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## Effects of Powdery Mildew on Quantity and Quality of Some Barley Cultivars under Egyptian Condition

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### ABSTRACT

Field experiments were conducted based on ten Egyptian barley cultivars (Giza 2000, Giza123, Giza 126, Giza 130, Giza131, Giza 132, Giza133, Giza134, Giza 135, Giza 136) sown in pure stands. No fungicide was used, and under natural infection, we carried out field tests throughout two seasons of growth at Giza station in 2021/2022 and 2022/2023, environmental conditions made it a hot spot for powdery mildew. Barley powdery mildew disease caused by a biotrophic air-born fungus *Blumeria graminis* f. sp. hordei. It is the most widespread disease in most barley cultivars worldwide. The results showed that six barley cultivars (Giza 131, Giza 132, Giza 133, Giza134, Giza135 and Giza 136) showed an adequate level of powdery mildew disease resistance during this study as they recorded a small percentage of disease severity did not surpass 50.5, and the AUDPC's lowest values (less than 300), whereas the barley cultivars; Giza 123, Giza 126, Giza 130 and Giza 2000 displayed high susceptibility to powdery mildew disease. High percentages of disease severity reached (59.5) and the high area under the disease progress curve (AUDPC) estimates more than (345.4). The research evaluates the relationship between disease severity and various grain yield traits of ten Egyptian barley cultivars. It employs statistical analyses and biplot graphs to interpret the correlations among the traits. Furthermore, the study examines the performance of barley genotypes and their resistance to the disease. The findings suggest that the GT biplot analysis is valuable for this study.

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### INTRODUCTION

Barley (*Hordeum vulgare*L.) is considered one of the major cereal crops in Egypt and worldwide. It ranks fourth in terms of cultivation cereal crops after wheat, maize, and rice as it is an important source of daily nutritional needs for both humans and animals in the majority of developing countries, including Egypt (Malcolmson *et al.* 2005).

In Egypt, barley is grown extensively in the North Coastal Region and recently reclaimed areas with saline soils and little water. Barley cultivars are generally under a severe and continuous challenge from several biotic and abiotic stresses that have a major impact on the annual yield production of commercial barley cultivars in Egypt. One of the most biotic constraints is the powdery mildew biotrophic fungal disease as it is the major challenge to sustain and successfully gain a satisfactory barley production (Tratwal and Bocianowski 2014 and Abdullaev *et al.*, 2021). In humid, fairly temperate areas, powdery mildew can cause output losses of up to 30%, on average (Agostinetto *et al.*, 2014). The disease can be managed in several ways. The first is the application of genetically modified mildew-resistant genotypes. This is an inexpensive, safe method for the environment. Many identified resistance genes have the potential to protect control

against barley powdery mildew infection. In barley, more than 85 race-specific resistance genes against powdery mildew have been found by Jørgensen (1994).

In Egypt, the problem with powdery mildew is the tile susceptibility of most of the commercial barley cultivars to this disease (Ghobrial *et al.* 1990). The most significant and negative impact on grain yield is the severe infection that can lead to substantial yield losses (Royse *et al.*, (1980). However, the severely infected barley plants and evaluation variability potential of ten commercial cultivars for resistance to powdery mildew elucidate that a plant may be much shorter than healthy plants, which can lead to a reduction in grain yield. Powdery mildew infection can reduce thousand kernel weight, leading to the lowest quality of grains (Cao *et al.* (2014). The severity level of powdery mildew disease severity can vary depending on factors such as weather conditions, cultivar susceptibility, and disease management practices. Higher disease severity is typically associated with greater yield losses than that of lower disease severity (%).

A plant breeding decision based only on the correlation coefficients between the desired traits might not always work because it just offers one-

dimensional data, ignoring the intricate interactions between these significant plant characteristics. (Carlos and Osva, 2022)

Therefore genotype x trait (GT) biplot analysis, as a novel and important procedure, permits the illustration showing the actual relationship between the evaluated characteristics and a good, complete, and full understanding of the relationships between these traits, that facilitate an obvious identification of these useful traits that can be well used in a correct and profitable indirect selection for an adequate level of disease resistance and a high grain yield of the target cultivars (Yan and Rajcan, 2002; Yan and Tinker, 2005; and Yan, 2014). Furthermore, GT biplot analysis provides information on the evaluated cultivars' production utility as well as information that in the detection of the less important (redundant) traits. In the previous study of (Swelam 2012), I mainly Utilized the GT biplot chart to display the connections between barley genotypes, various agronomic characteristics, and their relationships. The GT biplot graph can effectively aid in selecting multiple traits for barley breeding programs. Although there has been a recent curiosity in the GT biplot graph for interpreting genotype and trait data in Egypt, it is not commonly used in yield trials. Therefore, fewer or little numbers of references were found in the literature concerning this important technique. The primary goal of this research was to evaluate and characterize more precisely a host-genetic resistance to powdery mildew in ten Egyptian barley cultivars. The second objective was to assess the negative effect of powdery mildew on both quantitative and qualitative grain yield of these barley Egyptian cultivars through an accurate estimation of the two widely used i.e disease severity (%) and (AUDPC) disease parameters, yield components, and some chemical properties of barley grains.

Another aim of this study was also to identify a combination of the important traits, namely, grain

yield and disease severity (%)

The ultimate goal of this study was to illustrate the real relationship between the two disease parameters and yield components, under study to provide valuable insights to barley breeding programs and the development of disease-resistant barley varieties. Also, the correlation coefficient approach and genotype trait (GT) biplot analysis a valuable tools for understanding the relationships between these desired agronomic traits and powdery mildew disease parameters. GT biplot graph can be a viable alternative analytical method instead of using the correlation coefficient approach.

