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Determination of Grain Yield and Nutrition Traits in Hull-less Barley Genotypes

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Abstract

Naked barley is a multi-purpose cereal crop grown for feed, food and malting worldwide. In recent years, with the understanding of health benefits and significance in human nutrition, there is an increasing interest in quality characteristics as well as grain yield of naked barley. In this study, grain yield, yield components and some quality traits of 25 naked barley genotypes grown in three consecutive years were studied. The study was carried out during the 2016–2017 and 2017–2018 growing seasons in Turkey. The combined variance analysis results showed that the years and genotypes had highly significant effects on all the examined characteristics. As the average of years, mean grain yield of genotypes ranged from 2.40 (G21 numbered genotypes) to 4.18 (G18 numbered genotypes) t ha^{-1}. The genotype G5 had values greater than the averages in all traits, except for thousand-grain weight, fat, starch content and asit detergent fibre while the genotype G3 and G5 had values greater than the averages in all traits, except for hectoliter weight, fat content and protein content. The biplot analyses revealed that grain yield had positive correlations with spike length, plant height, number of grains per spike, protein, β-glucan, neutral detergent fibre

Keywords Genotypes · Grain yield · Naked barley · Protein · β-glucan

Introduction

Barley (*Hordeum vulgare* L.) is an important crop and has been used in animal feeding, production of fermented drinks and human nutrition since the ancient times. Although majority of barley production is used in animal feeding today, it was used in human nutrition in the past. Among the cereals, barley has the greatest adaptation capacity to different ecologies and it is highly tolerant to cold and dry conditions. Especially in dry areas, barley is preferred by majority of poor-resource farmers. Worldwide, barley is grown over 47.9 million ha land area with the average yield of 2950 kg ha^{-1}. Barley is also among the most cultivated cereals in Turkey, and is grown over 2.6 million ha land area with an average yield of 2691 kg ha^{-1}. There are two basic barley species according to the lateral florets of spikelets: Two-row and six-row barleys. In two-row barleys, lateral florets are infertile, but six-row barleys have three fertile florets per spikelet (Roljević-Nikolić et al. 2020). Besides, barley is classified into covered or hulled and naked or hulless according to the grain type (Ghimire et al. 2019).

Naked barley or hulles barley (*Hordeum vulgare* L. var. *nudum* Hook.f.) has the loose glumes that are easily separable during threshing (Eshghi et al. 2012). Well-adapted naked barley cultivars have long been cultivated in many regions of the world. Although naked barley is mostly used as animal feed, its importance is increasing as human foodstuff in recent years (Balouchi et al. 2005). This crop has many advantages in processing due to the absence of grain glumes. Therefore, naked barley has been accepted as more economic and valuable in food industry (Bleidere et al. 2013; Polišenská et al. 2019).

Bhatty and Rossnagel (1998) worked on chemical composition of naked barleys and reported protein contents as between 13–18%, starch content as between 60–74%, β-glucan contents as between 4–8%, total dietary fibre con-

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Data availability This manuscript has not been published and is not under consideration for publication elsewhere. All authors have approved of and have agreed to submit the manuscript to this journal.

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tents as between 12–17% and soluble fibre contents as between 3–6%. Naked barleys are quite rich in vitamins, minerals and tocopherols. Naked barley grains were reported to reduce glycemic index that stabilize blood glucose and insulin levels. Besides, barley grains were reported to reduce the risk of heart disease, cancer and age-related diseases (Bleidere et al. 2013). Because of these properties, naked barley has various beneficial effects on human health. Naked barley is widely used in animal feed. For this reason, ADF and NDF values related to nutrition are also important. ADF and NDF increase feed intake by promoting dry matter consumption in ruminants, and protect animals against metabolic diseases by increasing rumen pH. It also plays a role in obtaining milk with a higher fat ratio by maintaining the acetic acid/propionic acid ratio. In addition, ADF and NDF increase the production of quality protein by protecting the bacterial microflora in rumen (Tekce and Gul 2014). Despite of all these positive traits, the naked barley cultivars still have lower grain yields than the covered cultivars (Sturite et al. 2019). The number of studies about the performance of naked barley cultivars under different environmental conditions and diverse agricultural practices is quite limited. It was reported that cultivation systems and environmental conditions significantly influenced the quality traits of naked barley cultivars (Ehrenbergerová et al. 1997).

There are only two naked barley cultivars registered in Turkey. New naked barley cultivars should be developed to provide higher yield and grain quality. The objective of this study was to determine the yield, yield components and quality traits of naked barley lines/cultivars grown in different environments in Turkey.

