

Proximal canopy sensing of twenty-two bread wheat genotypes for nutritional quality, yield attributes and grain yield under Mediterranean climate

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Abstract

To ensure nutritional security of rapidly increasing population, research interest has revitalized in determining the nutritional quality traits of staple food crops, especially wheat. Besides higher yield potential, research gaps exist regarding nutritional quality assessment of promising wheat genotypes grown under the Mediterranean climate. A field study was conducted to determine the relationship between yield components and quality characteristics of 22 bread wheat genotypes using the SPAD meter, GreenSeeker (NDVI), and CM-1000 chlorophyll meter at different growing stages (Stem elongation, Heading, Anthesis and Milk stage). The recorded findings revealed that G-41 genotype surpassed the rest of bread wheat genotypes by recording the maximum grain yield, whereas G-60 genotype exhibited the highest protein and wet gluten content. Among response variables, SPAD and NDVI values at the heading stage and CM-1000 values at the milk stage were found to be statistically insignificant. According to the correlation and biplot analysis, a significant positive correlation was found between the SPAD values measured for the stem elongation, anthesis and milk stage and yield and quality characteristics. Significant positive correlations were found between the NDVI values at the stem elongation, anthesis, and milk stages and the yield components, and between the CM-1000 value at the heading stage and the grain yield.

Keywords: Bread Wheat, SPAD, GreenSeeker, CM-1000, Yield, Quality

INTRODUCTION

Under changing climate and rapidly increasing human population, crop production has become immensely vital to ensure food and nutritional security globally (Siddiqui et al., 2019; Iqbal, 2020; Oakes et al., 2024). Among staple food crops, wheat (*Triticum aestivum* L.) constitutes of one of the most strategic crops by feeding over half of the world's human populace (Arsoy, 2011; Chowdhury et al., 2021; Iqbal et al., 2021; Yildirim et al., 2022; Abbas et al., 2023). There are many wheat species, however, bread wheat is the most produced among wheat species (Iqbal et al., 2018; Choudhary et al., 2021; Sorour et al., 2021). Approximately one-third of the world's population depends on wheat as their primary food as it provides over 20% of daily calories and 55% of carbohydrates in nutrition worldwide (Alghawry et al., 2021; Kizilgeci, 2021; Zahoor et al., 2021). Previously, there has been persistent focus on boosting wheat grain yield under varying agro-climatic and soil conditions, whereas its nutritional quality assessment has got comparatively meager attention. A number of research findings have explicitly established that wheat genotypes differ pronouncedly in terms of nutritional quality traits by virtue of differences in their genetic make-up (Chowdhury et al., 2021; Darwish et al., 2024). Conventional breeding techniques primarily rely heavily on grain yield for identification and selection of wheat

genotypes having superior genetic make-up. Regan et al. (1992), Jansone et al. (2024) and Hassan et al. (2019) opined that destructive sampling techniques traditionally used to sort-out superior genotypes of wheat for desirable traits could be effective only in case when a small number of genotypes is under investigation. However, these sampling techniques tend to be labor-intensive, tedious, expensive and time-consuming. Moreover, it has been reported that sampling errors lead to misleading results in detecting and differentiating crop genotypes (Elliot and Regan, 1993; Ma et al., 2001; Babar et al., 2006; Kiran et al., 2015; Marino and Alvino, 2019; Zsebő et al., 2024).

Recently, proximal canopy sensing techniques hold bright perspectives for assessing wheat genotypes based on desired traits and that too without employing destructive sampling procedures. In breeding studies conducted in recent years, spectral reflection tools such as GreenSeeker and SPAD are preferred by many researchers as important selection tools in determining many parameters monitored in the cultivation of wheat (Yıldırım et al., 2009; Kızılgeçi et al., 2017). The GreenSeeker device is one of the most used spectral reflection instruments. Determination of efficiency parameters in studies using unmanned aerial vehicles is mainly based on NDVI analyzes (Gündoğan, 2018). Normalized difference vegetation index (NDVI) is used to characterize plant green area index, leaf area index, biomass and nutrient content via portable land devices or satellite. NDVI values can be used to determine physiological factors such as growth rate, vegetation area, earliness, plant leaf yellowing and yield. The NDVI technique can effectively determine the efficacy of farm inputs like irrigation water, fertilizers, etc. by determining their effect on plant canopy and photosynthesis rates (Pask et al., 2012).

