moderately susceptible.

Table 6. Means of biological yield (ton fed^{-1}) and grain yield (ton fed^{-1}) for the ten studied genotypes during the 2020/2021 and 2021/2022 seasons.

Genotypes	Biological yield (ton fed^{-1})		Grain yield (ton fed^{-1})	
	Season1	Season2	Season1	Season2
Line 1	5.933	5.500	2.266	1.990
Line 2	6.733	5.966	2.433	2.200
Line 3	5.566	5.686	2.066	1.320
Line 4	5.133	3.893	2.033	1.393
Line 5	5.300	4.900	2.100	1.503
Line 6	6.333	6.400	2.166	2.286
Line 7	3.833	3.600	1.433	1.423
Line 8	5.233	4.566	1.600	1.503
Giza 126	4.716	3.953	1.433	1.596
Giza 134	6.100	5.666	2.216	1.850
G LSD 0.05	420.62	710.34	178.02	183.97

Table 7. Means of 1000 kw (g) and net blotch for the ten studied genotypes during the 2020/2021 and 2021/2022 seasons.

Genotypes	1000 kw (g)		Net blotch	
	Season1	Season2	Season1	Season2
Line 1	55.07	62.23	5.33	6.00
Line 2	62.93	61.03	2.67	1.67
Line 3	53.67	58.67	7.33	7.67
Line 4	59.07	57.51	5.33	5.67
Line 5	52.43	60.41	1.67	2.33
Line 6	52.23	57.32	2.67	3.33
Line 7	52.03	62.11	7.33	7.67
Line 8	49.00	49.00	8.67	9.00
Giza 126	56.23	60.19	7.67	8.00
Giza 134	54.77	62.02	1.33	1.67
G LSD 0.05	**2.75**	**0.36**	**0.98**	**1.15**

The correlation coefficient between the studied traits:

Fig (2) shows the correlation between all pairs of the studied traits in the first and second seasons. Positive and highly significant correlation between heading date and maturity date (r = 0.85), a positive and highly significant correlation between grain yield with spike length (r = 0.83), and a positive significant correlation between spike length with 1000 kernel weight in the first season. In addition, the positive and extremely significant correlation between heading date and maturity date (r = 0.91), the positive significant correlation between plant height with both spike length (r = 0.67) and net blotch (r = 0.68), also between spike length with kernel weight (r = 0.71) and biological yield with grain yield (r = 0.73). On the other hand, a negative significant correlation between the heading date and maturity date with net blotch (r = -0.73 and r = -0.67, respectively) in the second season.

Molecular diversity:

Polymorphism of SSR analysis:

Table (8) shows the data obtained from seven microsatellite primers to detect polymorphism level of ten barley genotypes. A total of 16 alleles were generated from the seven SSR primers in which 13 primers with polymorphic alleles, representing a level of polymorphism of 85.71%. Each primer generates two except for GBM1078 primer generate was four. The number of polymorphic alleles per primer pairs ranged from 1 in (GBM1419) to 2 in all primers. The average of the total alleles per primer was 2.3, while the average of polymorphic alleles per primer was 1.86. Major allele frequency (MFA) ranged from 0.08 to 0.83 in all primers. Also, common alleles ranged from 0.03 to 0.69 with an average of 0.27. As presented in Table (9), the values of polymorphic information content (PIC) ranged from 0.25 to 0.87 indicating a uniform polymorphism rate among the primers.