Material and Methods

Plant Material

In this study, twenty-five naked barley genotypes were used. These naked barley genotypes were supplied from the International Center for Agricultural Research in Dry Areas-ICARDA (23 lines and Atahualpa cultivar) and from the Republic of Turkey Ministry of Agriculture and Forestry

Table 1 Pedigrees and spike types of the cultivars and lines used in the study

No	Pedigree	Spike types
G1	M104/3/LEGACY//PENCO/CHEVRON-BAR **CBSS05M00017S-5M-0Y-0M-0AP-0TR**	6
G2	RECLA 6O/BICHY2OOO//LIMON/BICHY2OOO/3/CHERI CBSS06Y00339S-28Y-0M-0AP-0TR	2
G3	PENCO/CHEVRON-BAR//PENCO/CHEVRON-BAR **CBSS05M00139S-10M-0Y-0M-0AP-0TR**	6
G4	PETUNIA 1/RITA PELADA CBSS05M00363S-3M-OY-OM-OAP-OTR	6
G5	ZIGZIG/PETUNIA 1 CBSS06Y00249S-22Y-0M-0AP-0TR	6
G6	ZIGZIG/PETUNIA 1 CBSS06Y00254S-6Y-0M-0AP-0TR	6
G7	PENCO/CHEVRON-BAR/3/LEGACY//PENCO/CHEVRON-BAR **CBSS05Y00202S-17Y-0M-0Y-0M-1AP**	6
G8	PENCO/CHEVRON-BAR/3/LEGACY//PENCO/CHEVRON-BAR **CBSS04Y00047S-26Y-2M-OY-OM-OY**	6
G9	PENCO/CHEVRON-BAR/3/LEGACY//PENCO/CHEVRON-BAR **CBSS04Y00048S-23Y-2M-0Y-0M-0Y**	6
G10	BICHY2000/PRTL CBSS04B00111S-7M-0Y-0M-2Y-0M-0AP	2
G11	PENCO/CHEVRON-BAR/3/LEGACY//PENCO/CHEVRON-BAR **CBSS05Y00202S-9Y-0M-0Y-0M-4AP**	6
G12	PENCO/CHEVRON-BAR/3/LEGACY//PENCO/CHEVRON-BAR **CBSS05Y00202S-27Y-0M-Y-0M-3AP**	6
G13	PENCO/CHEVRON-BAR/3/LEGACY//PENCO/CHEVRON-BAR **CBSS05Y00202S-37Y-OM-OY-OM-4AP**	6
G14	PETUNIA 1/3/LEGACY//PENCO/CHEVRON-BAR **CBSS05Y00208S-6Y-0M-0Y-0M-4AP**	6
G15	PETUNIA 1/3/LEGACY//PENCO/CHEVRON-BAR **CBSS05Y00208S-23Y-OM-OY-OM-1 AP**	6
G16	6B89.2027/3/LEGACY//PENCO/CHEVRON-BAR **CBSS05M00445S-12M-0Y-0M-0AP-0TR**	6
G17	CHAMICO/TOCTE//CONGONA/3/LEGACY//PENCO/CHEVRON-BAR **CBSS05M00392S-11M-0Y-0M-0AP-0TR**	6
G18	PENCO/CHEVRON-BAR//FALCON-BAR CBSS05M00405S-7M-OY-OM-OAP-OTR	6
G19	PENCO/CHEVRON-BAR//BICHY2000 CBSS05M00406S-6M-0Y-0M-0AP-0TR	6
G20	FRESA/PETUNIA1/7/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA1/6/LEGACY//PENCO/CHEVRON-BAR **CBSS05M00686D-I-2M-0Y-0M-0AP-0TR**	6
G21	LIMON/BICHY2000/5/MERIT,B/4/GOB/HUMAMO//CANELA/3/ALELI **CBSS05Y00211S-3Y-OM-OY-OM-2AP**	2
G22	TRADITION//PENCO/CHEVRON-BAR CBSS05M00405S-7M-OY-OM-OAP-OTR	6
G23	PENCO/CHEVRON-BAR/3/LEGACY//PENCO/CHEVRON-BAR **CBSS05Y00202S-37Y-OM-OY-OM-4AP**	6
G24	ATAHUALPA (Ecuador)	2
G25	YALIN (Turkey)	2

Field Crops Central Research Institute (Yalın). Pedigrees of genotypes were given as Table 1.