The correlation between leaf chlorophyll content and SPAD meter measurements might provide valuable information pertaining to growth attributes and nature of association among them. In these studies, it was reported that leaf chlorophyll and leaf nitrogen concentration had a positive correlation with SPAD measurement data in barley, corn, rice and wheat (Schepers et al., 1992; Peltonen et al., 1995; Wienhold and Krupinsky, 1999). CM-1000 Chlorophyllmeter indirectly measures the chlorophyll content in the leaf without contacting the plant. CM-1000 measurement data is one of the spectral reflection instruments used in recent years to monitor plant development, predict yield, monitor plant health, and detect plant nutrient deficiencies and stress conditions. In this study, the usability of the values measured with the help of GreenSeeker, SPAD and CM-1000 chlorophyll meters in some developmental periods of bread wheat genotypes grown in semi-arid conditions in determining the relationship between yield and quality elements was investigated. However, a significant research gap exists pertaining to nutritional profiling of promising wheat genotypes sown in the Mediterranean climate. Therefore, it was hypothesized that wheat genotypes might vary in their nutritional quality traits based on a typical genetic make-up along with their varying potential to respond to typical agronomic management practices. Thus, the prime aim of this study was to screen out promising wheat genotypes for boosting productivity under semi-arid conditions, while another strategic objective was to comparatively evaluate bread wheat genotypes in terms of their nutritional quality traits.

MATERIAL AND METHOD

The research was conducted in the research area of Teknobiltar R&D company in Diyarbakır province during the growing season of 2021-2022. The planting material of the trial included 22 bread wheat genotypes (8 commercial varieties and 14 advanced bread wheat lines). According to the physical and chemical analysis results of the soil samples taken from the trial area at a depth of 30 cm, the pH value was 7.87, the texture was clayey loamy, the organic matter content was low and the lime amount was moderately calcareous. The average monthly temperature values were above the long-term average during the crop-growing period. While the total amount of precipitation was determined as 319.20 mm, the total amount of precipitation was below the average for the long-term (492.6 mm). The research was set up according to the randomized complete blocks design (RCBD) with 4 replications. The sowing density was calculated as 550 seeds per m², and the experimental plots had a net area of 1.2 × 4 m. Sowing was done with a drill machine in 6 rows and the distance between rows was 20 cm. In the research, 60 kg of nitrogen and 60 kg of phosphorus were applied per hectare with planting. During the tillering period, 60 kg of nitrogen per hectare was applied twice during the growing season. Chemical control was carried out against weeds and pests. The study was carried out in rain-fed conditions. Harvesting was done with a combine harvester in the last week of June. Measurements of response variables were made with spectral reflection instruments were carried out during stem elongation, heading, anthesis and milk periods. Chlorophyll content was determined by taking the average of the measurements taken between 10:00 and 14:00 hours in sunny outdoors, in the middle region of the flag leaf of 5 plants in each experimental unit, using the SPAD-502 instrument, in a way that did not coincide with the transmission vein. The NDVI measurements were made with the help of the GreenSeeker (Handheld Crop) device in windless and cloudless weather, when the plant surface was not affected by any precipitation or weather conditions, between 10:00 and 14:00 of the day when sunlight was high. Leaf chlorophyll content was found by averaging the measurements of 5 plants in each parcel using the CM-1000 chlorophyll meter (Field Scout) instrument, which detects light at wavelengths of 700 nm and 840 nm, to estimate the amount of chlorophyll in the leaves. In the study grain yield, thousand grain weight, hectoliter weight, protein content, wet gluten content and sedimentation value were

measured. For quality analysis, samples taken from each plot were measured with Perten Inframatic 9500 NIR device without milling. The data were collected for all response variables under investigation that were subjected to one-way analysis of variance (ANOVA). Correlation analysis was also performed with the JMP Pro (10) statistical package program according to the randomized complete block design. Thereafter, significant difference comparisons between the mean values were determined according to the least significant difference (LSD) test employed at 5% probability level. Relationships among response variables were also determined using a biplot analysis.

RESULTS AND DISCUSSION

Thousand grain weight (g)

The recorded findings revealed that statistically significant ($p < 0.001$) differences existed in terms of thousand grain weight among the bread wheat genotypes examined in the study (Table 1). When the average values were examined, it was recorded that the genotypes had thousand grain weights between 23.27 g (G-18) and 40.14 g (Empire Plus). The general average of the genotypes was found to be 33.65 g. These findings corroborate with the conclusions made by many researchers who inferred pronounced effects of environment and genotype on the thousand grain weight of wheat (Aydođan et al., 2008; Aktar, 2011; Kizilgeci et al., 2021). Likewise, Yildirim (2005) also inferred after comparatively assessing different bread wheat varieties that thousand grain weight of bread wheat varieties differed significantly and it was attributed to varying genotypic make-up of wheat genotypes which resulted in a typical grain weight. Moreover, Aktaş (2014), in a study conducted on 15 bread wheat varieties under rain-fed and irrigated conditions in Diyarbakır, Mardin and Malatya locations, reported that thousand grain weights varied between 30.4 - 40.8 g.

