Fatty Acids Contents & Nutritional Compositions of Grains of Different Barley Genotypes

Selim Ozdemir[1]
Seyithan Seydosoglu[2]
Kagan Kokten[3] ✉
Abdullah Cil[4]
Nizamettin Turan[2]

[1] Department of Crop and Animal Production
Vocational School of Food,
Agriculture and Livestock
Bingol University - Bingol, Türkiye

[2] Department of Field Crops
Faculty of Agriculture
Siirt University - Siirt, Türkiye

[3] Department of Plant Production
and Technologies
Faculty of Agricultural
Sciences and Technology
Sivas University of Science and Technology
Sivas, Türkiye

[4] Republic of Türkiye
Ministry of Agriculture and Forestry
Western Mediterranean
Agricultural Research Institute - Adana, Türkiye

✉ CORRESPONDING AUTHOR
Kagan Kokten
Department of Plant Production
and Technologies
Faculty of Agricultural
Sciences and Technology
Sivas University of Science and Technology
Sivas, Türkiye
Fax: +90 4262160030
Tel: +90 5379352592
E-mail: kahafe1974@yahoo.com

Received: October 23, 2023
Accepted: August 7, 2024

Barley is an important cereal in the world regarding its utilisation and extensive production as a feed and food grain in many countries. But little information is available on barley oil in terms of its composition. The aim of this study was to describe the importance of barley seeds by extracting their oil and determine its composition regarding lipids along with evaluations on composition, nutrient content, feed value and quality parameters. The crude ash, crude protein, ADF, NDF and ADL ratios of the seeds of barley genotypes varied between 3.5-7.1%; 8.3-13.4%; 13.5-26.0%; 23.8-36.3% and 1.99-8.78%, respectively. The DMD ratios, DMI ratios, RFV values, TDN ratios, DE and ME values of genotypes varied between 68.7-78.4%; 3.30-5.05%; 175.9-304.0%; 62.9-72.3%; 3.21-3.63 MJ/kg and 9.67-11.33 Mcal/kg, respectively. The total lipid content of the examined genotypes varied between 1.7 and 3.9%. Several fatty acids were detected; Palmitic, stearic and arachidic acids from saturated fatty acids were detected in the seeds of all barley genotypes examined in the study. The seed lipids of some barley genotypes contain palmitic (16.80-25.56%) and stearic (1.33-3.70%) acids as the major component of fatty acids, among the saturated acids, with small amounts of arachidic (0.24-0.54%) and behenic (0.06-0.90%) acids. The major unsaturated fatty acids found in the seed lipids were oleic (15.30-33.78%), linoleic (41.92-55.28%) and linolenic (2.84-5.43%) acids. Palmitoleic, erucic, docosahexaenoic and nervonic acids were shown to be lower than 1%. Eicosenoic and erucic acids were detected in all barley genotypes. Barley seeds may be used as a source of edible oil due to the presence of several unsaturated and essential fatty acids.

Keywords: Barley, nutrients, quality, fatty acids, saturated, unsaturated

1. INTRODUCTION

Cereal-based foods are the primary source of energy and nutrients for the vast majority of people worldwide [1]. Exploiting the nutritional potential of cereal grains, particularly their starch, protein, and lipid fractions, is receiving increased attention as the global need for nutrients, food, and feed increases [2]. There has been very little scientific interest in identifying the fatty acids and lipid fractions in barley grain and other cereals, even though lipids have a 7significant influence on the functional and storage characteristics of cereal products, on processing [1, 2]. From a nutritional and technological point of view, barley and other cereal grain lipids in general deserve a more focused interest than the few reports available [3]. Conventional barley offers superior nutritional value compared to other cereals in terms of protein, carbohydrate, and mineral content. The nutritional value of conventional barley is great; however, it contains fewer lipids than oat [2]. The largest lipid concentrations in cereals are in oat, with 2-18% lipids [4], and in maize, with 5-22% [5] of the whole grain weight. Barley has approximately 2-4% lipids of the total grain weight. Nevertheless, barley lipids deserve a focused

interest due to their fatty acid composition and their vitamin E composition [2]. When we look at the previous studies on the lipid content and fatty acid composition of cereal grains in Turkey; it was seen that the fatty acid contents were investigated in the seeds of selected cereals cultivated in Turkey [6], Turkish sorghum landrace [7], *Sorgum bicolor* genotypes [8], some pearl millet genotypes [9].
The aim of this study was to determine the lipid contents and fatty acid compositions of the seeds of some barley genotypes along with standard chemical analysis such as crude ash, crude protein, ADF, NDF, ADL, Relative feed value, dry matter digestibility and dry matter intake.

2. MATERIALS AND METHODS

2.1. PLANT MATERIAL

The names of some barley genotypes grown in the farmer's field in the 2020-2021 growing season in Elazig after being obtained from different institutions and organisations are given in Table I.

2.2. METHODS

2.2.1 Chemical Analyses

Seeds of the barley genotypes were ground in a mill and passed through 1 mm sieve for chemical analysis. Chemical analyses were performed in three repetitions. Crude ash ratio of barley grain samples was determined by burning at 550°Cfor 8 hours [10]. Crude protein analyses were performed by the methods specified in AOAC [11]. The ADF, NDF and ADL constituting the cell wall were performed by the method specified in Van Soest [12] and Van Soest and Wine [13]. Relative feed value (RFV), dry matter digestibility (DMD) and dry matter intake (DMI) of barley grains were calculated according to the following formulas [14].
DMD% = 88.9 - (0.779 × ADF%);
DMI% = 120 / NDF%;
RFV = (DDM% × DMI%) /1.29
The total digestible nutrients (TDN) ratios and metabolic energy (ME) values of the seeds of barley genotypes were determined according to the method specified by Moore and Undersander [15], and the digestible energy (DE) value was determined by Fonnesbeck et al. [16] according to the method specified.

2.2.2 Oil Extraction and Preparation of Fatty Acid Methyl Esters (FAME)

Impurities were removed from the barley seeds, and the clean seeds were ground into powder using a ball mill. Lipids were extracted with hexane/isopropanol (3:2) [17]. The lipid extracts were centrifuged at 1 g for 10 min and filtered; then the solvent was removed on a rotary evaporator at 50°C.

2.2.3 Capillary GLC

Fatty acids in the lipid extracts were converted into methyl esters by means of 2% sulfuric acid in methanol [18]. The fatty acid methyl esters were extracted with 2.5 ml hexane. Then the methyl esters were separated and quantified by gas chromatography and flame ionisation detection (Agilent brand 7890A model GC, 5975C model MS) coupled to a glass GC 10 software computing recorder. Chromatography was performed with a capillary column (100 m in length and 0.25 mm in diameter, BPX90: SGE 054596) using nitrogen as carrier gas (flow rate 3 ml/min). The temperatures of the column, detector, and injector valve were 120-250°C and 230-270°C, respectively. Identification of the individual method was performed by frequent comparison with authentic standard mixtures that were analysed under the same conditions.
The data obtained was analysed by one-way analysis of variance (ANOVA) with the Jump-Pro13 statistical package program, and the differences between the means were compared according to the Tukey test. Correlation analysis was performed between the examined features. Correlation analysis and colour map were made in Jump-Pro13 and Biplot graphics in Genstat 12th (Copyright 2011, VSN International Ltd.).