## MATERIALS AND METHODS

Ten commercially barley cultivars (*Hordeum vulgare*L.), kindly provided by Barley Res. Department Field Crops Res. Institute, Agric. Res. Center, Egypt, were used in the field experiment. The study at Giza Agriculture Research Station in the two consecutive growing seasons, 2021/2022 and 2022/2023. The name and pedigree of these local cultivars are shown in Table (1).

The above-mentioned barley cultivars were planted in plots as a Randomized Complete Block Design( RCBBD) with three replications was implemented, where the plot size (experimental unit) was 2.4 m<sup>2</sup> (6 rows x 0.2 m x 2.0 m).The sowing rate of barley in Egypt is 50 kg/fed sown by using the broadcasting method.

### Disease assessment under field conditions:

Natural powdery mildew infections on barley plants were assessed every 7–10 days during the growing season (on mature plants. The intensity of the disease infection was assessed using the following:

In each trial, ten plants at the heading stage from each barley cultivar under study were assessed visually disease on a 0–10 scale for the percentage of leaf area covered by powdery mildew disease (Large, 2007).

**Table 1: Name and pedigree of the ten barley cultivars, used in the field experiments of the study.**

No.	Name	Pedigree
1	Giza 2000	C .C 89/3/Alanda/Hamra//Alanda-01
2	Giza 123	Giza 117/FAO 86
3	Giza 126	BaladiBahteem/S D729-Por12762-BC.
4	Giza 130	Comp.cross"229//Bco.Mr./DZ02391/3/DeirAlla 106
5	Giza 131	CM67B/CENTENO//CAMB/3/ROW906.73/4/GLORIABAR/COME-B/5/FALCON BAR/6/LINO
6	Giza 132	Rihane-05//AS 46/Aths*2Athe/ Lignee 686
7	Giza 133	Carbo/Gustoe
8	Giza 134	Alanda-01/4/W12291/3Api/CM67//L2966-69
9	Giza 135	ZARZA/BERMEJO/4/DS4931//GLORIABAR/COPAL/3/SEN/5/AYAROS
10	Giza 136	Plaisant/7/Cln-B/Ligee640/3/S.P-B//Gloriaar/ Come B/5/Falconbar/6/LinoCln-B/A/S.P/Lignee640/3/S.P-B//Gloria-Bar/Come B/5/Falconbar/6/Lino

Disease scores were converted for analysis by (Hafez *et al.*, 2014). i.e. 0 = 0 %, 1 = 0–3 %, 2 = +3–6 %, 3 = +6–12 %, 4 = +12–25 %, 5 = +25–50 %, 6 = +50–75 %, 7 = +75–88 %, 8 = +88–94 %, 9 = +94–97 % and 10 = +97–100 %. The disease severity index (DSI) was calculated using the following formula:

$$DSI = \frac{\sum \text{Ratings of each plant}}{10 \times \text{Number of plants rated}} \times 100$$

D.S.I= Disease severity index

#### Area under disease progress curve (AUDPC):

The (AUDPC) was calculated using a simple formula adopted by Pandey *et al.*, (1989) as a more reliable estimator follow:

$$AUDPC = D \left[ \frac{1}{2}(Y_1 + Y_k) + (Y_2 + Y_3 + \dots + Y_{k-1}) \right]$$

Whereas: D = days between two consecutive scores (time intervals)

$Y_1 + Y_k$  = sum of the first and last disease scores

$Y_2 + Y_3 + \dots + Y_{k-1}$  = sum of all in-between disease scores.

The RAUDPC for mixtures was determined by comparing the disease area under mixtures with that of cultivars in pure stands (mixture components).

#### Yield components:

Ten Egyptian barley varieties (*Hordeum vulgare* L.) were used in this study. These varieties were grown at Giza Research Station during two growing seasons 2021/2022 and 2022/2023. They were planted in a Randomized Complete Block Design (RCBD) with three replicates. Mature grain was harvested from each plot using a combine. Weigh to grain from each plot was measured and used to calculate the yield

At harvest time, grain yield (GY) was determined from the yield of the central area of the plot and then transformed to the unit of (Ton hectare<sup>-1</sup>). Grain yield-related traits were measured such as Spike length (SL, cm), Spike weight (SW), Grain spike number (GSN), Grain spike weight (GSW), and thousand kernel weight (TKW),

#### Assessment of qualitative traits:

Quality traits of each of the tested barley cultivars were also measured as total protein (TP), total lipid (TL), total fiber (TF), total carbohydrates (TC), (TDF) total dietary fiber, B- glucan and S.B glucan according to AOAC (2000) and crude ash was measured by weight 100 g seed and set them in an oven at 80°C for three days and later at 750 °C for five hrs. that turned it into ash.

#### Statistical analysis:

At first, an analysis of variance (ANOVA) was applied, and after that, a combined analysis of variance was computed over the two growing seasons of the study according to Snedecor and Cochran (1981). Before running the combined analysis, the Levene (1960) test was used to satisfy the assumption of homogeneity of variances. Mean

comparisons were done using least significant difference (LSD) values at a 5% level of probability (Steel and Torrie 1984).

The simple correlation coefficient approach was used to compare grain yield (as the resultant variable) and its related characters (as casual variables) this procedure was studied using simple correlation coefficients between all pairs of the studied traits, as suggested by Steel *et al.* (1997).

GGE Biplot analysis could be used for all types of two-way data sets such as genotypes with multiple traits. Gabriel (1971) and Yan and Rajcan (2002) used the genotype by trait (GT) biplot, analysis which is an application of the GGE biplot to study the genotype by trait data. Because the traits were measured in different units, the biplot procedure was generated using the standardized values of the trait means. All statistical analyses were performed using the computer software Gen Stat Program V.19.