Table 1. Average yield and quality values of bread wheat genotypes examined in the study

Genotypes	Thousand grain weight(g)	Grain yield (kg ha ⁻¹)	Hectolitre weight (kg L ⁻¹)	Protein Content (%)	Wet Gluten Content (%)	Zeleny Sedimen. (ml)
Beyazhan	37.62 abc	5079.2 b-g	78.53 ab	15.48 def	35.98 def	62.50 cde
Ceyhan 99	34.66 fgh	5610.4 abc	77.63 b-e	15.03 e-j	35.03 e-j	54.00 e-i
DZ-20-4	37.53 bcd	4347.9 fg	78.25 abc	15.03 e-j	35.00 e-j	56.50 c-h
DZ-20-6	35.01 d-g	5502.1 abc	77.85 a-d	14.25 hij	33.28 hij	47.75 hi
DZ22-06	37.44 b-e	4795.8 c-g	75.15 fgh	15.23 d-h	35.43 d-h	58.25 c-g
DZ22-10	39.54 ab	4938.5 b-g	75.45 fg	15.38 d-g	35.73 d-g	57.75 c-g
Empire Plus	40.14 a	5563.5 abc	76.40 def	14.65 f-j	34.10 f-j	53.50 f-i
G-12	34.99 efg	4283.3 g	70.28 kl	16.13 cd	37.45 cd	63.25 bcd
G-18	23.27 k	4432.3 efg	71.93 jk	17.20 ab	39.90 ab	75.50 a
G-27	35.86 c-g	4512.5 d-g	79.60 a	15.35 d-g	35.68 d-g	58.50 c-g
G-3	37.14 b-f	4578.1 d-g	76.55 c-f	14.45 g-j	33.63 g-j	51.00 ghi
G-32	33.91 gh	5007.3 b-g	76.73 c-f	15.48 def	36.05 def	57.75 c-g
G-37	27.89 i	5189.6 b-e	76.00 efg	15.18 d-i	35.33 d-i	54.50 d-i
G-41	38.59 ab	6067.7 a	78.60 ab	14.88 e-j	34.68 e-j	53.75 e-i
G-47	24.87 jk	5674.0 ab	73.60 hij	14.88 e-j	34.65 e-j	52.50 f-i
G-48	25.98 ij	5467.7 abc	74.25 ghi	14.13 j	32.98 j	46.00 i
G-54	34.83 fg	5143.8 b-f	72.75 ij	14.18 ij	33.08 ij	47.25 i
G-60	24.19 jk	2962.5 h	65.48 m	18.05 a	41.80 a	79.75 a
G-70	32.27 h	5276.0 a-d	77.88 a-d	14.70 f-j	34.28 f-j	52.75 f-i
Hüseyin Bey	28.17 i	4262.5 g	69.80 l	15.40 d-g	35.80 d-g	60.00 c-f
Tekin	38.34 abc	5459.4 abc	78.22 abc	15.85 de	36.85 de	63.75 bc
Toros 1003	38.08 abc	5125.0 b-f	77.88 a-d	16.93 bc	39.25 bc	71.75 ab
General mean	33.65	4967.2	75.40	15.35	35.72	58.10
Mean square	116.11**	18123.7***	49.76***	3.92***	19.89***	303.56***
C.V.	5.32	11.68	1.66	4.68	4.54	10.66

** , *** significant at 1% and 0.1% respectively

Hectoliter weight (kg L⁻¹)

There were statistically significant ($p < 0.001$) differences in terms of hectoliter weight among bread wheat genotypes used in this study (Table 1). It was determined that the average hectoliter weight values of the genotypes varied between 65.48 kg L⁻¹ and 79.60 kg L⁻¹. The highest hectolitre weight value was detected for G-27 genotype and the lowest value was detected in the G-60 genotype. The average of all genotypes was found to be 75.40 kg L⁻¹. Many researchers have reported that factors such as variety, ecological conditions and cultural practices impart pronounced influence on hectoliter weight of cereal crops including wheat (Aktar, 2011; Kendal et al., 2011) and it was also inferred that higher grain weight might be utilized as a reliable indicator to predict the grain yield potential of bread wheat genotypes.