Field Experiments

The barley genotypes were grown in Agricultural Research Center of Bozok University located in Yozgat in Turkey. Yozgat is the province in the middle of Turkey (39°45′10″ N, 34°48′13″ E; altitude: 1266 m). The experiments were established in 2016–2017 and 2017–2018 growing seasons in Yozgat provinces Turkey. Soil samples were taken from 0–30 cm depth. Experimental soils were clayey in texture and soil pH was 7.09, salt content 0.178 dSm^{-1}, lime content 7.15%, P_2O_5 content 0.78 kg ha^{-1}, K_2O content 5.93 kg ha^{-1} and organic matter content 2.49%. The climate parameters of the experimental province are provided in Table 2.

Experimental Design and Cultural Practices

Sowing dates were 14 October 2016 and 17 October 2017 respectively. The experiments were conducted in a randomized complete block design with 4 replications. Plant densities are adjusted to be 450 plants per square meter. Each plot had 8 rows of 4 m long with a row spacing of 20 cm. Fertilizers were applied according to soil analysis results. A dose as 60 kg ha^{-1} N and 60 kg ha^{-1} P_2O_5 (di-ammonium phosphate) were applied at sowing. During plant tillering, the plots were fertilized with 40 kg ha^{-1} N (urea). Plants were cultivated without any supplementary irrigation. Samples of all the plots were harvested close to the ground by hand using with a sickle on July 19 in the first year, on July 12 in the second year. Then these samples were threshed by plot threshing machine.

Traits Measurements and Chemical Analysis

Measurements were made on 10 randomly selected plants and average of these 10 plants was taken. Plant height was measured for each genotype at maturity from the ground to the spike tip. Spike length was measured as the distance from the base of the spike to the peak of the spike on the same main stem. The number of grain in the spike was determined by counting the grains in ten spikes. The number of grains per spike was calculated by taking the average of the grains in these spikes. Plants were harvested at maturity. Plot yield (g m^2) was recorded as the average grain weight measured after all harvested plants from the plot were threshed. Grain yield (t ha^{-1}) was calculated by converting the plot yield into ton per hectare. Thousand kernel weight (g): one hundred seeds were randomly counted from each plot, the seeds were then weighed and resultant weight was multiplied by 10. Hectolitre weight was determined by a hectolitre device and expressed in kilograms.

The grain samples were weighed for chemical analysis and dried for 5 h in an oven at 105 °C. Before the analysis of fat, starch, protein, β-glucan, acid detergent fibre (ADF), neutral detergent fibre (NDF) and ash samples were ground in a hammer mill to pass a 0.5 mm sieve. Starch content: Total starch content was determined with the aid of an enzymatic test kit (Megazyme International Ireland Ltd., Wicklow, Ireland). Fat content of naked barley grains was determined by the Soxhlet method. Nitrogen contents of the naked barley grains were determined in accordance with Kjeldahl method and resultant values were converted into protein contents by multiplying with a coefficient of 6.25. This method is accepted by the AACC method 46.12.01 (AACC 2010). The β-D-glucan contents were determined with the use of β-D-glucan enzymatic assay kit (Megazyme Kit) (Kamboj et al. 2020). The ADF and NDF contents were determined with an ANKOM 220 Fibre Analyzer using the method described by Van Soest et al. (1991).

Table 2 Climatic information of experimental locations

	Temperature (°C)			Rainfall (mm)		
	2016–17	2017–18	Long term (30 years)	2016–17	2017–18	Long term (30 years)
October	11.0	10.0	10.2	2.6	32.5	42.6
November	5.0	4.6	4.2	34.9	66.6	63.8
December	–3.3	3.4	0.0	68.3	55.5	76.6
January	–3.5	0.2	–2.0	52.8	98.7	65.1
February	–0.4	4.6	–0.9	11.6	30.0	61.5
March	5.1	7.5	3.0	87.6	147.7	62.1
April	8.3	12.2	8.3	46.8	20.6	69.5
May	12.4	14.8	12.9	99.5	114.6	62.1
June	17.6	24.5	16.8	56.5	38.8	42.2
July	6.6	21.3	19.8	0.7	3.0	14.8
Mean\Total	5.9	10.3	7.2	461.3	608	560.3

Statistical Analysis

Data were analyzed combined years. Statistical analysis was performed with the use of GenStat 12th Edition release software program. Significant means were compared with the use of least significant difference (LSD) test. Pearson's correlation coefficients were calculated for the correlations between the investigated traits. The mean values of the 25 genotypes for investigated traits were subjected to genotype-by-trait, principal components (PC) factor analysis and biplot analysis of PC1 and PC2.