Table I - Names of barley genotypes used in the study

No	Genotypes	No	Genotypes	No	Genotypes	No	Genotypes
G1	Baris	G11	Onder	G21	Novosadski-565	G31	Bravo
G2	Caca Bey	G12	Burakbey	G22	Nonius	G32	Finola
G3	Akar	G13	Anka-11	G23	Dara	G33	Larende
G4	Cetin-2000	G14	Altikat	G24	Erginel-90	G34	Tosunpasa
G5	Lord	G15	Bozlak	G25	Altinay	G35	Bozlak
G6	Sladoran	G16	Altinorak	G26	Sentosa	G36	Anka-10
G7	Sur-93	G17	Scarpia	G27	Champie	G37	Aydan Hanim
G8	Anka-08	G18	Samyeli	G28	Inbat	G38	Sahin-91
G9	Anka-06	G19	Anka-09	G29	Kendal	G39	Ince-04
G10	Asil	G20	Hevsel	G30	Tarm-92	G40	Avci-2002
						G41	Unver

3. RESULTS AND DISCUSSION

3.1. BASIC CHEMICAL ANALYSIS

Crude ash, crude protein, acid detergent fibre (ADF), neutral detergent fjibre (NDF), acid detergent lignin (ADL), dry matter digestibility (DMD), dry matter intake (DMI) and total digestible nutrients (TDN) ratios and relative feed value (RFV), digestible energy (DE) and metabolic energy (ME) values determined in the grains of some barley genotypes were found to be statistically significant at the 1% level (Table II).

The crude ash and crude protein ratios of the seeds of barley genotypes varied between 3.5-7.1% and 8.3-13.4%, respectively. The highest crude ash content of barley genotypes was obtained in Altinay variety, followed by Kendal and Dara varieties, which are statistically in the same group. The highest crude protein ratios were found in Altikat and Burakbey varieties, which were in the same group statistically. On the other hand, the lowest crude ash and crude protein ratios in grains belonging to barley genotypes were statistically obtained in Aydan Hanim and Avci-2002 varieties, which are in the same group. While it was reported that crude protein ratios of hulled and hulless barley were obtained as 13.41% and 14.62-16.65%, respectively [19], crude protein ratios of winter barley grain were reported to obtained as 8.2-12.1% [20], and as 10-20% in barley seed [21]. On the other hand, crude ash and crude protein rates were obtained as 6.4% and 21.9%, respectively, in barley [22], as 2.0-2.7% and 9.6-11.5%, respectively, in batches of barley [23], as 2-4% and 11.4-14.3%, respectively, in Tunisian barley varieties [24], as 2.6% and 12.0%, respectively, in grain of barley [25], as 0.51-2.03% and 8.3-9.2%, respectively, in whole barley flour [26], as 2.01-4.65% and 8.68-10.74%, respectively, in highland barley flour [27].

The ADF, NDF and ADL ratios of the seeds of barley genotypes varied between 13.5-26.0%, 23.8-36.3% and 1.99-8.78%, respectively. While the lowest ADF, NDF and ADL ratios were obtained from Unver, Caca Bey and Aydan Hanim varieties, respectively; the highest ADF and NDF rates were found in Bozlak cultivar, and the highest ADL rate was found in Kendal, Dara, Sentosa and Larende cultivars, which are statistically in the same group. In the study in which the chemical composition of winter barley grain was examined, it was reported that the crude fibre, ADF, NDF and lignin values of barley seed were obtained as 45.6-53.4 g/kg DM, 57.2-69.1 g/kg DM, 186-259 g/kg DM and 8.7-13.1 g/kg DM, respectively [20], while in the study examining the nutritional values of some grain species, it was reported that the crude fibre, ADF, NDF and ADL values of barley grain were obtained as 50 g/kg DM, 105 g/kg DM, 253 g/kg DM and 25 g/kg DM, respectively [25]. On the other hand, crude fibre values were obtained as 38-64 g/kg DM in barley grain [23], as 4.21% in whole barley flour [26], as 11-34% in barley seeds [21].

The DMD and DMI ratios and RFV values of barley grains differed statistically by 1% among genotypes and varied between 68.7-78.4%, 3.30-5.05% and 175.9-304.0%, respectively. The highest DMD rate was obtained from the Unver cultivar, and the highest DMI rate and RFV value were obtained from the Caca Bey cultivar, while the lowest DMD, DMI rates and RFV value were determined from the Bozlak cultivar. The TDN ratio, DE and ME values of barley seeds differed statistically at the level of 1% among genotypes. The TDN ratios, DE and ME values of grains of barley genotypes varied between 62.9-72.3%, 3.21-3.63 MJ/kg and 9.67-11.33 Mcal/kg, respectively. While the highest TDN ratios and DE values were obtained from the Unver cultivar, the highest ME value was obtained from the Baris cultivar. The lowest TDN rate and DE value were determined from the Bozlak cultivar, and the lowest ME value from the Unver cultivar. While it has been reported that the ME of barley grain was obtained as 13.4 MJ/kg DM [22], the apparent metabolisable energy value of barley seeds was obtained as 10.5-13.7 Mcal/kg DM [23].

With biplot analysis methods, the relationship between genotypes and the characters examined in the research can be presented graphically. In these graphs, PC1 represents the efficiency of genotypes and PC2 represents the stability of genotypes [28]. For this reason, it is desired that the PC1 value of an ideal genotype/variety should be high in terms of the characters in question, and the PC2 value should be close to zero [29]. The study found that the total variation between genotypes and traits was 92.09%, where 80.33% was sourced from PC1 and 11.76% was sourced from PC2. Demirel et al. [30] showed that the PC1+PC2 variation was 73.32% in the graphics obtained from the biplot analysis in their study, Akcura et al. [31] 82.2%, Yorulmaz et al. [32] found that this value was 47.07%. Since the angle between the vectors representing the examined features DMI, RFV, DMD, TDN, DE and ME is lower than 90°, there is a high positive relationship between these parameters. In addition, there was a high negative relationship between ADF and NDF, ADL and ash content. The distance of the vectors expressing the features and the distance of these vectors from the centre point of the coordinate plane are due to the weakness of the relationship between these characters [33]. When the vector graphic of this study is examined; it can be seen that the variation between varieties was low in terms of ADL ratio, but the variation was high in terms of other characteristics. In addition, it was seen that RFV and DMI features were in the first mega environment, DMD, TDN, DE and ME features were located in the second mega environment, ash and protein features were located in the third mega environment and ADL, ADF and NDF features were located in the fourth mega environment.