Grain yield (kg ha⁻¹)

It was observed that there were statistically significant ($p < 0.001$) differences between bread wheat genotypes in terms of grain yield. It was recorded that the average grain yield values of the genotypes vary between 2962.5 and 6067.7 kg ha⁻¹. The highest yield value was detected in the G-41 genotype and the lowest value in the G-60 genotype. The average of all genotypes was found to be 4967.2 kg ha⁻¹. The G-60 genotype included in the study had the lowest grain yield due to its late flowering and insufficient rainfall. These findings corroborate with those of Iqbal et al. (2021) who opined that genetic differences among wheat genotypes might be attributed to a typical grain yield recorded for different wheat genotypes. It was also inferred that different genotypes hold varying potential to respond and utilize farm input (irrigation water, fertilizers, etc.) which resulted in pronounced differences in their grain yield potential under similar agronomic management plans and agro-climatic conditions.

Protein content (%)

It was observed that there were statistically significant ($p < 0.001$) differences in protein content between bread wheat genotypes. The average protein content values of the genotypes varied between 14.13% and 18.05%. While the highest protein value was obtained in the G-60 genotype, the lowest value was obtained in the G-48 genotype. The general average of genotypes was found to be 15.35%. These findings are in agreement with those of Walsh et al. (2023) who inferred that proximal canopy analysis revealed a significant difference in protein content of wheat genotypes and also opined that these techniques resulted in more precise findings in comparison to destructive sampling techniques and thus these could be suggested for assessing genotypic difference among wheat genotypes in terms of protein content. It was also inferred that protein content of bread wheat genotypes was a complex quantitative trait that is generally controlled by multiple genes and also get influenced by the interaction effects of genotype and environment. Therefore, non-destructive sampling techniques become vital to evaluate bread wheat genotypes to identify high-performing and stable genotypes in order to recommend them for cultivation in target areas.

Wet gluten content (%)

It was observed that there were statistically significant ($p < 0.001$) differences between bread wheat genotypes in terms of wet gluten content. It is seen that the average wet gluten values of the genotypes vary between 32.98% and 41.80%. The highest gluten value was detected in the G-60 genotype and the lowest value was detected in the G-48 genotype. The average of all genotypes was found to be 35.72%. In bread production, the amount and quality of gluten in the structure of the grain is an effective factor in the formation of bread during the fermentation stage. Özen and Akman (2014) stated that the amount of gluten in the grain structure varies according to the variety and ecological conditions.

Zeleny sedimentation (ml)

When Table 1 was examined, it was seen that there were statistically significant differences ($p < 0.001$) in terms of sedimentation content among the bread wheat genotypes used. It is seen that the average sedimentation values of the genotypes vary between 46.00 ml and 79.75 ml. The highest sedimentation value was detected in the G-60 genotype and the lowest value in the G-48 genotype. The average of all genotypes was found to be 58.10 ml. The sedimentation value, which determines the protein quality of wheat grain and has a high degree of heritability, provides information about the bread quality of wheat and is an important quality criterion (Koçak et al., 1992).

Normalized differences vegetation index (NDVI)

Based on recorded findings, it was determined that there existed statistically significant differences among bread wheat genotypes in terms of NDVI values measured during stem elongation. The average NDVI values of the genotypes varied between 0.29 and 0.67. The highest NDVI value was determined in the DZ22-10 genotype and the lowest value in the G-60 genotype. The general average of the genotypes was found to be 0.54. G-60 genotype had the lowest

NDVI value because it was a late flowering genotype compared to other genotypes and could not adequately cover the soil surface. However, there was no statistically significant difference between the bread wheat genotypes under investigation in terms of NDVI values measured during the heading stage.

Table 2. NDVI values measured at different developmental periods of bread wheat genotypes examined in the study

Genotypes	Stem Elongation	Heading	Anthesis	Milky
Beyazhan	0.59 a-f	0.73	0.69 b-e	0.63 b-e
Ceyhan 99	0.53 b-g	0.74	0.71 a-d	0.67 ab
DZ-20-4	0.50 c-g	0.74	0.69 b-e	0.61 ef
DZ-20-6	0.50 c-g	0.73	0.71 a-d	0.64 b-e
DZ22-06	0.60 a-e	0.72	0.69 b-e	0.59 f
DZ22-10	0.67 a	0.72	0.66 e	0.60 ef
Empire Plus	0.63 a-d	0.72	0.71 a-d	0.62 def
G-12	0.61 a-e	0.75	0.72 abc	0.64 b-e
G-18	0.43 gh	0.74	0.74 a	0.66 abc
G-27	0.53 a-g	0.75	0.71 a-d	0.63 c-f
G-3	0.61 a-e	0.72	0.70 a-e	0.60 ef
G-32	0.65 ab	0.74	0.70 a-e	0.66 a-d
G-37	0.55 a-g	0.75	0.71 a-d	0.66 a-d
G-41	0.58 a-f	0.74	0.72 a-d	0.65 a-d
G-47	0.48 efg	0.73	0.73 ab	0.69 a
G-48	0.45 fg	0.73	0.71 a-d	0.66 a-d
G-54	0.54 a-g	0.72	0.71 a-d	0.65 a-d
G-60	0.29 h	0.70	0.68 cde	0.64 b-e
G-70	0.50 c-g	0.73	0.74 a	0.66 a-d
Hüseyin Bey	0.49 d-g	0.70	0.68 de	0.63 c-f
Tekin	0.55 a-g	0.74	0.69 b-e	0.63 cde
Toros 1003	0.64 abc	0.74	0.73 ab	0.63 b-e
General mean	0.54	0.73	0.71	0.64
Mean square	0.03	ns	0.0001*	0.0001
C.V.	18.54**	3.67	4.05*	4.51