## RESULTS AND DISCUSSION

#### Analysis of variance

Before operating a combined analysis of variance, using of Levene test (1960) proved the homogeneity of separate error variances for all studied characters. Results in Table(2) exhibited that mean squares due to year, cultivar, and interaction between them were highly significant (0.05 or 0.01 probability levels) for characters, The significant cultivar × year interaction indicated that differences among cultivars were not stable from 1 year to another, and these interactions are unavoidable in agricultural investigations (Yan and Kang, 2003), Therefore, it is enough to present the combined averages across the two seasons without showing its seasonal averages. These results reflect the different genetic backgrounds of the studied cultivar for disease traits and yield characteristics.

The results of the combined analysis of variance (Table 3) indicated high significance for quantitative and disease traits such as. Spike length, Spike weight, Grain Yield t h<sup>-1</sup>, Grain spike number, Grain spike weight, 1000kernel weight(TKW), Disease Severity(D S%), and Area under disease progress curve (AUDPC). Analysis of variance of the six yield-related traits; Spike length, Spike weight, Grain Yield t. h<sup>-1</sup>, Grain spike number, Grain spike weight, and 1000kernel weight showed that all the Egyptian barley cultivars had highly significant genotypic differences for all yield traits as shown in Table (2). There were highly significant variations in the thousand kernel weight (TKW) of barley cultivars based on their spike type and other genotypic traits. The highest (TKW) was found in Giza 136 (53.49 g) and the lowest in Giza 2000 (40.16 g).

**Table 2: Analysis of variance of disease traits in 10 evaluated barely cultivar**

Separate years					
Source of variation	d.f.	DS%		AUDPC	
		MS		MS	
		Y1	Y2	Y1	Y2
R	2	0.00108	0.00049	3.333	10
C	9	36.775**	35.48605**	28475.34**	26570.43**
Residual	18	0.00138	0.00351	3.333	6.296
Total	29				
Combined					
Source of variation	d.f.	DS%	AUDPC		
		MS	MS		
R	2	0.00079	1.667		
Y	1	0.618135**	305.553**		
Residual	2	0.00079	11.667		
C	9	72.21967**	55017.39**		
Residual	18	0.00244	5.37		
Y.C	9	0.041172**	28.381**		
Residual	18	0.00244	4.259		
Total	59				

\*, \*\* = Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.

C :cultivars Y: years AUDPC: Area under disease progress curve

DS%disease severity

Means of (KW) trait ranged from 40.16 g (Giza 2000) to 53.49 g (Giza 136) among all cultivars with a grand mean of 49.6 g. Concerning the Spike length, the results in Table (2) showed that Giza 136 gave the highest Spike length with values of (16.26 cm, but Giza 2000 and Giza 123 showed the lowest S length (11.32cm and 11.44cm).

Giza 2000 and Giza 123 showed the lowest S lengths (11.32cm and 11.44cm).

Regarding the number of grains spike-1 (GSN), data in Table (4) showed that Giza 130 recorded the highest GSN with the value of (54 grains/spike) however, the lowest GSN value (44.49 grains/spike) was detected by Giza 123.

The G.s.w data in Table (3) showed that Giza 133 recorded the highest G.s.w with a value of (2.78 gm) however; the lowest G.s.w value (1.07 gm) was detected by Giza 2000. Regarding SW the highest value is 3.4 gm in Giza 135 and the lowest value are 2.27 gm in Giza 2000

In this study, a significant difference was found among all cultivars with a grain yield mean of 5.37 tons h<sup>-1</sup>. The highest grain yield value was determined by Giza 136 with 5.93-ton followed by Giza 135 (5.83-ton h<sup>-1</sup>) and the lowest value is 4.35-ton h<sup>-1</sup> in Giza 2000 as shown in Table (3), Our results indicated high performance for Egyptian cultivars (Giza 136, Giza 135, Giza 133, Giza132 and Giza 130 in almost of studied traits. This results in a good harmony with (Mariey *et al.*, 2023).

Concerning the disease traits D S% and AUDPC gave the highest value at 9.42% and 290.4 with Giza 123 followed by Giza 2000 8.58% and 281 respectively and the lowest value were 0.55%,59.65,0.55%, and 61.32 in Giza 126 and Giza 135. the results show that the cultivars most susceptible to disease are Giza 123 and Giza 2000.

Characterization of powdery mildew disease resistance in the ten barley cultivars under field conditions. To precisely characterize during the two growing seasons of this study, the two widely used and more reliable estimators for disease resistance i.e. disease severity (%) and area under the disease progress curve were accurately estimated for each of the studied cultivars (Table 3).

#### **Effect of Powdery mildew disease on barley grain quality traits of the tested cultivars:**

Barley grains are used primarily as the source of energy for both humans and animals, Thus the main components of the barley grain are, protein, lipid, and carbohydrate and some minor components significantly affect the food-use quality of barley.

In this investigation, the analysis of variance of grain quality traits such as. Protein, t. lipid, t. fibres, crude ash.t. carbo, TDFB- glucan, and S.B glucan showed high difference significance among all the Egyptian cultivars for all the studied traits as shown in Table (5). the two varieties, Giza 135 and Giza 136 gave the best quality traits and the least disease severity.

**Table 3: Powdery mildew disease parameters i.e disease severity (%) and area under disease progress curve (AUDP) assessed in the ten barley cultivars of the study, under field conditions during the two growing seasons 2021/2022 and 2022/2023**

Cultivar	DS%			AUDP		
	Y1	Y2	comb.	Y1	Y2	comb.
Giza 123	59.5	59.33	59.415	345.4	335.4	340.4
Giza 126	55.3	54.85	55.075	232.2	229.5	230.85
Giza 130	54.87	54.33	54.6	233.53	226.2	229.87
Giza 131	20.92	20.82	20.87	50.3	59.1	59.7
Giza 132	21.2	21.1	21.15	65.7	57.87	61.78
Giza 133	20.6	20.5	20.55	60.1	59.3	59.7
Giza 134	21.18	20.93	21.055	55.8	50.8	53.3
Giza 135	20.57	20.53	20.55	50.5	52.13	51.32
Giza 136	20.6	20.5	20.55	50.1	52.2	51.15
Giza 2000	58.67	58.49	58.58	336.5	325.5	331
Mean	35.34	35.14	35.23	148.01	139.4	153.65
L.S.D of C	0.06	0.101	0.05997	3.13	4.3	2.81
Y			0.03113			3.795
CXY			0.07895			3.965

AUDPC: Area under disease progress curve DS% disease severity

C: cultivars y: years

The data showed that the relation between DS and AUDPC was significant Giza 123 was high susceptibility to powdery mildew and Giza 131 was resistance.