Results and Discussion

In present study, significant differences were observed in investigated traits of the genotypes (Tables 3 and 4). Genotypic and phenotypic relationships among the traits are examined and the coefficients are given in Table 5. Grain yield and quality traits of naked barley genotypes vary widely with the genotypes, years and growing conditions (Bleidere et al. 2013). Climate conditions significantly influence the productivity of field crops. Although total precipitation of 2017–2018 growing seasons was higher than the long-term averages, it was lower in 2016–2017 growing season than the long-term averages. The amount of precipitation was measured as 461.3 and 608.0 mm in 2016–2017, 2017–2018 growing season, respectively (Table 2).

Yield is controlled by several genes, thus it is considered as a polygenetic trait. Besides, yield is greatly affected by the environment, too. There were significant differences in grain yields of the genotypes and the years ($p<0.01$). The combined data over two years revealed that the grain yields of the genotypes ranged from 2.40 t ha^{-1} (G21) to 4.21 t ha^{-1} (G3). In terms of grain yield, genotypes G3, G5, G11, G14, G15, G18, G22 and Yalın were placed in the same statistical group. Bahrami et al. (2008) reported significant effects of genotype × environment interactions on grain yield of barley. Low grain yields of the genotypes could be attributed to low number of grains per spike in these genotypes (Balouchi et al. 2005). Balouchi et al. (2005) reported grain yields of barley genotypes as between 1.71 and 3.96 tons.

Plant height, spike length, thousand-kernel weight and hectolitre weight are important traits of cereals, and these traits affect significantly the grain yield (Eshghi et al. 2012). There were significant differences in plant heights of the genotypes. The plant heights of the genotypes varied between 64.09 cm (G21) and 92.53 cm (Yalın). The spike length of naked barley genotypes varied between 6.05 (G15) and 7.38 cm (G12). The number of grains per spike values varied between 14.35 (G12) and 40.00 (G17) with an average value of 31.17 in 2016–17 and between 16.25 (G12) and 48.30 (G18) with an average value of 38.98 in 2017–18.

The combined data over the two years showed that the number of grains per spike values of the genotypes ranged from 15.30 (G12) to 43.36 (G8). The thousand-grain weight of the genotypes ranged from 34.28 to 47.14 g. twelve genotypes had thousand-grain weights greater than the overall average (40.05 g), while thirteen genotypes had hectolitre weights greater than the overall average (75.31 kg). The average value of the thousand-grain weight in first and second year were determined as 39.42 g and 40.67 g, while the average value of the hectolitre weight was determined as 75.26 kg and 75.36 kg respectively (Table 3). Since these traits were primary yield components, they can be used in indirect improvement of the grain yield of studied genotypes. The values obtained in the third year were significantly greater than in the first and the second years. So, these traits were significantly influenced by genotype and environmental factors. Previous studies attributed the differences in yields to differences in genotypes (Akgun 2016; Yuksel and Ikincikarakaya 2020), environmental factors (Eticha et al. 2010) or agronomic practices (Balouchi et al. 2005; Bleidere et al. 2013). Eshghi et al. (2012) assessed the genetic diversity of 63 oat genotypes and reported the plant heights as between 68.20 and 113.6 cm. Roljević-Nikolić et al. (2020) reported spike length of hulles barley genotypes as 9.18, 8.68 and 9.75 cm in the first, second and third years, respectively. The number of grains per spike of the genotypes was reported as 18.95, 18.05 and 22.23 in the first, second and third years, respectively. Balouchi et al. (2005) reported the number of grains per spike and thousand-grain weight of genotypes as between 21–54 and 24–47 g, respectively. Bleidere et al. (2013) reported the hectolitre weight of husked barley genotypes as 73.5 kg in the first year and 79.1 kg in the second year.