*, 5% and **, 1% significant. ns: non significant

It was observed that there were statistically significant differences at the 5% level in terms of NDVI values measured during the anthesis stage. It was determined that the average NDVI values of the genotypes varied between 0.66 and 0.74. The highest NDVI value was detected in the G-18 genotype and the lowest value in the DZ22-10 genotype. The general average of the genotypes was found to be 0.71. NDVI values measured during the flowering period were determined to have statistically significant differences at the 1% level. It was determined that the average NDVI values of the genotypes varied between 0.59 and 0.69. The highest NDVI value was detected for G-47 genotype, whereas the lowest value was recorded for DZ22-06 genotype. The general average of the genotypes was found to be 0.64. These results are in concurrence with those of Lopes and Reynolds (2012) and Zsebő et al. (2024) who inferred that NDVI values remained effective in differentiating the wheat genotypes and could be preferred over destructive sampling techniques to sort out the most performing genotypes. Moreover, Swoish et al. (2022), Guan et al. (2019) and Naser et al. (2020) determined the NDVI index by employing red and near-infrared spectra from GreenSeeker sensor measurements and inferred that it remained effective in quantifying the crops' canopies greenness and assessing plant health changes over time.

Chlorophyll content (SPAD)

It was observed that there were statistically significant differences between bread wheat genotypes in terms of SPAD values measured during the stem elongation period. The average SPAD values of the genotypes varied between 45.90 and 53.05. The highest SPAD value was detected in the G-60 genotype and the lowest value in the DZ-20-4 genotype. The general average of the genotypes was found to be 49.96. It was determined that there was no statistically significant difference in terms of SPAD values measured during the heading period. It was observed that there were statistically significant differences at the 0.1% level between genotypes in terms of SPAD values measured during the flowering period. The average SPAD values of the genotypes varied between 50.55 and 56.93. The highest SPAD value was detected in the G-60 genotype and the lowest value in the Ceyhan 99 variety. The general average of the genotypes was found to be 52.82.

Table 3. SPAD average values of bread wheat genotypes examined in the study

Genotypes	Stem Elongation	Heading	Anthesis	Milky
Beyazhan	48.28 c-f	47.43	51.25 ef	51.25 h
Ceyhan 99	50.05 bc	49.85	50.55 f	52.15 gh
DZ-20-4	45.90 f	48.28	51.25 ef	50.90 h
DZ-20-6	51.88 ab	49.10	52.23 def	56.03 bcd
DZ22-06	48.58 cde	49.35	50.98 ef	53.00 e-h
DZ22-10	49.58 bcd	51.00	52.65 def	55.10 b-f
Empire Plus	48.60 cde	49.43	51.35 ef	53.53 d-h
G-12	51.78 ab	48.85	54.38 bcd	56.05 bcd
G-18	51.50 ab	48.38	52.90 cde	54.30 c-g
G-27	52.90 a	53.33	55.18 abc	55.83 b-e
G-3	46.03 ef	48.58	52.83 def	54.30 c-g
G-32	50.30 bc	49.10	52.13 def	52.95 e-h
G-37	51.73 ab	49.18	55.85 ab	55.83 b-e
G-41	49.90 bc	49.68	52.53 def	54.65 c-g
G-47	49.73 bcd	51.70	50.78 ef	51.13 h
G-48	47.23 def	48.30	51.33 ef	52.60 fgh
G-54	51.38 ab	52.10	53.95 bcd	57.93 ab
G-60	53.05 a	48.63	56.93 a	59.78 a
G-70	50.78 abc	50.63	52.88 c-f	53.78 c-h
Hüseyin Bey	48.28 c-f	52.60	55.90 ab	56.58 bc
Tekin	49.85 bc	53.23	52.73 def	55.85 b-e
Toros 1003	51.80 ab	50.78	51.60 ef	52.25 fgh
General mean	49.96	49.98	52.82	54.35
Mean square	16.37***	11.63 ^{ns}	13.2***	20.79***
C.V.	3.67	5.86	3.13	3.82