Scatterplot biplot graphics provide a visual output by

Table II - Means of the examined characteristics

Genotype	CA	CP	ADF	NDF	ADL	DMD (Dry Matter Digestibility	DMI (Dry Matter Intake)	RFV (Relative Feed Value)	TDN (Total Digestible Nutrients)	DE (Digestible Energy)	ME (Metabolic Energy)
	(%)	(%)	(%)	(%)	(%)	(%)	(%)		(%)	(MJ/kg)	(Mcal/kg)
G1	5.2 k-m	11.0 kl	15.9 f-n	25.3 ı-m	5.03 n-q	76.5 a-ı	4.74 a-g	281.1 a-g	70.4 a-ı	3.54 a-ı	11.33 a
G2	4.3 rs	10.4 mn	14.6 l-n	23.8 m	4.07 r	77.6 a-c	5.05 a	304.0 a	71.4 a-c	3.59 a-c	11.29 ab
G3	5.8 g-ı	12.0 ef	18.3 d-j	27.5 d-k	8.33 cd	74.7 e-k	4.36 f-k	252.4 f-k	68.7 e-k	3.47 e-k	11.29 ab
G4	5.7g-j	12.8 bc	15.7 h-n	26.6 f-m	7.62 f	77.0 a-g	4.51 b-ı	268.0 a-ı	70.6 a-g	3.55 a-g	11.26 a-c
G5	5.5 ı-k	10.3 no	16.0 f-n	26.0 g-m	5.34 l-n	76.5 a-ı	4.61 a-h	273.5 a-ı	70.4 a-ı	3.54 a-ı	11.19 a-c
G6	5.4 j-l	11.1 jk	13.8 mn	24.2 lm	3.81 r	78.2 ab	4.97 a-c	301.4 a-d	72.0 ab	3.62 ab	11.13 a-d
G7	6.2 ef	10.7 lm	17.1 e-l	25.4 ı-m	5.33 l-n	75.5 c-j	4.73 a-g	277.3 a-h	69.5 c-j	3.50 c-j	11.13 a-d
G8	5.2 lm	9.5 dt	18.4 d-ı	27.6 d-j	6.35 ıj	74.5 f-k	4.35 f-k	251.7 f-k	68.5 f-k	3.46 f-k	11.11 a-e
G9	5.5 g-j	12.3 de	16.7 f-m	27.1 d-l	5.31 l-n	75.8 b-ı	4.42 e-k	260.2 e-j	69.8 b-ı	3.52 b-ı	11.11 a-e
G10	5.4 j-l	11.7 f-h	16.7 f-m	27.1 d-l	6.85 gh	75.9 b-ı	4.43 d-j	260.4 e-j	69.8 b-ı	3.52 b-ı	11.05 a-f
G11	5.9 f-h	13.0 b	16.1 f-n	25.1 ı-m	5.68 k	76.3 a-ı	4.78 a-g	283.0 a-g	70.3 a-ı	3.54 a-ı	11.04 a-g
G12	5.8 g-ı	13.1 ab	16.8 e-m	27.2 d-l	4.81 q	75.8 b-j	4.41 e-k	259.0 e-j	69.7 b-j	3.51 b-j	11.03 a-h
G13	4.6 qr	11.7 fg	15.8 g-n	26.1 f-m	5.21 l-o	76.6 a-h	4.60 a-h	273.1 a-ı	70.5 a-h	3.55 a-h	11.02 a-h
G14	6.5 c-e	13.4 a	18.8 c-g	29.2 b-f	8.04 de	74.2 h-l	4.11 h-l	236.3 ı-l	68.2 h-l	3.45 h-l	11.00 a-ı
G15	5.9 fg	10.6 m	26.0 a	36.3 a	6.04 j	68.7 n	3.30 m	175.9 m	62.9 n	3.21 n	11.00 a-ı
G16	5.7 g-j	10.7 lm	16.6 f-n	27.2 d-l	6.48 ı	76.0 a-ı	4.42 e-k	260.5 e-j	69.9 a-ı	3.52 a-ı	10.99 a-ı
G17	6.2 de	12.0 ef	17.0 e-l	25.9 h-m	6.65 hı	75.6 c-j	4.63 a-h	271.4 a-ı	69.6 c-j	3.51 c-j	10.98 a-ı
G18	6.5 c-e	11.5 g-ı	19.9 b-e	30.3 b-d	8.06 de	73.4 j-m	3.96 j-l	225.2 j-l	67.4 j-m	3.41 j-m	10.98 a-ı
G19	4.6 p-r	10.2 no	14.9 k-n	25.3 ı-m	4.85 pq	77.2 a-d	4.74 a-g	284.1 a-g	71.1 a-d	3.58 a-d	10.92 a-ı
G20	6.3 de	11.1 k	17.9 d-k	28.3 c-ı	7.13 g	75.0 d-k	4.25 g-l	247.0 f-l	68.9 d-k	3.48 d-k	10.90 b-ı
G21	5.4 j-l	11.1 k	16.9 e-m	27.3 d-l	6.12 j	75.7 b-j	4.40 e-k	258.1 e-j	69.7 b-j	3.51 b-j	10.90 b-ı
G22	6.5 cd	11.8 fg	17.9 d-k	28.3 c-ı	7.84 ef	75.0 d-k	4.25 g-l	247.1 f-l	69.0 d-k	3.48 d-k	10.90 b-ı
G23	6.9 ab	11.2 ı-k	22.1 b	30.9 bc	8.76 ab	71.6 m	3.88 kl	215.6 k-m	65.7 m	3.34 m	10.89 b-ı
G24	6.7 bc	13.0 b	18.8 c-h	29.2 b-g	7.92 ef	74.2 g-l	4.12 h-l	237.0 h-l	68.2 g-l	3.45 g-l	10.88 b-j
G25	7.1 a	12.6 cd	19.1 b-f	28.0 c-j	8.34 cd	74.0 ı-m	4.29 f-k	246.6 g-l	68.1 ı-m	3.44 ı-m	10.87 b-j
G26	5.5 hıj	10.0 o-q	17.0 e-l	26.1 f-m	8.67 ab	75.6 c-j	4.60 a-h	269.5 a-ı	69.6 c-j	3.51 c-j	10.86 c-j
G27	6.2 de	10.2 n-p	20.6 b-d	29.0 b-h	8.44 bc	72.8 k-m	4.14 h-l	233.8 ı-l	66.9 k-m	3.39 k-m	10.86 c-j
G28	5.2 lm	11.8 f	16.1 f-n	27.1 d-l	5.16 m-p	76.3 a-ı	4.42 e-k	261.8 c-j	70.2 a-ı	3.54 a-ı	10.84 c-j
G29	7.0 ab	11.7 f-h	21.8 bc	32.1 b	8.78 a	71.9 lm	3.73 lm	208.3 lm	66.0 lm	3.35 lm	10.75 d-k
G30	4.9 m-p	10.6 m	15.8 g-n	26.2 f-m	1.99 u	76.6 a-h	4.58 a-h	271.9 a-ı	70.5 a-h	3.55 a-h	10.75 d-k
G31	4.7 o-q	9.6 r-t	15.6 ı-n	24.2 lm	3.86 r	76.8 a-f	4.97 a-d	295.9 a-e	70.7 a-f	3.56 a-f	10.69 e-k
G32	5.0 m-o	9.3 t	16.0 f-n	27.1 d-l	3.34 s	76.4 a-ı	4.42 e-k	262.1 b-j	70.3 a-ı	3.54 a-ı	10.67 f-k
G33	4.8 n-q	9.7 q-s	20.6 b-d	30.0 b-e	8.65 a-c	72.9 k-m	4.01 ı-l	226.5 j-l	66.9 k-m	3.39 k-m	10.62 g-l
G34	4.1 s	9.9 p-r	15.1 j-n	25.0 j-m	5.32 l-n	77.1 a-e	4.81 a-f	287.6 a-f	71.0 a-e	3.57 a-e	10.62 h-l
G35	4.8 n-q	10.2 no	13.8 mn	24.1 lm	5.04 n-q	78.2 ab	4.98 ab	301.9 a-c	72.0 ab	3.62 ab	10.59 ı-m
G36	5.0 mn	12.3 de	15.1 j-n	25.0 j-m	3.06 s	77.1 a-e	4.81 a-f	287.6 a-f	71.0 a-e	3.57 a-e	10.47 j-m
G37	3.7 t	8.3 u	14.0 l-n	24.4 k-m	2.66 t	78.0 a-c	4.93 a-e	298.1 a-e	71.8 a-c	3.61 a-c	10.39 k-m
G38	5.4 j-l	11.4 h-j	17.0 f-m	27.1 e-l	7.85 ef	75.9 b-ı	4.44 b-j	261.1 d-j	69.8 b-ı	3.52 b-ı	10.38 k-m
G39	5.1 mn	11.7 f-h	16.7 f-m	27.1 e-l	4.94 o-q	75.9 b-ı	4.43 c-j	260.7 d-j	69.8 b-ı	3.52 b-ı	10.23 lm
G40	3.5 t	8.4 u	15.0 k-n	25.0 j-m	5.48 kl	77.2 a-d	4.80 a-f	287.4 a-f	71.1 a-d	3.58 a-d	10.18 m
G41	4.6 p-r	9.4 t	13.5 n	24.1 lm	5.36 k-m	78.4 a	4.98 a-c	302.6 ab	72.3 a	3.63 a	9.67 n
Av.	**5.5**	**11.1**	**17.1**	**27.0**	**6.06**	**75.6**	**4.50**	**262.6**	**69.5**	**3.50**	**10.85**
TUKEY$_{(0.05)}$	**0.080****	**0.079****	**0.783****	**0.789****	**0.078****	**0.610****	**0.134****	**10.059****	**0.589****	**0.026****	**0.103****
CV (%)	**1.64**	**0.815**	**5.555**	**3.548**	**1.567**	**0.979**	**3.570**	**4.691**	**1.350**	**0.857**	**1.107**

** significant at the P≤0.01 level. There is no statistical difference between the averages shown with the same letter.

evaluating the relationship between genotypes based on average data. However, it cannot provide information about the importance level of the relationship between features. In addition to biplot graphics, our research was supported by a pairwise correlation table and a correlation colour map resulting from the correlation to reveal the importance of the relationship between features (Table III; Figure 3). While there was a positive and high relationship between the research CA rate and CP, ADF, NDF and ADL, a negative and high relationship was found between other features (Table III).