Naked barley is a multi-purpose cereal crop grown for feed, food and malting in the world. In recent years, with the understanding of its health benefits and significant in human nutrition, there is a growing interest in quality characteristics as well as grain yield of naked barley genotypes. In this study, the combined analysis of variance ($P<0.001$) for fat, protein, starch and β-glucan contents traits showed significant differences between the genotypes and the years (Table 3). According to the average of two years, fat contents of genotypes varied between 1.97% and 2.72%. The genotypes G16 (2.75%), G1 (2.67%), G4 (2.71%), G1 (2.70%) and G17 (2.67%) had the greatest fat contents. The average values of the fat content in the first and second years were respectively determined as 2.67% and 1.99% (Table 3). The mean starch contents of the genotypes varied between 57.32% and 65.54%. The genotypes G21 (63.45%), G7 (63.56%) and G14 (65.54%) had the greatest starch contents. The average starch content

Table 3 Average values of some investigated traits the naked barley genotypes[a]

Genotypes	GY		PH		SL		GS		TGW		HW		FAT	
G1	3.81	b–f	85.60	a–d	6.21	efg	38.45	abc	39.11	g–k	71.76	jk	2.70	a
G2	3.34	hi	80.22	def	6.67	b–g	27.33	gh	45.88	ab	78.03	cd	2.11	c–f
G3	4.21	a	85.95	a–d	6.72	a–f	40.08	abc	39.36	f–j	75.36	e	2.29	b–f
G4	3.75	c–g	83.74	b–e	7.02	a–d	41.11	abc	36.37	k–n	75.35	e	2.71	a
G5	4.11	ab	86.45	a–d	7.27	ab	38.04	a–d	34.28	n	79.58	b	1.97	f
G6	3.60	d–h	77.39	efg	6.49	d–g	35.95	c–f	35.27	lmn	71.25	kl	2.52	ab
G7	3.80	b–f	82.97	cde	6.66	b–g	38.40	abc	38.04	i–l	73.22	ghi	2.21	b–f
G8	3.56	e–i	83.73	b–e	6.80	a–e	43.36	a	41.31	c–h	71.80	jk	2.08	ef
G9	3.33	hi	88.77	abc	6.67	b–g	31.94	d–g	41.51	c–g	78.53	c	2.24	b–f
G10	2.61	kl	69.05	hi	7.19	abc	30.15	fg	42.31	Cde	80.61	a	2.39	a–e
G11	3.93	abc	86.53	a–d	6.98	a–d	42.03	abc	41.24	c–h	72.47	ij	2.44	a–d
G12	3.67	c–h	83.27	cde	7.38	a	15.30	j	43.84	bc	74.86	ef	2.38	a–e
G13	2.88	jk	81.74	cde	6.98	a–d	39.28	abc	42.78	cd	70.66	l	2.22	b–f
G14	3.89	a–e	85.80	a–d	6.76	a–f	37.78	a–e	40.80	d–i	73.50	gh	2.09	def
G15	3.47	f–i	74.52	fgh	6.05	g	40.05	abc	38.60	h–k	75.50	e	2.44	a–d
G16	3.72	c–g	84.08	b–e	6.56	c–g	37.64	a–e	34.37	mn	77.56	cd	2.72	a
G17	3.42	ghi	88.03	abc	7.08	a–d	42.10	abc	42.06	c–f	74.18	fg	2.67	a
G18	4.12	ab	90.68	ab	7.18	abc	42.93	ab	35.51	lmn	75.62	e	2.09	def
G19	3.39	ghi	87.66	abc	6.24	efg	37.04	b–e	37.39	jkl	72.93	hi	2.52	ab
G20	3.21	ij	72.27	gh	6.12	fg	31.56	efg	37.15	j–m	77.08	d	2.08	ef
G21	2.40	l	64.09	i	6.44	d–g	23.13	hi	47.14	a	80.06	ab	2.45	abc
G22	4.02	abc	84.67	bcd	6.81	a–e	37.40	a–e	37.88	jkl	72.53	hij	2.31	b–f
G23	3.70	c–g	88.66	abc	7.04	a–d	38.00	a–d	39.48	e–j	78.04	cd	2.07	ef
Atahualpa	2.74	kl	82.00	cde	6.53	c–g	19.94	ij	42.44	cd	71.73	jk	2.22	b–f
Yalın	3.88	a–e	92.53	a	7.24	ab	28.01	gh	47.06	a	80.45	ab	2.42	a–e
2016–2017	3.45	b	74.67	b	6.25	b	31.17	b	39.42	b	75.26		2.67	a
2017–2018	3.63	a	90.96	a	7.28	a	38.98	a	40.67	a	75.36		1.99	b
Mean	3.54		82.82		6.76		35.08		40.05		75.31		2.33	
CV	10.25		8.62		9.93		9.97		7.20		1.38		15.37	
LSD	0.36		7.06		0.66		6.23		2.85		1.03		0.33	
Genotypes (G)	**		**		**		**		**		**		**	
Year (Y)	**		**		**		**		**		ns		**	
Y × G int	**		**		ns		ns		**		**		**	