***, significant at 0.1%. ns: non significant

It was observed that there were statistically significant differences at the level of 0.1% in terms of SPAD values measured during the milk maturation period. The average SPAD values of the genotypes varied between 50.90 and 59.78. The highest SPAD value was detected in the G-60 genotype and the lowest value in the DZ-20-4 genotype. The general average of the genotypes SPAD value was 54.35. Carlson and Ripley (1997) reported similar findings whereby spectral techniques remained effective in determining the phenotypic and yield potential difference among genotypes of field crops and also inferred that phenotype measurements using these techniques especially SPAD could produce accurate and precise results free of sampling errors as in case of destructive sampling of bread wheat genotypes.

Leaf chlorophyll content (CM-1000)

The results revealed that statistically significant differences existed among bread wheat genotypes in terms of CM-1000 values measured during the stem elongation period. The average CM-1000 values of the genotypes varied between 384.00 and 605.00. The highest CM-1000 value was detected in the G-54 genotype, and the lowest value was detected in the G-60 genotype. The general average of the genotypes was found to be 487.68.

It was observed that there were statistically significant differences in terms of CM-1000 values measured during the heading period. The average CM-1000 values of the genotypes varied between 400.50 and 689.25. The highest CM-1000 value was detected in the G-47 genotype, and the lowest value was detected in the G-60 genotype. The general average of the genotypes was found to be 526.97.

It was observed that there were statistically significant differences between bread wheat genotypes in terms of CM-1000 values measured during the flowering period. The average CM-1000 values of the genotypes varied between 347.00 and 714.25. The highest CM-1000 value was detected in the G-3 genotype, and the lowest value was detected in the Tekin genotype. The general average of the genotypes was determined as 559.78.

It was also observed that there existed no statistically significant difference in terms of CM-1000 values measured during the milky stage.

Table 4. CM-1000 average values of bread wheat genotypes examined in the study

Genotypes	Stem Elongation	Heading	Anthesis	Milky
Beyazhan	423.50 ef	559.50 b-g	414.50 ef	466.00
Ceyhan 99	504.50 cd	525.25 c-i	529.75 b-e	530.25
DZ-20-4	413.75 ef	440.25 jk	406.50 ef	421.50
DZ-20-6	453.75 def	525.25 c-i	501.50 de	457.50
DZ22-06	454.50 def	496.50 f-j	539.00 b-e	405.50
DZ22-10	455.75 def	522.25 d-j	504.50 cde	420.25
Empire Plus	536.50 abc	443.50 jk	594.75 a-d	464.75
G-12	468.25 cde	460.25 h-k	607.50 a-d	473.75
G-18	471.50 cde	545.00 b-g	608.50 a-d	500.00
G-27	525.75 bcd	548.50 b-g	634.75 a-d	484.00
G-3	470.50 cde	484.00 f-j	714.25 a	464.25
G-32	506.25 cd	527.75 c-h	593.25 a-d	477.75
G-37	503.00 cd	562.00 b-f	618.00 a-d	525.75
G-41	410.25 ef	478.25 g-k	651.25 abc	473.00
G-47	602.50 ab	689.25 a	639.25 a-d	542.50
G-48	520.50 cd	617.00 ab	573.00 a-d	528.50
G-54	605.00 a	601.75 bcd	568.75 a-d	435.00
G-60	384.00 f	400.50 k	622.75 a-d	475.00
G-70	530.75 a-d	498.00 e-j	498.50 de	486.00
Hüseyin Bey	515.00 cd	605.50 bc	652.75 ab	445.75
Tekin	459.75 c-f	484.00 f-j	347.00 f	440.75
Toros 1003	513.75 cd	579.00 b-e	495.25 de	460.75
General mean	487.68	526.97	559.78	471.75
Mean square	12822***	18052***	32951**	5482 ^{ns}
C.V.	11.39	11.01	18.65	13.10

** , 1% and *** , 0.1% significant. ns: non significant

Correlation Analysis

NDVI Correlation Analysis

A significant negative correlation of 5% was determined between the NDVI values measured during the stem elongation period with protein ($r = -0.216$) and wet gluten content ($r = -0.214$). A positive significant relationship was determined between NDVI measurement values and grain weight ($r = 0.218$) between hectolitre ($r = 0.375$) at the level of 1% and between thousand kernel weight ($r = 0.530$) at the level of 0.1%. A significant positive relationship was found only between the NDVI values measured during the heading period and the hectoliter ($r = 0.245$) and no significant relationship was detected between the other examined characteristics. A significant positive correlation was also found between the NDVI values measured during the anthesis period and grain yield ($r = 0.246$) but no significant correlation was found between the other examined characteristics. A significant negative correlation was found between NDVI values measured during the milky period and thousand grain weight ($r = -0.363$) and a positive correlation between grain yield ($r = 0.234$).