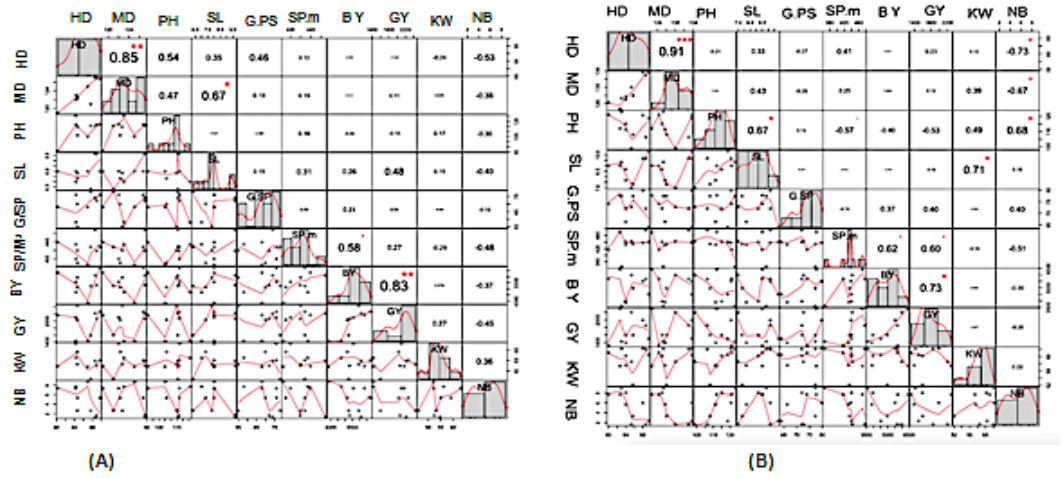

Fig. 2. The correlation analysis between the studied traits. (A): First season, (B): Second season. ". ", *,**, and *** are *P* values of 0.001, 0.01, 0.05, 0.1, 1. DH: days to heading, DM: days to maturity, PLH: plant height, SL: spike length, Sp/M^2: no. of spikes m^{-2}, G/S: no. of grain spike^{-1}, Kw:1000 Kernel weight, BY: biological yield, GY: grain yield, NB: net blotch.

The dendrogram explaining the genetic relationships among the tested genotypes is presented in Fig. (3). The results revealed that the set of genotypes tested was divided into two clusters. The first cluster consisted of Line 8 (Net blotch susceptible cultivar) and the other cluster is divided into two sub-clusters. The first sub-cluster consisted of two branches. For Principal Component Analysis based on the polymorphic results (PCA) three possible groups can be distinguished that are group I which contained the most resistant genotypes to net blotch disease Giza 134, Line 2, Line 5 and Line 6, group II comparing the moderately susceptible genotypes Giza 126, Line 1, Line 3 and Line 7, respectively and group III Line 8 (Fig. 4).

Table 8. Number of the amplified DNA bands as well as the polymorphism percentage generated by the eight SSR primers.

Primer name	Ch.	position	No. of alleles		Polymorphism %	Mol. size range of alleles (bp)	Allele freq	Common allele	PIC
			Total	Polymorphic					
GBM1078	3H	68.16	4	2	50.0	730- 1640	0.17- 0.83	0.03- 0.69	0.25
EBMAC0695	1H	65.31	2	2	100.0	50- 86	0.25- 0.50	0.06- 0.25	0.69
SCSSR10477	1H	79.09	2	2	100.0	143- 215	0.08- 0.75	0.01- 0.56	0.43
GBM1405	3H	68.33	2	2	100.0	50- 86	0.17- 0.75	0.03- 0.56	0.41
GBM1419	7H	95.75	2	1	50.0	143- 215	0.58- 0.83	0.34- 0.59	0.87
GBM1461	1H	129.70	2	2	100.0	50- 86	0.17- 0.67	0.03- 0.44	0.53
GBM1516	7H	81.21	2	2	100.0	143- 215	0.33- 0.50	0.11- 0.25	0.64
	Total		**16**	**13**					**3.82**
	Average		**2.3**	**1.86**	**85.71**			**0.27**	**0.55**