**Table 4: Effect of powdery mildew infection on grain yield, and its related traits of the 10 tested Egyptian barley cultivars overall two growing seasons, under study 2021 /2022 and 2022/2023.**

Barley Cultivar	Grain yield component					
	Spike length	Spike weight	grain yield t. h-1	Grain spike number	Grain spike weight	1000 kernal weight
Giza 123	11.44	2.56	4.8	44.69	2.29	45.86
Giza 126	13.35	2.73	5.04	49.05	2.4	49.78
Giza 130	13.23	2.71	5.2	54	2.51	50.53
Giza 131	13.83	2.69	5.55	52.67	2.27	52.66
Giza 132	16	2.61	5.64	53.83	2.71	51.4
Giza 133	15.5	3.29	5.7	52.33	2.78	51.4
Giza 134	13.8	2.99	5.72	52.32	2.59	50.27
Giza 135	14.48	3.4	5.83	53.17	2.71	50.89
Giza 136	16.26	3.35	5.93	52.47	2.5	53.49
Giza 2000	11.32	2.27	4.35	47.69	1.07	40.16
Mean	13.92	2.38	5.37	51.22	2.86	49.6
L.S.D	0.79	0.09	0.09	0.79	0.04	0.97
Analysis of variance (F Test) varieties	**	**	**	**	**	**

\*, \*\* significant at the 0.05 & significant at the 0.01 probability levels, respectively

AUDPC: Area under disease progress curve DS% disease severity

While Giza 123 and Giza 2000 gave the lowest quality traits and the highest disease severity.

#### Correlation studies:

#### Correlation between powdery mildew disease parameters and quantitative agronomic traits of the tested barley cultivars

The relationship between a disease severity (%) of powdery mildew and some quantitative and

qualitative grain yield traits of the tested barley cultivars were fully determined and interpreted. Through conducting the two main and highly effective statistical analyses i.e. simple correlation coefficient and genotype by trait (GT) biplot, two pivotal techniques were greatly used and effectively used to visualize and explain more accurately. Simple correlation coefficients for all comparisons among

the barely studied traits are presented in Table (6). Results showed that there was a highly significant and positive correlation between KW, GYH (0.859\*\*), GSW (0.787\*\*), and SPL (0.674\*\*), GSN, GYH (0.729\*\*). This strong correlation suggested that KW may be raised through selection for more spikes. These findings indicate that

selection for KW and GSW would be accompanied by high-yielding ability Gab Alla *et al* (2018), Heru *et al* (2018), and Yassin *et al* (2022). On the other hand, DS% and AUDPC in powdery mildew disease susceptibility highly significantly correlated and negatively with all traits, while the relation between DS% and AUDPC was highly positive (995\*\*).

**Table 5: Effect of powdery mildew disease infection on grain quality traits of the 10 tested Egyptian barley cultivars overall two growing seasons 2021 /2022 and 2022/2023**

Barley Cultivars	Grain barley quantitative traits							
	Total protein	Total lipid	Total fiber	crude ash	Total carbo	TDF	B-glucan	S.B glucan
Giza 123	6.51	1.46	6.67	3.89	64.15	11.23	4.45	3.24
Giza 126	10.53	2.39	8.65	4.56	77.18	13.15	5.46	3.1
Giza 130	12.55	2.77	10.33	5.55	77.49	12.65	5.78	4.09
Giza 131	12.44	2.94	8.95	4.975	77.68	12.15	5.46	3.69
Giza 132	10.63	2.55	8.85	4.77	77.33	13.25	5.32	3.84
Giza 133	10.75	2.8	9.25	4.77	75.14	13.41	5.48	3.79
Giza 134	9.49	2.09	7.98	4.74	75.6	13.52	5.44	3.77
Giza 135	10.67	2.25	9.16	4.53	76.43	13.57	5.48	4.33
Giza 136	10.93	2.75	9.38	4.64	78.37	13.76	5.48	4.4
Giza 2000	6.26	1.4	7.945	4.7	55.96	12.04	4.05	3.89
Mean	10.07	2.34	8.72	4.71	73.53	12.87	5.24	3.81
LSD	0.39	0.03	0.03	0.003	0.03	0.003	0.01	0.01

Analysis of variance

(F Test) varieties

\*\* \*\*

\*, \*\* significant at the 0.05 & significant at the 0.01 probability levels, respectively

(TDF) total dietary fiber, (DS) disease severity, (TP) Total protein, (TL) Total lipids, (SBG) Soluble bête glucan.

**Table 6: Correlation coefficients for all comparisons among the barely**

**Studied traits across the two growing seasons, .e. 2021/2022 and 2022/2023.**

	SL	SW	GYH	GSN	GSW	1000KW	DS
SW	.619**						
GYH	.729**	.659**					
GSN	.621**	.515**	.729**				
GSW	.654**	.662**	.742**	.578**			
KW	.674**	.514**	.859**	.659**	.787**		
DS	-.704**	-.538**	-.900**	-.748**	-.630**	-.825**	
AUDPC	-.697**	-.511**	-.894**	-.731**	-.625**	-.828**	.995**

\*, \*\* significant at the 0.05 & significant at the 0.01 probability levels, respectively.