Savaşlı et al. (2012) reported that the correlation between NDVI measurement values and grain yield was high, especially in the early period. Sultana et al. (2014) found a positive relationship between NDVI measurement values and grain filling time, ripening time, and yield. Karaman (2017) reported that there is a positive relationship between NDVI measurement values made during milking stages of wheat and grain yield. Kizilgeci and Yildirim (2021) determined a significant correlation between NDVI and grain yield at anthesis stage under rain-fed conditions.

SPAD Correlation Analysis

A significant positive correlation was determined between SPAD values measured during the stem elongation period and sedimentation ($r = 0.231$) at the 5% level and between protein ($r = 0.276$) and wet gluten ($r = 0.274$) at the 1% level. There was no significant positive or negative relationship between the SPAD measurement data at the heading stage and the examined traits. Kızılgeçi et al. (2017) reported that there was a high correlation between SPAD measurement data and thousand grain weight values during the heading period. SPAD values measured during the anthesis stage were significantly correlated with thousand grain weight ($r = -0.248$) at negative 5% level, with hectolitre ($r = -0.410$) and grain yield ($r = -0.452$) at negative 0.1% level. A significant relationship was found between SPAD measurement values

and protein ($r= 0.257$), wet gluten ($r= 0.258$) and sedimentation ($r= 0.227$) at the 5% level.

Debaeke et al. (2006) reported that there was a linear correlation between the SPAD measurement data observed during the anthesis stage of the wheat plant and the grain yield and protein content of the grain. Fotovat et al. (2007) stated that there was a positive correlation between SPAD measurement data and yield values in bread wheat. A significant negative relationship was determined between SPAD values measured during the milky stage and grain yield ($r= -0.235$) at the level of 5%. and between hectoliter ($r= -0.417$) at the level of 0.1%. Bahar and Bahar (2016) reported that there was a positive correlation between the SPAD measurement data observed in the anthesis and dough formation stages of the wheat plant and the quality parameters protein, wet gluten and zeleny sedimentation values.

Table 5. Correlation coefficient values showing the relationships of yield and quality characteristics based on data obtained with spectral reflectance instruments

		Protein	Hectoliter	Wet Gluten	Zeleny Sedim.	TKW	Grain yield
NDVI	Stem Elongation	-0.216*	0.375**	-0.214*	-0.186	0.530***	0.183
	Heading	0.091	0.245*	0.099	0.090	0.033	0.154
	Anthesis	-0.048	0.094	-0.045	-0.055	-0.144	0.246*
	Milky	-0.025	-0.017	-0.022	-0.068	-0.363**	0.234*
SPAD	Stem Elongation	0.276**	-0.147	0.274**	0.231*	-0.158	-0.183
	Heading	-0.089	0.053	-0.089	-0.095	0.034	-0.002
	Anthesis	0.257*	-0.410***	0.258*	0.227*	-0.248*	-0.452***
	Milky	0.199	-0.417***	0.201	0.171	-0.139	-0.235*
CM-1000	Stem Elongation	-0.176	-0.043	-0.175	-0.196	-0.175	0.197
	Heading	-0.183	0.036	-0.183	-0.194	-0.279**	0.294**
	Anthesis	0.132	-0.347**	0.124	0.087	-0.348**	-0.174
	Milky	0.095	-0.067	0.096	0.046	-0.366**	0.192

*, **, *** are significant at 5%, 1%, 0.1% respectively

CM-1000 Correlation Analysis

The results revealed that there was no significant relationship between the CM-1000 values measured during the stem elongation stage and the examined characteristics. A significant negative correlation of 1% was found between CM-1000 values measured during the heading period and thousand grain weight ($r= -0.279$). A positive significant relationship was found between CM-1000 measurement values and grain yield ($r= 0.294$) at the 1% level. A significant negative relationship was determined at the 1% level between CM-1000 values measured during the flowering period and hectoliter ($r= -0.347$) and thousand grain weight ($r= -0.348$). A negative significant relationship was found at the 1% level between CM-1000 values measured during the milky period and thousand grain weight ($r= -0.366$).