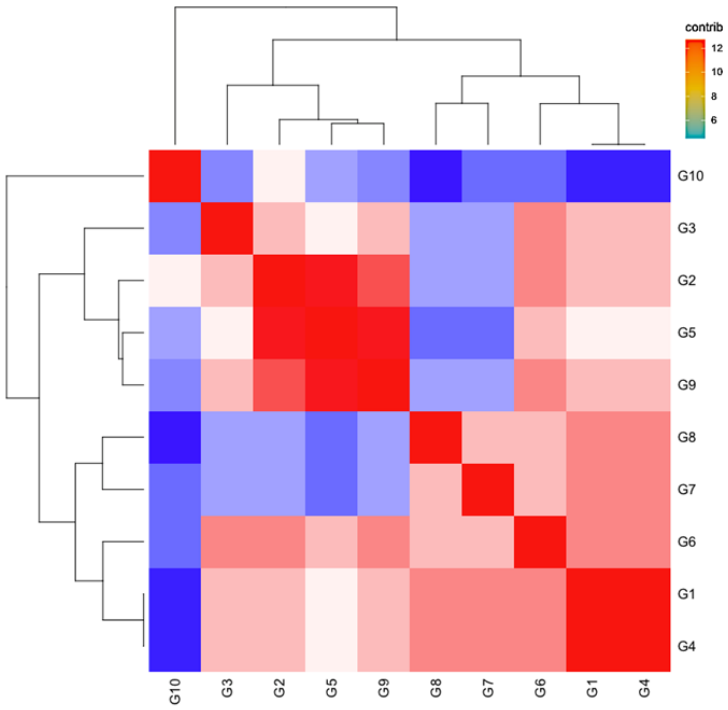

Fig. 3. Genetic relationships dendrogram among the tested genotypes. G1=Giza134, G2=Giza126, G3=line1, G4=line2, G5=line3, G6=line4, G7=line5, G8=line6, G9=line7 and G10=line8.

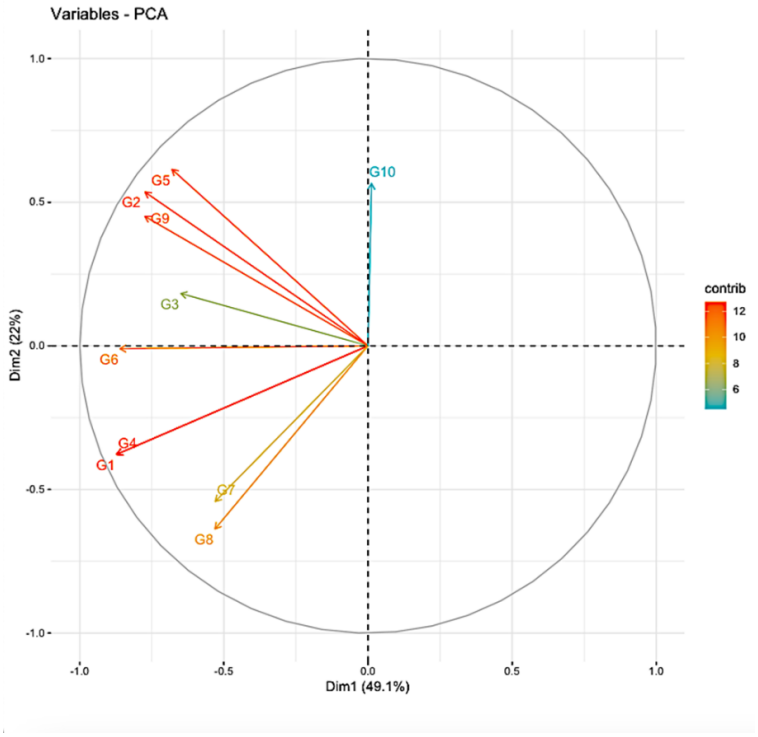

Fig. 4. Principal Component Analysis based on the polymorphic results (PCA). G1=Giza134, G2=Giza126, G3= Line 1, G4= Line 2, G5= Line 3, G6= Line 4, G7= Line 5, G8= Line 6, G9= Line 7 and G10= Line 8.