GY grain yield (t ha^{-1}), *PH* plant height (cm), *SL* spike length (cm), *GS* number of grains per spike (no), *TGW* thousand-grain weight (g), *HW* hectoliter weight (kg), *FAT* Fat content (%), *ns* non-significant

[a] The difference between the averages shown with the same letters is not significant at the $P \le 0.05$ level

** significant at $P \le 0.01$

in first and second years was determined as 58.80% and 63.94% respectively (Table 4). The protein contents of the genotypes ranged from 12.65 to 17.31%. The genotypes, G4 (16.09%), G3 (16.11%), Atahualpa (16.16%), G1 (16.20%), G18 (17.04%) and G19 (17.31%) were placed into the same statistical group in terms of protein contents. Average protein contents in first and second years were determined as 15.4% and 14.50%, respectively (Table 4). The β-glucan contents (βG) of genotypes ranged from 4.42 to 5.98%. The genotypes G4, G5, 23 and Yalın were placed into the same statistical group in terms of β-glucan content Average β-glucan content in first and second years were determined as 4.90% and 3.63%, respectively (Table 4). The combined analysis of variance for ADF and NDF showed that there were significant differences ($P < 0.001$) between the genotypes and the years. The ADF contents of the genotypes ranged from 2.62 to 4.81%. The NDF contents of the genotypes ranged from 22.31 to 26.04%. Average values of the ADF and NDF contents in the first and second years were determined as 3.71–24.35% and 3.26–24.95%, respectively (Table 4).

Polišenská et al. (2019) reported that fat, starch, protein and β-glucan contents of hulless barley cultivars significantly varied with the environments, years and agronomic

Table 4 Average values of some investigated traits the naked barley genotypes[a]

Genotypes	SC		PC		βG		ADF		NDF	
G1	58.75	ghi	16.20	abc	5.38	b–e	3.98	abc	24.51	b–e
G2	59.82	fgh	12.65	j	5.34	cde	4.81	a	26.04	a
G3	60.66	d–g	16.11	abc	5.25	de	3.36	b–g	24.49	b–e
G4	58.20	hi	16.09	abc	5.84	ab	3.78	b–e	24.93	abc
G5	62.42	b–e	15.15	c–g	5.98	a	3.37	b–g	25.25	ab
G6	59.73	f–i	15.12	c–g	5.38	b–e	4.11	ab	24.98	abc
G7	63.56	ab	14.55	d–h	4.97	e	3.58	b–e	23.44	e–h
G8	62.84	b–e	13.68	hij	5.39	b–e	3.11	d–g	24.10	b–f
G9	61.67	b–f	15.24	c–g	4.99	e	3.21	c–g	23.06	fgh
G10	62.53	b–e	15.46	cde	5.24	de	2.93	efg	23.81	c–f
G11	61.15	b–g	15.31	c–f	5.22	de	3.29	b–g	24.35	b–e
G12	62.40	b–e	14.09	f–i	5.40	b–e	3.36	b–g	23.51	d–g
G13	62.16	b–f	15.19	c–g	5.54	a–d	3.47	b–g	24.40	b–e
G14	65.54	a	13.01	ij	5.28	cde	3.27	b–g	23.46	e–h
G15	61.55	b–f	13.94	g–j	5.32	cde	3.49	b–f	24.18	b–f
G16	62.91	bcd	13.65	hij	4.42	f	3.71	b–e	22.37	gh
G17	61.81	b–f	14.03	f–i	5.37	b–e	3.60	b–e	23.65	def
G18	59.74	f–i	17.04	ab	5.42	b–e	2.62	g	24.39	b–e
G19	57.32	i	17.31	a	5.55	a–d	3.91	bcd	25.15	ab
G20	62.63	b–e	14.45	e–h	5.74	abc	3.64	b–e	23.67	def
G21	63.45	abc	13.45	hij	5.35	b–e	3.85	bcd	22.31	h
G22	60.41	e–h	15.10	c–g	5.52	a–d	3.00	efg	24.53	b–e
G23	61.05	c–g	15.85	bcd	5.66	a–d	2.68	fg	24.68	bcd
Atahualpa	60.40	e–h	16.16	abc	5.41	b–e	3.55	b–e	24.24	b–f
Yalın	61.62	b–f	15.92	bc	5.55	a–d	3.44	b–g	24.21	b–f
2016–2017	58.80	b	15.48	a	4.90	b	3.71	a	24.35	a
2017–2018	63.94	a	14.50	b	5.86	a	3.26	b	23.95	b
Mean	61.37		14.99		5.38		3.48		24.15	
CV	4.07		9.21		7.26		4.80		4.96	
LSD	2.46		1.31		0.49		0.85		1.18	
Genotypes (G)	**		**		**		**		**	
Year (Y)	**		**		**		**		*	
Y × G int	**		**		**		ns		ns	