In the biplot chart (Figure 2), which makes it easy to express which genotype is at the forefront at which point, in terms of the parameters examined, it has been determined that varieties that stand out were: 1) Variety number 15 (Bozlak) in terms of ADF, NDF, 2) Variety numbers 23 (Dara) and 29 (Kendal) in terms of ADF, NDF and ADL, 3) Variety numbers 21 (Novosadski-565) and 25 (Altinay) in terms of protein and ash content. The absence of any feature in the regions with varieties 4 (Cetin-2000), 6 (Sladoron), 11 (Onder), 15 (Bozlak) and 37 (Aydan Hanim) located at the diagonal points of the polygon indicates that these varieties are not in an ideal environment for any feature. Numbers 2 (Caca Bey), 5 (Lord), 13 (Anka-11), 18 (Samyeli), 25 (Altinay), 28 (Inbat), 29 (Kendal) and 35 (Bozlak) were located close to the centre point of the coordinate plane. It

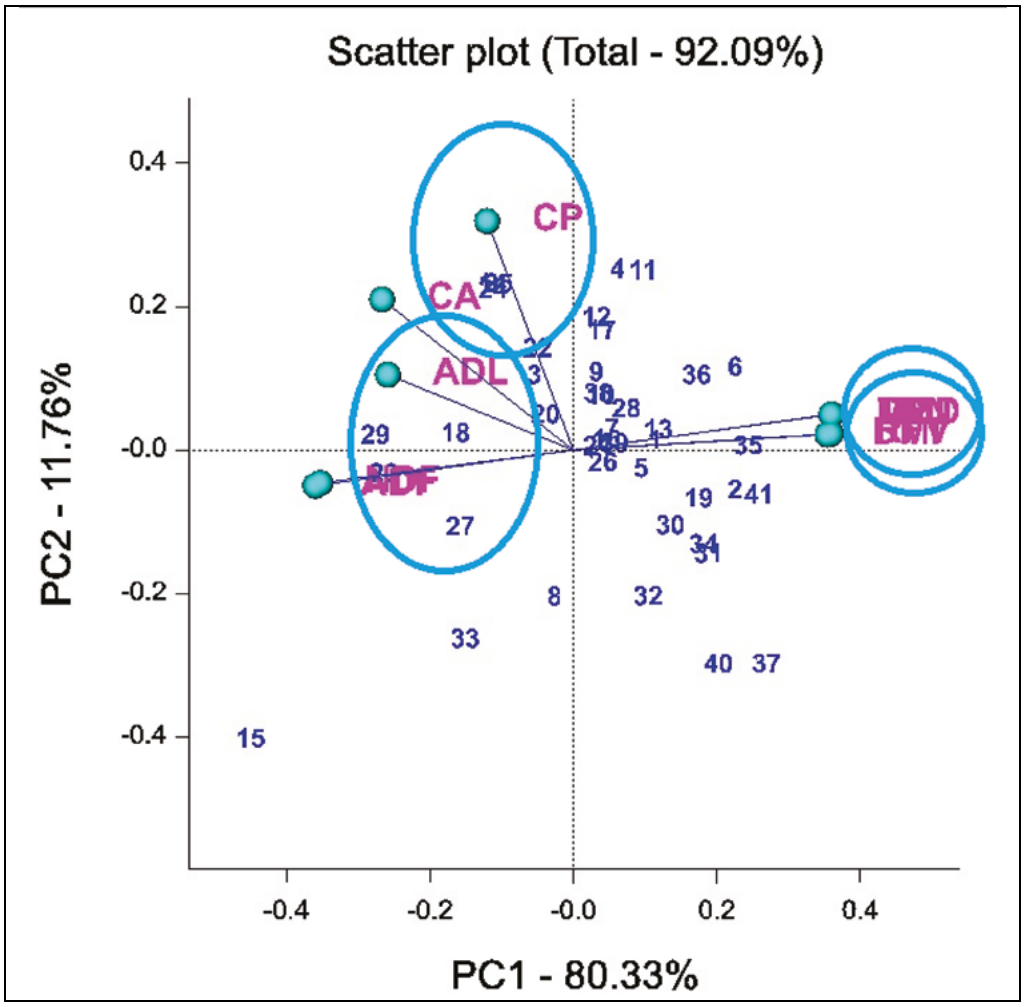

Fig. 1 - Vectoral representation of the relationship between the features examined in terms of average data. Abbreviations: CP; crude protein, ADF; Acid detergent fiber, NDF; Nötral detergent fiber, ADL; Acid detergent lignin, DMD; Dry Matter Digestibility, DMI; Dry Matter Intake, RFV; Relative Feed Value, TDN ;Total Digestible Nutrients, DE; Digestible Energy, ME; Metabolic Energy.

shows that the varieties have reasonable results in all examined traits and give higher than average values.
There is a positive and significant relationship between ADL and CP, a positive and significant relationship between ADF and NDF and ADL, and a negative and significant relationship between other features. A positive and significant relationship was found between NDF and ADL, a negative relationship between NDF and other features, and a negative and high relationship between ADL and other features. A direct (R=1) relationship was detected between DMD and DMI, RFV, TDN, DE and ME. A positive and high relationship was found between DMI and RFV, TDN, DE and ME, and a positive and high relationship was found between RFV and TDN, DE and ME. A direct relationship (R=1) was found between TDN and DE and ME, and between DE and ME (Table III). In the colour mapping system obtained based on the correlation between features, those with a correlation R value equal to 1 are dark red, while as they approach 0, their colour becomes lighter. As the R value moves away from 0, the colours turn dark blue (Figure 3).