SL(Spike length), SW (Spike weight), GYH (Grain Yield t h<sup>-1</sup>), GSN (Grain spike number), GSW (Grain spike weight), KW(1000 kernel weight), DS(Disease Severity) AUDPC (Area under disease progress curve)

**Table 7: Correlation coefficients among qualitative traits across two seasons 2021 /2022 and 2022/2023.**

	TP	TL	TF	Crud ash	TC	TDF	B glucan	SBG
TL	.904**							
TF	.802**	.763**						
C.ash	.630**	0.579**	.740**					
TC	.785**	.744**	.549**	0.352**				
TDF	0.486**	0.495**	0.580**	0.379**	.528**			
B.glucan	.834**	.766**	.648**	0.486**	.900**	.549**		
SBG	0.268*	0.286*	0.378**	0.323*	0.340**	0.340**	0.364**	
DS	-.716**	-.728**	-0.525**	-0.325*	-.713**	-.723**	-.695**	-0.423**

\*, \*\* significant at the 0.05 & significant at the 0.01 probability levels, respectively.

(TP)Total protein, (TL) Total lipids, (TF)total fiber, (SBG)Soluble bête glucan, (TDF)total dietary fiber, (DS) disease severity, (CA)crude ash, (TC) Total carbohydrate, (BG)Beta glucan,

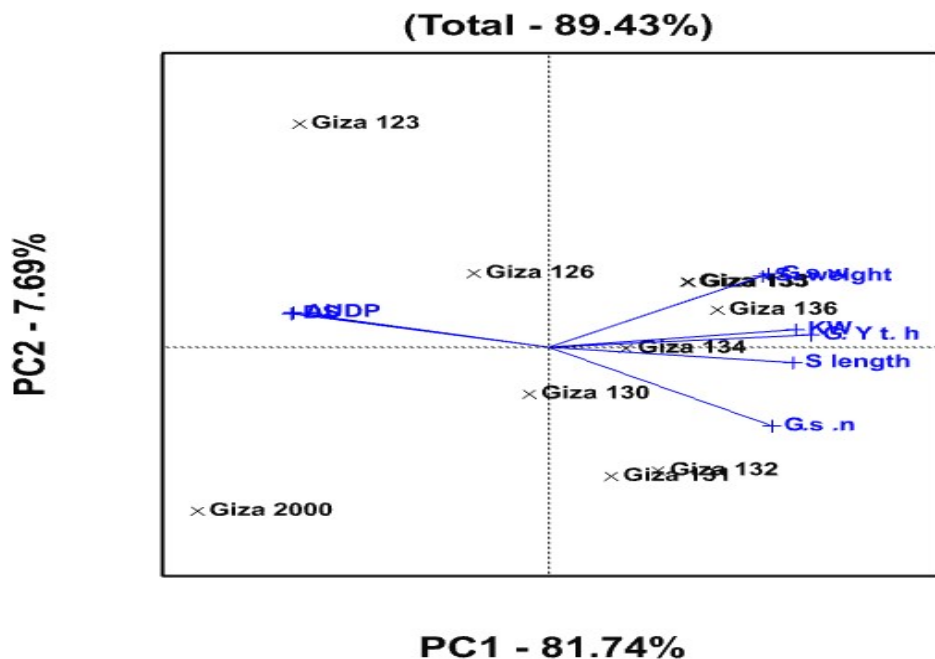
**Simple correlation between the powdery mildew disease parameters and qualitative traits of the tested barley cultivars**

Simple correlation coefficients among all studied traits are shown in Table (7) Results revealed high significant negative correlation coefficient among disease severity (DS%), T. protein, T. lipid, T. carbo, TDF and, B glucan and SBG Whereas, only significant negative correlation and non-significant was obtained with Crud ash. This shows the inverse relationship between disease severity and traits

**Genotype by trait (GT) Biplot analysis**

Figure (1) shows the relationship among the studied traits of the tested barely cultivars using the grain yield and its related traits, and disease severity susceptibility. The GT biplot of the mean performance of these traits could be explained by 89.43 % of the total variations, of the standardized data. The first and two principal components (PC1 and PC2) explained 81.74% and 7.69% of the total variation, respectively. This relatively large percentage demonstrates the intricate connections between genotypes and the associated traits that have been measured. The initial two PC values captured over 60% of the total variation, demonstrating a good fit for the GT biplot model. (Yan and Kang 2003). Similar results were also obtained in the previous study by (Darwish *et al*

2019). They stated that the treatment by trait (TT) biplot was considered an effective tool, resulting in useful information that was successfully used for helping the plant breeders to make a correct decision. The graph of GTbiplot (fig 1) showed that a vector is drawn from the biplot origin to each marker of the traits to visualize the relationships among these related traits (Yan and Tinker 2005). The obtained results revealed that spike length, spike. weight, grain yield t. h-1, grain spike number, grain spike weight, and 1000 k.w agronomic traits had acute angle ( $\theta < 90^\circ$ ) between their vectors, indicating to strong and positive correlation ( $r = \cos \theta: 0 < 1$ ). Meanwhile; the same traits were strong and negatively correlated with disease severity susceptibility (Ds) trait and AUDPC, because the angle between their trait vectors and Ds, AUDPC trait vector was obtuse ( $\theta > 90^\circ$ ), whereas ( $r = \cos \theta: -1 < \cos \theta < 0$ ). Therefore, the correlations among traits could be shown by the biplot graph (Yan and Kang, 2003). In comparing, these association results in the biplot graph would be confirmed by correlation coefficients between these traits (Table 6). These results agreed with results derived from the correlation matrix showing that GT biplot analysis is a good substitute and procedure for correlation coefficients as it could provide an interpretation and a good explanation of the interrelationships among the studied traits



**Fig. 1: Genotype by trait (GT) biplot in vector view, displaying the interrelation among the measured agronomic traits and disease parameters for some barely Egyptian cultivars over the two growing seasons 2021 /2022 and 2022/2023.**