SC Starch content (%), *PC* Protein content (%), *βG* β-glucan content (%), *ADF* Acid detergent fibre (%), *NDF* Neutral detergent fibre (%), *ns* non-significant

[a] The difference between the averages shown with the same letters is not significant at the $P \leq 0.05$ level

** significant at $P \leq 0.01$

practices. Erbas Kose and Mut (2019) reported that fat, protein, starch, ADF and NDF contents were significantly influenced by environmental and genetic factors and reported average fat, protein, starch, ADF and NDF content of barley genotypes respectively as 1.86%, 12.78%, 59.62%, 6.69% and 23.64%. Shaveta and Kaur (2019) reported significant effects of environmental conditions and Abdel-Haleem et al. (2020) reported significant effects of genetic factors on β-glucan content of the hulless barley genotypes. Naked barley is rich in nutritional components like β-glucan, total dietary fibre, protein, limiting amino acids and starch as compared to its covered types (Bleidere et al. 2013). In previous studies conducted on hulless barley genotypes, fat contents varied between 1.18 and 3.09% (Guo et al. 2020), starch contents ranged from 57.8 to 61.25% (Li et al. 2019), protein contents from 6.35 to 23.4% (Wang et al. 2011), β-glucan contents from 3.0 to 15.0% (Virkki et al. 2004) and ADF contents from 1.33 to 6.89% (Abdel-Haleem et al. 2010). Also, average NDF content of hulless barley genotypes was reported as 28.7% (Yang et al. 1997).

Correlations among the investigated traits are provided in Table 5. According to correlation coefficients, grain yield had positive correlations with plant height (r = 0.500**) and number of grains per spike (r = 0.774**) and negative correlations with thousand-grain weight (r = –0.467*). Plant height had significant positive correlations with protein

Table 5 Pearson's correlation coefficients of the relationship among investigated traits

	GY	PH	SP	GS	TGW	HW	FAT	SC	PC	βG	ADF
PH	0.530**	–	–	–	–	–	–	–	–	–	–
SP	–0.213	0.368	–	–	–	–	–	–	–	–	–
GS	0.774**	0.251	–0.414*	–	–	–	–	–	–	–	–
TGW	–0.467*	–0.157	0.306	–0.548**	–	–	–	–	–	–	–
HW	–0.181	–0.222	0.138	–0.282	0.186	–	–	–	–	–	–
FAT	0.078	0.144	–0.291	0.269	–0.207	–0.181	–	–	–	–	–
ST	–0.198	–0.398*	0.225	–0.172	0.132	0.247	–0.276	–	–	–	–
PC	0.179	0.397*	0.112	0.161	–0.296	–0.063	0.095	–0.603**	–	–	–
βG	–0.111	–0.086	0.108	–0.096	0.168	0.074	–0.380	–0.287	0.400*	–	–
ADF	0.068	–0.012	–0.337	–0.044	0.260	–0.259	0.261	–0.407*	–0.314	–0.201	–
NDF	0.218	0.306	–0.120	0.130	0.040	–0.275	–0.207	–0.734**	0.239	0.333	0.527**

GY Grain yield, *PH* Plant height, *SP* Spike length, *GS* number of grains per spike, *TGW* Thousand-grain weight, *HW* Hectolitre weight, *FAT* Fat content, *SC* Starch content, *PC* Protein content, *βG* β-glucan, *ADF* Acid detergent fibre, *NDF* Neutral detergent fibre

* significant at $P<0.05$, ** significant at $P<0.01$

content (r = 0.397**), but had significant negative correlations with starch content (r = –0.398*). Starch content had significant negative correlations with plant height (r = –0.398*), protein content (r = –0.603**), ADF value (r = –407*) and NDF value (r = –0.734**). Protein content had significant positive correlations with β-glucan content (r = 0.400*). ADF value had positive correlations with NDF value (r = 0.527**). Similar correlations were also reported among the present traits in previous studies (Table 4). Zaefizadeh et al. (2011) reported a positive correlation between plant height and number of grains per spike and a negative correlation between plant height and 1000-grain weight. Roljević-Nikolić et al. (2020) reported that grain yield had positive correlations with plant height, spike length, number of grains per spike, positive correlations were also reported between spike length and number of grains per spike and between stem height and spike length. Negative correlations were reported between protein and ADF contents (Abdel-Haleem et al. 2010).