3.2. LIPID CONTENTS AND FATTY ACID COMPOSITION

Lipid contents and fatty acid composition of 41 genotypes of barley were determined and the results are shown in Table IV.
The lipid content of the examined genotypes varied between 1.7 and 3.9% (Table IV). Scarpia (3.9%), Kendal (3.9%), Hevsel (3.8%), Onder (3.7%), Sahin-91 (3.7%) and Erginel-90 (3.6%) varieties were the highest for lipid content. The lowest percentages of lipid content were in Tarm-92 and Aydan Hanim varieties. It was reported that the lipid contents of 21 different barley strains grown in Ottawa varied between 2.5-3.1% [34], while the oil contents extracted from different barley grains varied between 1.90-2.87% [35]. In addition, it was reported that the oil content was obtained as 1.27% in the Larende barley variety grown in Turkey [6], the oil content was obtained as 1.73% in the barley grains obtained from a farmer's field in Konya [36] and oil content ranged from 3.71 to 4.69% in hulless and

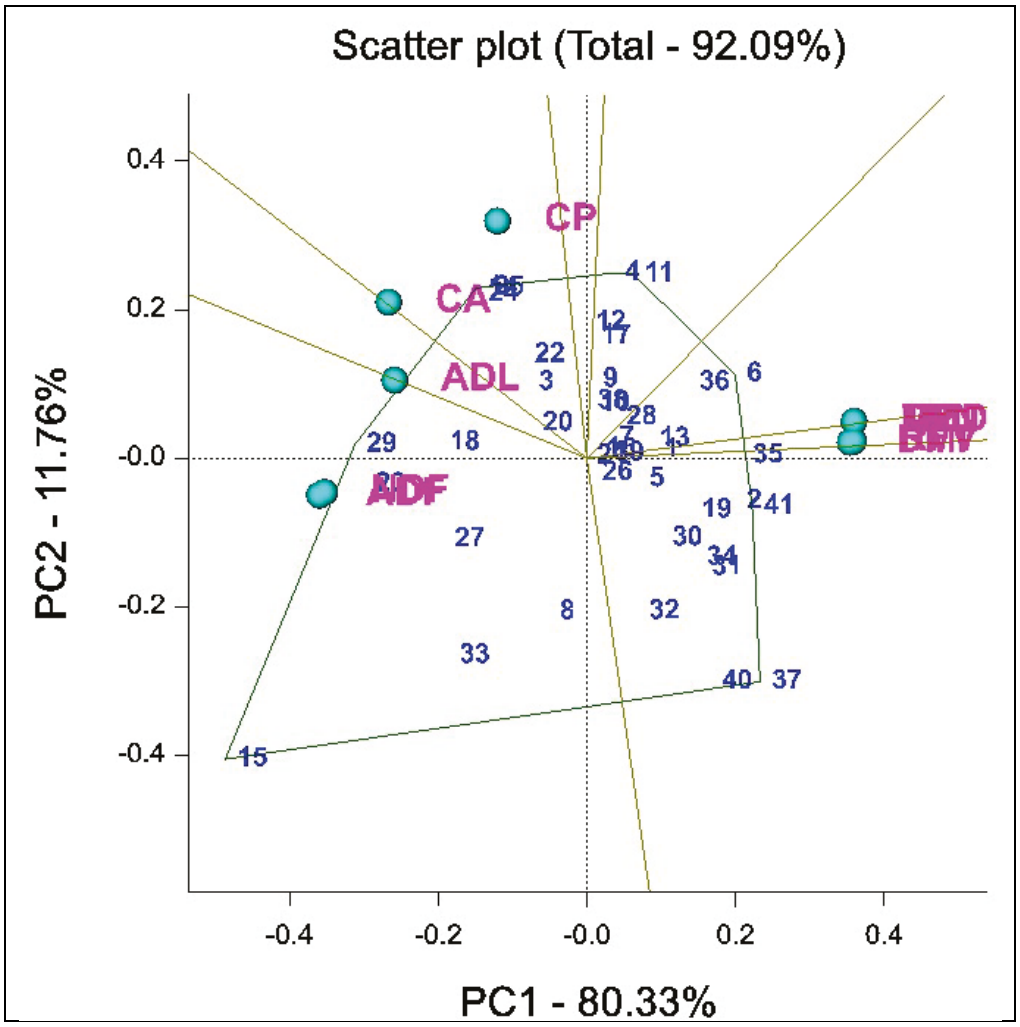

Fig. 2 - Fig. 2. Representation of the relationship between the examined features in terms of average data with polygon and sectors. Abbreviations: CP; crude protein, ADF; Acid detergent fiber, NDF; Nötral detergent fiber, ADL; Acid detergent lignin, DMD; Dry Matter Digestibility, DMI; Dry Matter Intake, RFV; Relative Feed Value, TDN ;Total Digestible Nutrients, DE; Digestible Energy, ME; Metabolic Energy.

Table III - Pairwise correlation analysis results of the relationship between features

	CA	CP	ADF	NDF	ADL	DMD	DMI	RFV	TDN	DE
CP	0.6425**	1								
ADF	0.6331**	0.1728	1							
NDF	0.5926**	0.2177	0.9538**	1						
ADL	0.6667**	0.3222*	0.6413**	0.5847**	1					
DMD	-0.6331**	-0.1728**	-1.0000**	-0.9538**	-0.6413**	1				
DMI	-0.6337**	-0.2621	-0.9412**	-0.9902**	-0.6363**	0.9412**	1			
RFV	-0.6497**	-0.2541	-0.9615**	-0.9885**	-0.6551**	0.9615**	0.9973**	1		
TDN	-0.6331**	-0.1728	-1.0000**	-0.9538**	-0.6413**	1.0000**	0.9412**	0.9615**	1	
DE	-0.6331**	-0.1728	-1.0000**	-0.9538**	-0.6413**	1.0000**	0.9412**	0.9615**	1.0000**	1
ME	-0.6331**	-0.1728	-1.0000**	-0.9538**	-0.6413**	1.0000**	0.9412**	0.9615**	1.0000**	1.0000**

* Significant at level P≤0.05; ** Significant at level P≤0.01

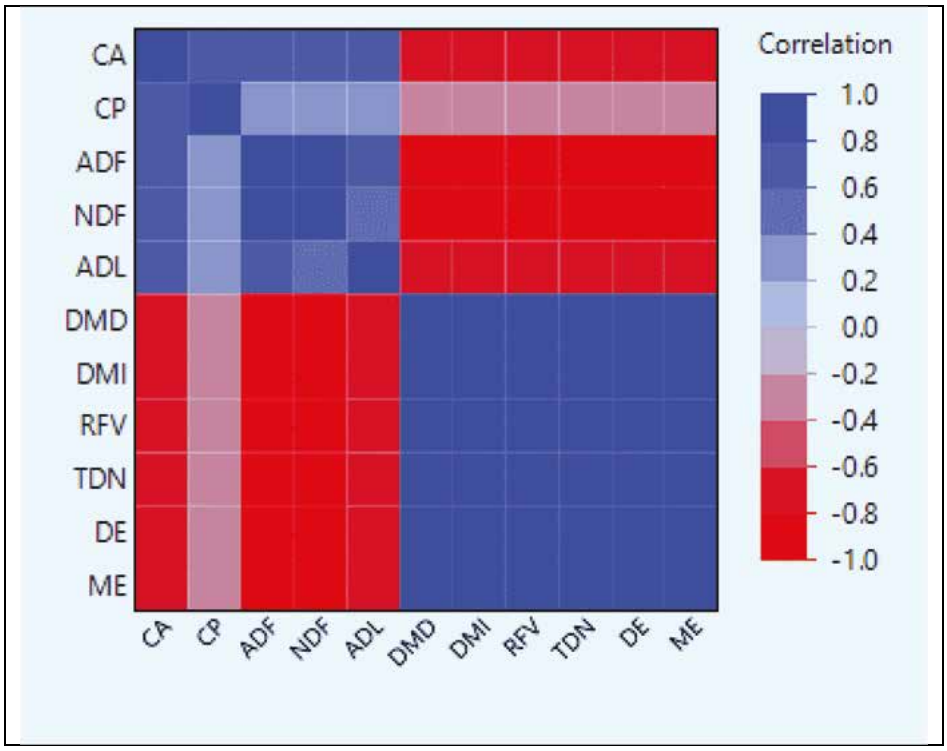

Fig. 3. Representation of pairwise correlation between features with color mapping system. Abbreviations: CP; crude protein, ADF; Acid detergent fiber, NDF; Nötral detergent fiber, ADL; Acid detergent lignin, DMD; Dry Matter Digestibility, DMI; Dry Matter Intake, RFV; Relative Feed Value, TDN ;Total Digestible Nutrients, DE; Digestible Energy, ME; Metabolic Energy.

covered barley grain under organic and conventional management regimens [37].