Meanwhile, the polygon view of the biplot (GT) describes the interaction between the genotype and the tested traits (Fig. 2). This graph was drawn by joining the outermost genotypes, which become the vertices of the polygon, to the origin, showing that the perpendicular genotypes to the polygon sides facilitate comparison between neighboring vertex genotypes. Genotypes G135, G136 G134, and G132 recorded high values of Spike length, Spike. weight, grain yield t. h-1, grain spike number, grain spike weight and 1000k.wtraits and at the same time they display an adequate level of powdery mildew disease resistance, as they recorded low percentages of disease severity (%) and least values of area under disease progress curve (AUDPC). Also, G130 and G126 located high values of the sector with reflected similar behavior toward the kernel weight, SPL, grain yield h<sup>-1</sup>, and grain spike number

Regarding Giza123 and Giza 2000 barley cultivars, it's highly infected with the disease, but they have moderate traits So it tolerates the infection. The current results are in harmony with those obtained by (Tiia *et al.*, 2017, Sanjaya *et al.* , 2019 and Yassin *and* Zeinab. 2022).

Figure (3) shows the relationship among the studied barely genotypes using the qualitative traits and disease severity susceptibility. 85.05 percent of the variation in the standardized data was explained by the GT biplot of the mean performance of these traits. Two principal components (PC1 and PC2) accounted for 21.40% and 63.65% of the

explanation, respectively. The intricacy of the connections between the genotypes and the measured correlated traits is reflected in this comparatively high proportion. By recording a high percentage (above 60%) of the total variation, the first two PCs' results achieved the GT biplot model's goodness of fit. (Yan and Kang, 2003). The graph of the GT biplot showed that a vector is drawn from the biplot origin to each marker of the traits to visualize the relationships among these related traits (Yan and Tinker 2005). Results revealed that protein, t. lipid, t. carbo, TDF, and B- glucan and traits had acute angle ( $\theta < 90^\circ$ ) between their vectors, indicating to strong and positive correlation ( $r = \cos \theta: 0 < 1$ ). Meanwhile; the same traits were strong and negatively correlated with disease severity susceptibility (Ds) trait because the angle between their trait vectors and Ds trait vector was obtuse ( $\theta > 90^\circ$ ), whereas ( $r = \cos \theta: -1 < \cos \theta < 0$ ). Therefore, the correlations among traits could be shown by the biplot graph (Yan and Kang. 2003). In comparing, these association results in the biplot graph would be confirmed by correlation coefficients between these traits (Table 6). These results agreed with those obtained by the correlation matrix, indicating that the GT biplot graph is a good substitute procedure for correlation coefficients for interpreting the interrelationships among the studied traits

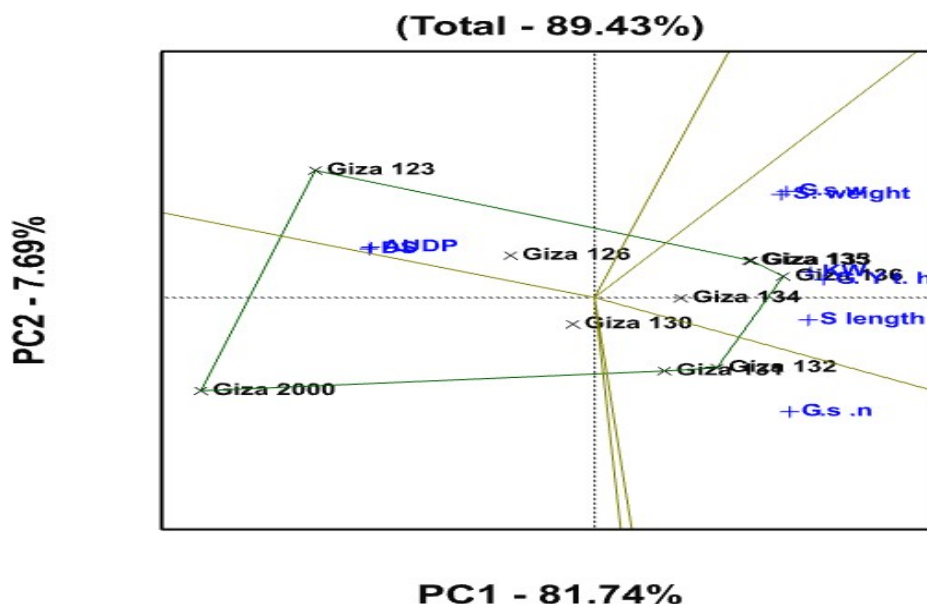


Fig. 2: Polygon view of genotype by trait (GT) biplot showing which barley cultivar had the highest values of which agronomic traits and low estimated of disease parameters for the tested (10) barely cultivars over th two growing seasons2021 /2022 and 2022/2023.