DISCUSSION

The differences among genotypes were significant or highly significant for studied traits except for days to maturity which were non-significant indicating that genotypes differed in their performance. Our results agree with those of Abaas *et al.* (2016) who found highly significant variances for the studied traits, except for no. of spikes plant^{-1}, for parents and days to maturity for parents vs. crosses also El-Refaey *et al.* (2017) found highly significant differences among genotypes for all the studied traits. The scored data displayed that the genotypes showed highly significant differences in grain yield (ton fed^{-1}). Line 2 and Line 6 gave the highest mean values, Line 7 scored the lowest mean values in both growing seasons. These results indicated that yield losses, caused by net blotch disease ranged from 10% to 40%. Liu, Z. *et al*. (2011) reported that yield losses, caused by net blotch disease were associated with yield losses ranging from 10% to 40%. Dora *et al*. (2021) found that the high-yielding genotypes showed high-yield component trait estimates (no. of grains spike^{-1}, no. of spikes plant^{-1} and 100-grain weight) compared with high net blotch foliar disease resistance. A positive and highly significant correlation between grain yield with spike length (r = 0.83), and a positive significant correlation between spike length with 1000 kernel weight in the first season. These results agreed with Ali *et al*. (2009) found positive significant and highly significant correlations between spike length and 100-kernel weight (r = 0.197) and number of kernels per spike (r = 0.629), respectively. The SSR marker GBM1419 showed the highest level of polymorphism with a PIC value of 0.87 whereas, SSR marker GBM1078 expressed the lowest level of PIC value (0.25). In this respect, Dora *et al*. (2017) differentiated 20 barley genotypes using SSR markers. These SSR primers produced 40 alleles ranging from two to eight alleles per locus with a mean value of 5 alleles per locus. Aboulila and Mansour (2017) reported that amplification products scored a polymorphism percentage of 94.44% for Triple-SCoT and 90.91% for SSR, while the average no. of polymorphic fragments/primer was 17 and 7.14 in the two marker systems, respectively. Khodayari *et al*. (2012) estimated the genetic diversity of 32 landraces barley using 17 microsatellite markers. A high level of polymorphism information content (PIC; average = 0.651) and an average of 8.1 alleles per locus were observed.

CONCLUSION

Generally, the most promising genotypes were Giza 134, Line 2, Line 5 and Line 6 for net blotch infection and grain yield, these genotypes would be important in breeding programs for improving both traits in barley.

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تقييم الانتاجية والمقاومة لمرض التبقع الشبكى لبعض التراكيب الوراثية من الشعير

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تم تقييم ودراسة الاختلافات بين عشرة تراكيب وراثية من الشعير للمحصول ومرض التبقع الشبكي في محطة البحوث الزراعية بسخا خلال موسيمي 2021/2020 و20222/2021 لتحديد افضل التراكيب الوراثية من الشعير والتي لها القدرة علي انتاج محصول عالي واكثر مقاومة لمرض التبقع الشبكي. تم دراسة صفات التبكير ومحصول الحبوب ومكوناتة بالإضافة للإستجابة للعدوي بمرض التبقع الشبكي. اظهر تحليل التباين وجود فروق معنوية أو عالية المعنوية بالنسبة للصفات المدروسة؛ ولقد اوضحت النتائج ان السلالة 2 والسلالة 6 سجلت اعلي القيم لمحصول الحبوب في كلا الموسمين. علاوة علي ذلك؛ كان الصنف جيزة 134 والسلالات 2 و5 و 6 كانو اكثر التراكيب الوراثية مقاومة حيث اعطوا اقل القيم لمرض التبقع الشبكي. بالنسبة للارتباط الخطي بين الصفات المدروسة فقد اظهرت النتائج وجود ارتباط معنوي موجب بين طول النبات ووالمقاومة للتبقع الشبكي (R0.68=) وفي الاتجاة الاخر؛ فكان هناك ارتباط معنوي سالب بين عدد الايام حتي الطرد؛ عدد الايام حتي النضج مع المقاومة للتبقع الشبكي (R=-0.73 ؛ 0.67R=-علي التوالي) في الموسم الثاني. اما بالنسبة للتحليل الجزيئي فقد تم استخدام سبعة ازواج من بادئات ال (GBM1078, EBMAC0695, 5SCSSR104770, GBM1405, GBM1419, GBM1461, GBM1516) لدراسة التباينات المختلفة للتراكيب الوراثية المقاومة والحساسة للتبقع الشبكي كل البوادئ اعطت تباينات مختلفة لتقييم التنوع الوراثي للعشرة تراكيب وراثية. لذالك فإن التراكيب الوراثية جيزة 134 والسلالة 2 والسلالة 5 والسلالة 6 يمكن الإستفادة منهم في برامج التربية للمحصول العالي واكثر مقاومة لمرض التبقع الشبكي.

الكلمات المفتاحية: الشعير ، الإنتاجية، التبقع الشبكى ، المقاومة، المعلمات الجزيئية، الإرتباط.