The seed lipids of some barley genotypes contain palmitic (16.80-25.56%) and stearic (1.33-3.70%) acids as the major component fatty acids, among the saturated acids, with small amounts of arachidic (0.24-0.54%) and behenic (0.06-0.90%) acids (Table IV). The major unsaturated fatty acids found in the seed lipids were oleic (15.30-33.78%), linoleic (41.92-55.28%) and linolenic (2.84-5.43%) acids (Table IV). Palmitoleic, erucic, docosahexaenoic and nervonic acids were lower than 1% in Table IV. In this study, the saturated fatty acids of some barley genotypes were between 19.48 and 28.54%, while the amounts of unsaturated fatty acids were between 71.46 and 80.52%.

Palmitic, stearic and arachidic acids from saturated fatty acids were detected in the seeds of all barley genotypes examined in the study. The highest palmitic, stearic and arachidic acids were in Akar (25.56%), Avci-2002 (3.70%) and Bravo (0.54%) varieties, respectively, while the lowest palmitic, stearic and arachidic acids were in Lord (16.80%), Tarm-92 (1.33%) and Finola (0.24%), respectively. It has been reported that the palmitic and stearic acids of winter and spring barley varieties vary between 21.7-23.6% and 0.59-1.81%, respectively [38], and the palmitic and stearic acids of 21 different barley strains vary between 18.3-27.0% and 2.5-3.1%, respectively [34], and the palmitic and stearic acids of barley oils are 120 g/kg and 6.9 g/kg, respectively [39]. While the palmitic and stearic acids of some barley cultivars were found to vary between 17.72-23.79% and 0.28-4.58%, respectively [35], the palmitic and stearic acids of Larende barley seeds in Turkey were reported to be 20.41% and 1.25%, respectively [6]. On the other hand, it was reported that the palmitic and stearic acids were obtained as 18.53 and 1.85%, respectively, in the barley grains obtained from a farmer's field in Konya [36] and, palmitic and stearic acids were ranged from 10.5 to 22.0% and from 0.3 to 1.1%, respectively, in hulless and covered barley grain under organic and conventional management regimens [37].

Palmitoleic acid was detected in all genotypes except Akar, Sladoran, Anka-08 and Burakbey genotypes; the highest level (0.15%) was found in the Dara variety, while the lowest level (0.07%) was found in the seeds of the Novosadski-565 variety. While the palmitoleic acid content of seeds of some barley cultivars was reported to vary between 0.31-2.87% [35], the palmitoleic acid content of Larende barley cultivar seeds was determined as 0.13% [6].

The major unsaturated fatty acids in the seed lipids of all barley genotypes were oleic, linoleic, and linolenic acids. The oleic, linoleic and linolenic acid contents were the highest in the seeds of Lord (33.78%), Bravo (55.28%) and Champie (5.43%) varieties, respectively and the lowest oleic, linoleic and linolenic acids in Champie (15.30%), Lord (41.92%) and Anka-10 (2.84%) genotypes, respectively. It has been reported

Table IV - The lipid contents and fatty acid compositions of seeds of some barley genotypes

No	Lipid	16:0	16:1	18:0	18:1	18:2	18:3	20:0	20:1	22:0	22:1	22:6	24:1	SFA	USFA
G1	3.1	21.90	0.11	1.56	16.21	54.01	4.35	0.36	1.07	0.09	0.22	0.12	-	23.91	76.09
G2	2.5	21.07	0.08	2.44	18.20	52.12	4.07	0.46	1.00	0.07	0.23	0.18	0.07	24.05	75.95
G3	3.1	25.56	-	2.54	20.59	45.41	3.87	0.44	0.95	-	0.20	0.23	0.19	28.54	71.46
G4	3.4	18.11	0.12	1.58	26.80	48.20	3.36	0.29	0.90	0.10	0.28	0.11	0.16	20.08	79.92
G5	3.3	16.80	0.12	2.67	33.78	41.92	3.13	0.35	0.74	0.08	0.24	0.10	0.07	19.90	80.10
G6	2.6	19.25	-	2.55	17.43	55.17	4.11	0.43	0.81	0.10	0.15	-	-	22.33	77.67
G7	3.2	19.38	0.11	1.59	20.31	52.55	4.38	0.34	1.07	0.08	0.19	-	-	21.39	78.61
G8	2.6	19.48	-	1.53	25.80	47.32	4.21	0.29	1.04	-	0.17	0.15	-	21.30	78.70
G9	3.1	19.82	0.09	2.34	18.55	53.22	4.15	0.40	0.87	0.07	0.20	0.29	-	22.63	77.37
G10	2.8	20.13	0.10	1.51	18.71	54.45	3.23	0.32	0.93	0.11	0.15	0.36	-	22.07	77.93
G11	3.7	19.46	0.10	3.04	18.23	52.93	4.34	0.53	0.85	0.07	0.23	0.21	-	23.11	76.89
G12	3.2	20.31	-	2.18	18.49	52.78	4.25	0.39	0.85	-	0.19	0.55	-	22.88	77.12
G13	2.4	19.86	0.08	2.07	18.27	53.06	4.62	0.40	0.95	0.08	0.22	0.38	-	22.41	77.59
G14	3.1	19.38	0.10	1.74	18.52	54.63	3.61	0.36	0.98	0.08	0.19	0.30	0.10	21.57	78.43
G15	2.7	19.60	0.09	2.58	18.30	53.15	4.40	0.42	0.88	0.10	0.21	0.19	0.07	22.71	77.29
G16	2.2	19.63	0.10	2.65	17.18	53.95	4.71	0.48	0.89	0.06	0.22	0.12	-	22.83	77.17
G17	3.9	20.38	0.09	2.71	16.97	54.24	3.98	0.39	0.84	0.08	0.19	0.12	-	23.56	76.44
G18	3.4	20.17	0.13	1.54	17.80	53.70	4.93	0.29	1.04	0.10	0.18	0.12	-	22.10	77.90
G19	3.0	20.26	0.11	1.38	17.45	53.68	5.24	0.26	1.10	0.08	0.14	0.17	0.12	21.98	78.02
G20	3.8	19.51	0.13	1.50	17.49	54.19	5.21	0.31	1.22	0.09	0.16	0.09	0.10	21.41	78.59
G21	2.4	20.14	0.07	2.18	17.03	54.44	4.54	0.40	0.91	0.08	0.20	-	-	22.80	77.20
G22	3.4	19.93	0.08	2.62	17.13	54.38	4.22	0.49	0.85	0.09	0.19	-	-	23.14	76.86
G23	3.2	21.06	0.15	1.96	23.22	47.99	3.60	0.31	1.00	0.08	0.22	0.28	0.13	23.41	76.59
G24	3.6	20.16	0.13	1.43	18.26	53.67	4.57	0.27	1.09	0.10	0.17	0.16	-	21.96	78.04
G25	3.4	20.67	0.11	2.64	23.63	47.51	3.43	0.48	0.87	0.08	0.30	0.15	0.13	23.87	76.13
G26	3.0	21.10	0.11	1.40	17.21	53.60	4.75	0.26	1.07	0.09	0.18	0.12	0.11	22.85	77.15
G27	2.9	21.57	0.10	2.15	15.30	53.73	5.43	0.32	1.00	0.11	0.19	0.10	-	24.16	75.84
G28	2.5	18.92	0.11	1.75	24.65	48.89	3.47	0.30	0.86	0.13	0.27	0.19	0.46	21.10	78.90
G29	3.9	17.17	0.09	1.89	29.62	45.71	3.85	0.24	0.78	0.18	0.27	0.20	-	19.48	80.52
G30	1.7	20.84	0.11	1.33	18.98	52.59	4.14	0.26	1.18	0.09	0.17	0.17	0.15	22.51	77.49
G31	2.2	19.10	0.09	2.72	16.60	55.28	4.24	0.54	0.85	0.09	0.28	0.12	0.08	22.45	77.55
G32	1.9	21.29	0.12	1.41	17.46	53.86	4.05	0.24	1.13	0.10	0.17	0.10	0.07	23.05	76.95
G33	2.9	19.36	0.09	1.56	18.06	54.87	4.14	0.37	0.93	0.25	0.15	0.14	0.08	21.53	78.47
G34	2.5	21.28	0.10	2.74	17.27	52.47	4.26	0.48	0.81	0.12	0.21	0.18	0.06	24.63	75.37
G35	2.5	20.73	0.10	3.00	17.07	53.02	4.08	0.52	0.80	0.14	0.26	0.20	0.07	24.40	75.60
G36	1.9	22.28	0.12	2.03	22.52	48.20	2.84	0.38	1.06	0.08	0.21	0.14	0.14	24.76	75.24
G37	1.7	20.58	0.11	3.05	17.42	52.91	3.91	0.52	0.79	0.11	0.29	0.21	0.09	24.26	75.74
G38	3.7	18.62	0.11	1.60	20.06	53.75	3.20	0.36	0.99	0.90	0.23	0.18	-	21.48	78.52
G39	2.5	21.24	0.10	1.46	17.29	53.61	4.41	0.29	1.03	0.13	0.16	0.17	0.10	23.12	76.88
G40	2.6	22.05	0.10	3.70	16.26	52.51	3.64	0.47	0.74	0.14	0.25	0.14	-	26.36	73.64
G41	3.0	21.00	0.11	1.71	19.60	51.10	4.43	0.37	1.01	0.13	0.24	0.18	0.11	23.21	76.79