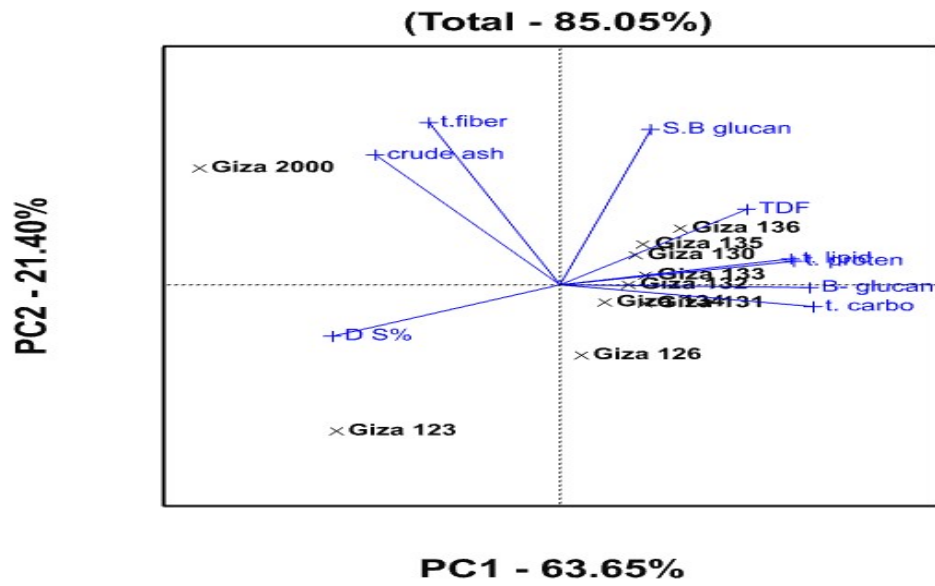


Fig. 3: Vector view for genotype by trait (GT) biplot, showing the interrelationship among the qualitative measured traits as well as the powdery mildew disease parameters for ten barely cultivars, over the two seasons 2021 /2022 and 2022/2023

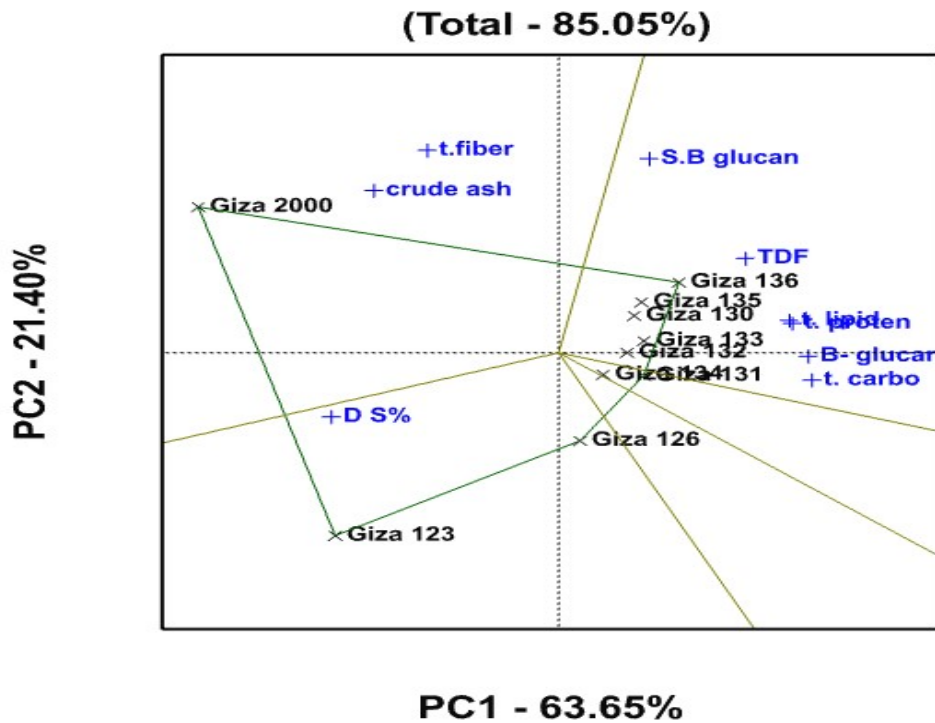


Fig. 4: Polygon view for cultivar by trait (GT) biplot, showing which the barley cultivars had the highest values for which qualitative traits with the lowest values of disease parameters for some barely genotypes over two seasons.

The polygon view of the biplot describes the interaction between the genotype and the traits (Fig.). This graph was drawn by joining the outermost genotypes, which become the vertices of the polygon, to the origin, showing that the perpendicular genotypes to the polygon sides facilitate comparison between neighboring vertex genotypes. Genotypes G126, G136, G134 and G131 recorded high values of t. protein, t. lipid, t. carbo, TDF and B- glucan qualitative traits, as well as the highest level of powdery mildew disease resistance. Also, G130, G132, G133, and G135, barley cultivars located in high values of the sector with reflected similar behavior for the same traits

Regarding Giza123 and Giza 2000 barley cultivars displayed high infection with the PM disease, during the two growing seasons of the study, but at the same time, they produced a relatively high yield quality, during this study. Where they are less affected by the powdery mildew disease infection. Therefore, the above two barley cultivars should be characterized as the tolerant barley cultivars. These results are in harmony with those obtained by (Tiia *et al.*, 2017, Sanjaya *et al.*, 2019 and Yassin *et al.*, 2022).

## DISCUSSION

Powdery mildew can have several detrimental effects on barley plants. The powdery mildew fungus interferes with photosynthesis, the process by which plants convert sunlight into energy. This can lead to stunted growth and reduced yield. Infected plants may experience premature aging, leading to early leaf yellowing and shedding. This can limit the plant's ability to produce grain. Powdery mildew can also affect grain quality. (Tucker *et al* 2013) Infected grains may be smaller, lighter, and have reduced germination rates. Powdery mildew can weaken plants, making them more susceptible to other diseases. Powdery mildew can negatively affect several yield components. Where yield losses can reach 40% (Chaure *et al* 2000).

Growing resistant cultivars of barley can significantly minimize the deleterious negative effects of the powdery mildew pathogen infection, under field conditions (Abdullaev *et al.*, 2021).

Further studies are needed to accurately explain the specificity in the interaction between the causal fungus and its host-plant. Also, it requires a continuous search for new donors of the desired yield characters with PM resistance traits in different barley genotypes.

During the two years of the current study, ten Egyptian commercial barley cultivars were precisely evaluated and accurately characterized for their host genetic resistance to PM under severe natural infection and disease pressure at the Giza

experiment station ( hot spot location for PM disease ). The genetic control of the *B. graminis* f. sp. hordei pathogen and the cultivation of host-genetic resistant barley cultivars in agriculture are considered to be the most effective control strategies that lead to a successful and great management his serious disease, consequently, these resistant genotypes are supposed to be less affected by a new dangerous pathogen race's attack produce a relatively high yield and quality ( **Abdullaev et al.2021**)

The concept of graphical display of matrices with, an application of principal component analysis of biplot was early developed by (**Gabriel 1971**). However as early as the second half of the twenty century ;(**Gabriel 1971**) used the biplot Procedure approach. Since then, the biplot analysis technique has been widely used or applied to display both genotype main effect (GT) and genotype trait (GT) interaction between the multiple traits of the target genotypes.