Genotype × trait biplot analysis (GT biplot) assesses genotypes based on multiple traits. The GT biplot has been used for a long time to understand the effect of genotype and environment on the relationships between yield and quality traits (Yan and Tinker 2006). It used to determine those that are superior to the desired genotypes and traits. Then this genotypes and traits can be used in breeding programs. A practical visualization of the associations between traits is also provided by this analysis (Yan and Frégeau-Reid 2018). In this study, the GT biplot (Fig. 1) display 46.0% of the information in the mean data of the 25 genotypes for the 12 investigated traits. This low rate indicate that the complexity of the relationships among the measured traits. Mean data of investigated traits were used to create a GT biplot. Since there was an acute angle between the grain yield (GY) and the vectors of the traits FAT, GS, ADF, PH, PC and NDF, grain yield was positively and highly correlated with these traits. But GY was negatively correlated with HW, TGW, SP, BG and ST. In addition, HW, TGW, SP and ST traits were positively related. βG was negatively correlated with TGW, SP, ADF, NDF, PC and PH. Positive and strong correlation was determined between the PC and βG content, too. Because the angles between these traits are less than 90°, these properties are

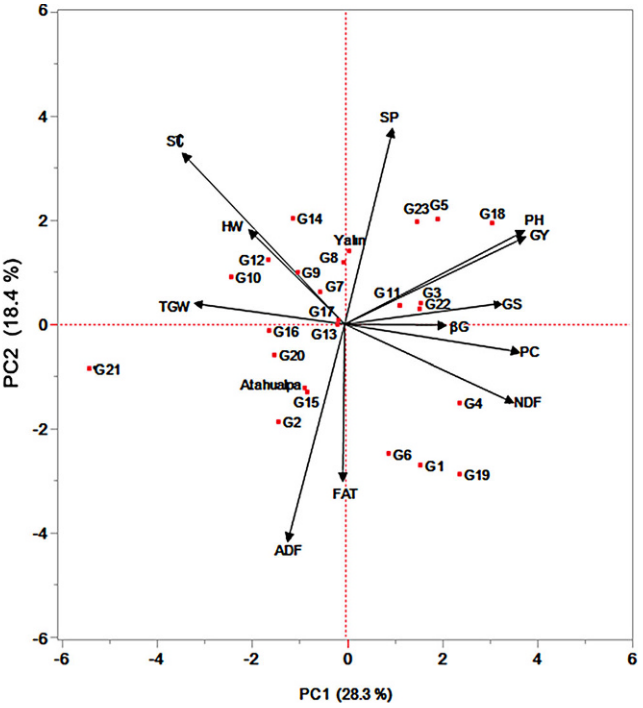

Fig. 1 View of genotype × trait biplot summarizing of yield and quality traits of 25 naked barley genotypes studied for 12 traits in according to the data of the combined years. (*GY* Grain yield, *PH* Plant height, *SP* Spike length, *GS* number of grains per spike, *TGW* Thousand-grain weight, *HW* Hectolitre weight, *FAT* Fat content, *ST* Starch content, *PC* Protein content, *βG* β-glucan, *ADF* Acid detergent fibre, *NDF* Neutral detergent fibre)

positively related. Yield is not the only trait in cereal studies that can determine the effectiveness of a single genotype. Seed quality (HW, TGW, SP) and nutrition traits (PC, βG, NT, FAT) are valuable for breeders when combined with high yield levels. Therefore, in selecting the best genotypes, the yield-trait combination effects are more significant than the effects of individual traits.

Conclusion

According to the average of years, the mean grain yield of the genotypes ranged from 2.40 to 4.21 t ha^{-1}, and the genotypes G3, G18, G5, G22, G11, G14 and Yalın respectively had the greatest grain yields. The genotype G3 and G5 had almost values greater than the averages in all traits. In terms of yield and some quality traits, many advanced lines with superior properties were identified. Present results will provide useful information for breeders conducting breeding researches to increase the yield and quality traits of the naked barley genotypes.

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Declarations

Conflict of interest Z. Mut, Ö.D. Erbaş Köse, Y.M. Kardes and H. Akay declare that they have no competing interests.

Ethical standards Not applicable. **Consent to participate** Not applicable. **Consent to publish** Not applicable.

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