C16:0 Palmitic acid; C16:1 Palmitoleic acid, C18:0: Stearic acid, C18:1 Oleic acid; C18:2 Linoleic acid; C18:3 Linolenic acid; C20:0 Arachidic acid; C20:1 Eicosenoic acid, C22:0 Behenic acid, C22:1 Erucic acid, C22:6 Docosahexaenoic acid, C24:1 Nervonic acid; SFA: Saturated fatty acid; USFA: Unsaturated fatty acid

that oleic, linoleic and linolenic acids in the seeds of winter and spring barley varieties vary between 9.4-12.6%, 58.2%-58.9% and 5.16-7.78%, respectively [38]. On the other hand, oleic, linoleic and linolenic acids were obtained as 12.2-21.2%, 50.7-58.5% and 4.3-7.1%, respectively, in 21 different barley strains [34], as 91 g/kg, 237 g/kg and 16.0 g/kg, respectively, in barley oils [39], as 13.96-22.40%, 39.49-53.40% and 4.65-25.07%, respectively, in grains of some barley varieties [35], as 17.08%, 55.20% and 4.69%, respectively, in Larende barley variety [6], as 19.94%, 51.74% and 0.97%, respectively, in barley oils [36], as 15.8-25.6%, 50.6-71.2% and 2.2-5.2%, respectively, in hulless and covered barley grain [37].

Eicosenoic and erucic acids were detected in all barley genotypes; the highest level was found in Hevsel (1.22%) and Altinay (0.30%), respectively, while the lowest level was found in the seeds of Lord and Avci-2002 (0.74%), and Anka-09 (0.14%) genotypes, respectively. Behenic acid was detected in all genotypes except Akar, Anka-08 and Burakbey genotypes, and docosahexaenoic acid was detected in all genotypes except Sladoran, Sur-93, Novosadski-565 and Nonius varieties. While the highest behenic and docosahexaenoic acids were found in Sahin-91 (0.90%) and Burakbey (0.55%), respectively, the lowest behenic and docosahexaenoic acids were detected in the seeds of Altinorak (0.06%) and Hevsel (0.09%) genotypes, respectively. On the other hand, Nervonic acid was detected in only 22 genotypes examined in the study;

While the highest value was found in Inbat (0.46%), the lowest value was determined in Tosunpasa (0.06%) genotype. While arachidic acid was detected in trace amounts in barley oil [39], it was found as 0.30% in Larende barley seeds [6] and as 0.31% in barley grains [36]. In the study carried out to determine the effects of malt processing steps on the bioactive properties and fatty acid composition of barley, green malt and malt grains, the behenic acid content was determined as 0.18% in barley grain, 0.33% in green malt and 0.25% in malt [36].

The saturated fatty acids (SFA) of barley genotypes were between 19.48 and 28.54%. The seeds of the Kendal variety had the lowest level of total saturated acid, and the seeds of the Akar variety had the highest saturated fatty acid (SFA) concentration. The unsaturated fatty acids (USFA) of barley genotypes were between 71.46 and 80.52%. The highest unsaturated fatty acid contents were detected in the seeds of the Kendal (80.52%), Lord (80.10%), Cetin-2000 (79.92%), Inbat (78.90%), Anka-08 (78.70%), Sur-93 (78.61%), Hevsel (78.59%) and Sahin-91 (78.52%) genotypes, respectively (Table IV).

4. CONCLUSIONS

The crude ash, crude protein, ADF, NDF and ADL ratios of the seeds of barley genotypes varied between 3.5-7.1%; 8.3-13.4%; 13.5-26.0%; 23.8-36.3% and 1.99-8.78%, respectively. The DMD ratios, DMI ratios, RFV values, TDN ratios, DE and ME values of genotypes varied between 68.7-78.4%; 3.30-5.05%; 175.9-304.0%; 62.9-72.3%; 3.21-3.63 MJ/kg and 9.67-11.33 Mcal/kg, respectively. The lipid content of the examined genotypes varied between 1.7 and 3.9%. Palmitic, stearic and arachidic acids from saturated fatty acids were detected in the seeds of all barley genotypes examined in the study. The seed lipids of some barley genotypes contain palmitic (16.80-25.56%) and stearic (1.33-3.70%) acids as the major component fatty acids, among the saturated acids, with small amounts of arachidic (0.24-0.54%) and behenic (0.06-0.90%) acids. The major unsaturated fatty acids found in the seed lipids were oleic (15.30-33.78%), linoleic (41.92-55.28%) and linolenic (2.84-5.43%) acids. Palmitoleic, erucic, docosahexaenoic and nervonic acids were shown to be lower than 1%. Eicosenoic and erucic acids were detected in all barley genotypes.

BIBLIOGRAPHY

[1] K. Liu, Comparison of lipid content and fatty acid composition and their distribution within seeds of 5 small grain species. Journal of Food Science 76(2), C334-C342 (2011).

[2] H.F. Seefeldt, F.H. Larsen, N. Viereck, M.A. Petersen, S.B. Engelsen, Lipid composition and deposition during grain filling in intact barley (*Hordeum vulgare*) mutant grains as studied by 1H HR MAS NMR. Journal of Cereal Science 54(3), 442-449 (2011).

[3] D. Cozzolino, S. Roumeliotis, J. Eglinton, Evaluation of the use of attenuated total reflectance mid infrared spectroscopy to determine fatty acids in intact seeds of barley (*Hordeum vulgare*). LWT-Food Science and Technology 56(2), 478-483 (2014).

[4] K.J. Frey, J.B. Holland, Nine cycles of recurrent selection for increased groat-oil content in oat. Crop Science 39(6), 1636-1641 (1999).

[5] P. Zheng, W.B. Allen, K. Roesler, M.E. Williams, S. Zhang, J. Li, ... B. Shen, A phenylalanine in DGAT is a key determinant of oil content and composition in maize. Nature Genetics 40(3), 367-372 (2008).