For analysis, more accurately, the obtained data of the tested barley genotypes' (10 cultivars) performance. a GT biplot analysis was proposed. Moreover, this approach was conducted to gain more detailed information on the actual correlation between a powdery mildew disease severity (%) and each of the different agronomic traits, under study..

This analytical technique was constructed from the first two principal components i.e. PC1 and PC2 and derived from PC analysis of both agronomic traits and powdery mildew disease severity and AUDPC.

Powdery mildew disease caused by the fungus *Blumeria graminis* f. sp. Hordei is a significant disease affecting barley understanding the genetic basis of tolerance and resistance to this disease is crucial for developing durable resistance varieties.

Mechanisms of resistance: Hypersensitive Response (HR) Some barley genotypes exhibit a hypersensitive response where infected cells undergo programmed cell death to limit the spread of the pathogen. This response is often associated with specific resistance genes (MIX) and other regulatory genes like Rar1 and Rar2 (peterhansel *et.al*.1997)

The development of tolerance genotypes in barley is crucial for ensuring crop productivity under adverse environmental conditions by understanding the genetic and physiological mechanisms underlying stress tolerance researchers can develop barley varieties that are more resilient to drought, heat, and salinity

In this part of the study, the GT biplot results revealed that yield and quality performances of barley cultivars understudy were highly influenced and severity affected by the level of host resistance

to powdery mildew disease. The barley cultivars Giza 131, 132, 133, 134, 135 and 136 demonstrated the best performance among the ten cultivars tested during the two growing seasons of the study. In contrast the lowest Giza 2000, 123, 126 and 130.

On the other hand, the obtained results also that GT biplot analysis permitted meaningful and useful information on GT interaction data. Also, it assisted in examining the real relationships between different genotype performance traits, which could be well used and effectively utilized in a suitable indirect selection for superior and advanced barley cultivars in the barley breeding program, in Egypt.

### CONCLUSIONS

- 1-Powdery mildew (*B. graminis* f. sp. *hordei*) was the lowest prevalent among other observed diseases, and Giza136, Giza 133 and Giza 135 cultivars were the most resistant to powdery mildew during two growing seasons.
- 2-Of the diseases that were observed, powdery mildew (*B. graminis* f. sp. *hordei*) was the most common. Giza 2000, and Giza 123 cultivars were the most susceptible to powdery mildew during two growing seasons.
- 3-The GT biplot graph is a valuable tool for understanding the relationships between traits and disease severity.

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## المخلص العربي

## تأثير مرض البياض الدقيقي على كمية وجودة لبعض اصناف الشعير تحت الظروف المصرية

شرين فيليب ميخائيل<sup>١</sup>، كريمة احمد<sup>٢</sup>، هدى العرابي<sup>٣</sup><sup>١</sup> قسم بحوث امراض الشعير- معهد امراض النباتات- مركز البحوث الزراعية<sup>٢</sup> قسم بحوث الشعير- معهد تربية المحاصيل- مركز البحوث الزراعية<sup>٣</sup> المعمل المركزي لتصميم وتحليل التجارب البحثية- مركز البحوث الزراعية

مرض البياض الدقيقي والمسبب المرضي فطر *Blumeria graminis f. sp. hordei* في أصناف الشعير. أجريت تجارب ميدانية على أساس عشرة أصناف من الشعير المصري وهي الجيزة ٢٠٠٠ الجيزة ١٢٣، الجيزة ١٢٦، الجيزة ١٣٠، الجيزة ١٣١، الجيزة ١٣٢، الجيزة ١٣٣، الجيزة ١٣٤، الجيزة ١٣٥، الجيزة ١٣٦ تم زراعتها في محطة الجيزة ولم يتم استخدام اي مبيدات وتحت العدوى الطبيعية. أجرينا اختبارات ميدانية على مدار موسمين من النمو في محطة الجيزة ٢٠٢١/٢٠٢٢ و ٢٠٢٢/٢٠٢٣، وذلك لان الظروف البيئية تجعلها منطقة ساخنة للإصابة بمرض البياض الدقيقي. أظهرت النتائج أن ستة أصناف من الشعير. الجيزة ١٣١ والجيزة ١٣٢ والجيزة ١٣٣ والجيزة ١٣٤ الجيزة ١٣٥ والجيزة ١٣٦ أظهرت انها مقاومة لمرض البياض الدقيقي خلال هذه الدراسة حيث سجلت شدة المرض لم تتجاوز ٥٠,٥ والتطور المرضي في المنطقة (أقل من ٣٠٠).

في حين أن أصناف الشعير الجيزة ١٢٣ والجيزة ١٢٦ والجيزة ١٣٠ والجيزة ٢٠٠٠ لها قابلية عالية للإصابة بمرض البياض الدقيقي تصل الى (٥٩,٥) والتطور المرضي (٣٤٥,٤) يقيم البحث العلاقة بين شدة المرض والصفات المختلفة للمحصول ونتاج الحبوب وجودتها التكنولوجية لعشرة أصناف من الشعير المصري. يستخدم التحليلات الإحصائية والرسوم البيانية لتفسير الارتباطات بين الصفات الحقلية والمكونات التكنولوجية. علاوة على ذلك، تبحث الدراسة في أداء الأنماط الوراثية للشعير ومقاومتها للمرض. تشير النتائج إلى GT biplot أن هذا التحليل هو أداة قيمة لهذه الدراسة ويساعد المربي على اتخاذ القرار.