[6] A. Kan, Characterization of the fatty acid and mineral compositions of selected cereal cultivars from Turkey. Rec. Nat. Prod. 9(1), 124-134 (2015).

[7] M. Kaplan, K. Kokten, R. Temizgul, S. Buyukkilic Beyzi, Assessment of oil content and fatty acid composition of Turkish sorghum landrace through GGT Biplot analysis. Fresenius Environmental Bulletin 26(3), 1924-1931 (2017).

[8] M. Kaplan, R. Temizgul, S. Buyukkilic Beyzi, K. Kokten, K. Karaman, Classification of different *Sorghum bicolor* genotypes depending on fatty acid composition with using Biplot analysis. Progress in Nutrition 20(4), 699-705 (2018).

[9] S. Seydosoglu, K. Kokten, A. Cil, Some macro elements and fatty acid compositions of seeds of some pearl millet (*Pennisetum glaucum*) genotypes. Chemistry of Natural Compounds 59(5), 524 (2023).

[10] AOAC, Official method of analysis. Association of official analytical chemists 15th. edition, Washington DC, USA (1990).

[11] AOAC, Official Methods of Analysis of AOAC International. 17th ed., 2nd Rev., Gaithersburg, MD, USA, Association of Analytical Communities (2003).

[12] P.J. Van Soest, The use of detergents in the analysis of fibre feeds. II. A rapid method for the determination of fibre and lignin. Journal of the Association of Official Analytical Chemists 46, 829-835 (1963).

[13] P.J. Van Soest, R. H. Wine, The use of detergents in the analysis of fibrous feeds. IV. Determination of plant cell wall constituents. Journal of the Association of Official Analytical Chemists 50, 50-55 (1967).

[14] D.A. Rohweder, R.F. Barnes, N. Jorgensen, Proposed hay grading standards based on laboratory

analyses for evaluating quality. Journal of Animal Science 47, 747-759 (1978).
[15] J.E. Moore, D.J. Undersander, Relative forage quality: An alternative to relative feed value and quality index. In Proceedings 13th Annual Florida Ruminant Nutrition Symposium 32, 16-29 (2002).
[16] P.V. Fonnesbeck, D.H. Clark, W.N. Garret, C.F. Speth, Predicting energy utilization from alfalfa hay from the Western Region. Proceeding of American Society of Animal Sciences (Western Section) 35, 305-308 (1984).
[17] A. Hara, N.S. Radin, Lipid extraction of tissues with a low toxicity solvent. Anal. Biochem. 90, 420-436 (1978).
[18] W.W. Christie, Gas Chromatography and Lipids: A practical guide. The Oily Press, Ayr, pp. 307 (1990).
[19] D. Boros, B. Rek-Cieply, M. Cyran, A note on the composition and nutritional value of hulless barley. Journal of Animal and Feed Sciences 5, 417-424 (1996).
[20] S. Wroblewitz, L. Hütler, R. Manderscheid, H.J. Weigel, H. Wätzig, S. Dänicke, The effect of free air carbon dioxide enrichment and nitrogen fertilisation on the chemical composition and nutritional value of wheat and barley grain. Archives of Animal Nutrition 67(4), 263-278 (2013).
[21] M.A. Farag, J. Xiao, H.M. Abdallah, Nutritional value of barley cereal and better opportunities for its processing as a value-added food: a comprehensive review. Critical Reviews in Food Science and Nutrition 62(4), 1092-1104 (2022).
[22] B. Svihus, R.K. Newman, C.W. Newman, Effect of soaking, germination, and enzyme treatment of whole barley on nutritional value and digestive tract parameters of broiler chickens. British Poultry Science 38, 390-39 (1997).
[23] B. Svihus, M. Gullord, Effect of chemical content and physical characteristics on nutritional value of wheat, barley and oats for poultry. Animal Feed Science and Technology 102, 71-92 (2002).
[24] L. Lahouar, F. Ghrairi, A. El Arem, S. Medimagh, M. El Felah, H.B. Salem, L. Achour, Biochemical composition and nutritional evaluation of barley rihane (*Hordeum vulgare* L.). Afr J Tradit Complement Altern Med. 14(1), 310-317 (2017).
[25] W. Biel, K. Kazimierska, U. Bashutska, Nutritional value of wheat, triticale, barley and oat grains. Acta Sci. Pol. Zootechnica 19(2), 19-28 (2020).
[26] A.A. Aly, F.E. El-Deeb, A.A. Abdelazeem, A.M. Hameed, A.A. Alfi, H. Alessa, A.F. Alrefaei, Addition of whole barley flour as a partial substitute of wheat flour to enhance the nutritional value of biscuits. Arabian Journal of Chemistry 14, 103112 (2021).
[27] Q. Zheng, Z. Wang, F. Xiong, Y. Song, G. Zhang, Effect of pearling on nutritional value of highland barley flour and processing characteristics of noodles. Food Chemistry X 17, 100596 (2023).
[28] W. Yan, L.A. Hunt, Q. Sheng, Z. Szlavnics, Cultivar evaluation and mega environment investigation based on the GGE biplot. Crop Science 40, 597-605 (2000).
[29] E. Farshadfar, M. Rashidi, M.M. Jowkar, H. Zali, GGE Biplot analysis of genotype × environment interaction in chickpea genotypes. Europ. J. Exp. Biology 3(1), 417-423 (2013).
[30] F. Demirel, A.M. Kumlay, B. Yıldırım, Evaluation of agromorphological characteristics of some bread wheat (*Triticum aestivum* L.) genotypes by biplot, clustering and path analysis methods. European Journal of Science and Technology (23), 304-311 (2021).
[31] M. Akcura, O. Hocaoglu, S. Aydogan, A.G. Akcacik, Determination of grain quality parameters of selected bread wheat varieties and pure lines derived from landraces of Türkiye. Turkish Journal of Agriculture-Food Science and Technology 10(11), 2173-2179 (2022).
[32] L. Yorulmaz, M. Oner, O. Albayrak, C. Akinci, Evaluation of yield and quality characteristics in bread wheat (*Triticum aestivum* L.) genotypes: Research of strategic products of economic importance in field crops. Iksad Publications 2, 33-46 (2022).
[33] F. Abate, F. Mekbib, Y. Dessalegn, GGE biplot analysis of multi-environment yield trials of durum wheat (*Triticum turgidum* Desf.) genotypes in North Western Ethiopia. American J. Exp. Agriculture 8, 120-129 (2015).
[34] G. Fedak, I. De La Roche, Lipid and fatty acid composition of barley kernels. Can. J. Plant Sci. 57, 257-260 (1977).
[35] R.O. Osman, F.M. Abd El Gelil, H.M. El-Noamany, M.G. Dawood, Oil content and fatty acid composition of some varieties of barley and sorghum grains. Grasas Y Aceites 51(3), 157-162 (2000).
[36] M.M. Ozcan, F. Aljuhaimi, N. Uslu, Effect of malt process steps on bioactive properties and fatty acid composition of barley, green malt and malt grains. J. Food Sci. Technol. 55(1), 226-232 (2018).
[37] L. Legzdina, E. Ivdre, D. Piliksere, A. Vaivode, I. Mierina, M. Jure, The impact of crop management regime on oil content and fatty acid composition in hulless and covered spring barley. Agronomy Research 20(1), 215-228 (20229.
[38] R.W. Welch, Fatty acid composition of grain from winter and spring sown oats, barley and wheat. J. Sci. Fd. Agric. 26, 429-435 (1975).
[39] L. Wang, R.K. Newman, C.W. Newman, L.L. Jackson, P.J. Hofer, Tocotrienol and fatty acid composition of barley oil and their effects on lipid metabolism. Plant Foods for Human Nutrition 43, 9-17 (1993).