Biplot Analysis

The Biplot analysis effectively examined and evaluated the relationships between spectral reflection instruments and yield and quality characteristics (Figure 1). In the vector representation of biplot analysis, each feature examined in the research is represented by a vector. It is understood that as the vector length that is the distance to the biplot starting point increases the variation between genotypes increases in terms of the characteristics examined and as the vector length shortens the variation between genotypes decreases (Karaman, 2019). In this regard, it was observed that the variation was generally high in all characteristics under investigation. When the vector representations of the data obtained with spectral reflection instruments were examined, it was elucidated that the variation between genotypes is high in terms of NDVI and CM-1000 values and the variation between genotypes is reduced in terms of SPAD values. Moreover, when quality parameters were examined, it was revealed that the variation between genotypes was recorded to be generally higher. In the biplot analysis technique, each feature examined has been represented by a vector. The cosine of the angle between the vectors indicated the value of the Pearson correlation between these two features. In other words, if the angle between the vectors was less than 90° , it indicated a positive correlation between the examined features, whereas greater than 90° indicated a negative correlation, and an angle of 90° exhibited absences of any correlation (Kendal and Sayar, 2016; Kendal et al. 2016). The biplot analysis performed for all features examined in the research is given in Figure 1. When the biplot chart was examined, PC1 (24.5%) and PC2 (13.2%) constituted 37.7% of the total variation. According to biplot analysis, it was determined that there was a positive relationship between the SPAD value measured during stem elongation, anthesis and milky stages and protein, wet gluten and zeleny sedimentation. According to biplot analysis, there is a positive relationship between the NDVI value measured during the stem elongation period and the hectoliter weight and thousand grain weight;

A positive relationship was determined between the NDVI value measured during the anthesis and milk periods and grain yield. According to biplot analysis, a positive correlation was found between CM-1000 measurement data during the heading period and grain yield.

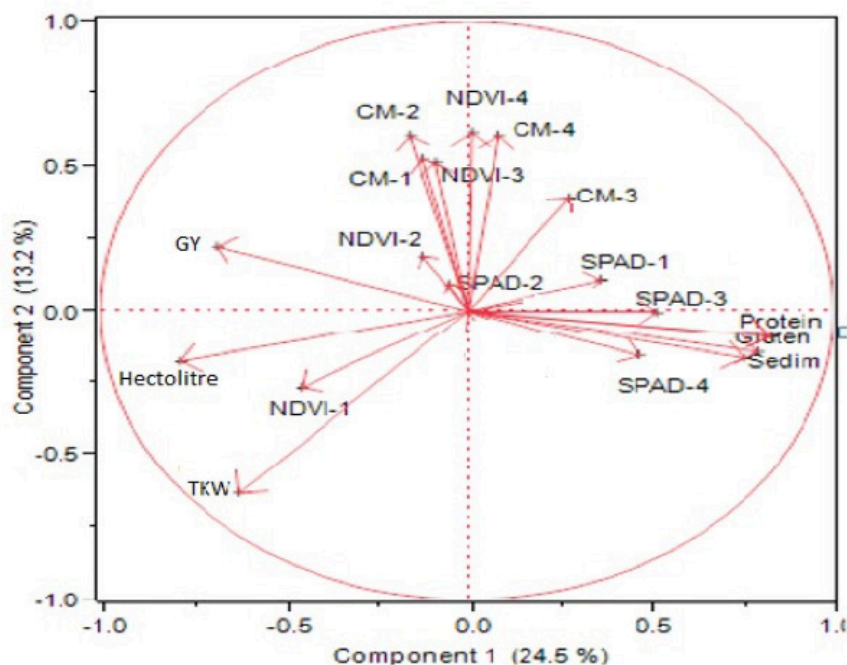


Figure 1. Biplot analysis showing recorded efficiency and quality standards achieved with spectral transmission tool NDVI-1: Normalized vegetation index in the stem elongation stage. NDVI-2: Normalized vegetation index in the heading stage. NDVI-3: Normalized vegetation index in the anthesis period. NDVI-4: Normalized vegetation index in the milk stage. SPAD-1: Chlorophyll content in the stem elongation stage. SPAD-2: Chlorophyll content in the heading period. SPAD-3: Chlorophyll content in the stem elongation stage. SPAD-4: Chlorophyll content in the milk stage. CM-1: Leaf chlorophyll content in the stem elongation period. CM-2: leaf chlorophyll content in heading period. CM-3: leaf chlorophyll content in anthesis period. CM-4: leaf chlorophyll content in milk stage. TKW: Thousand kernel weight. GY: Grain yield

According to correlation analysis and Biplot analysis, a positive correlation was determined between the SPAD value measured during stem elongation, anthesis and milk stages and protein, wet gluten and sedimentation. There is a positive relationship between the NDVI value measured during the stem elongation stage and the hectoliter weight and thousand grain weight; A positive correlation was determined between the NDVI value measured during the anthesis and milky stage and grain yield. It was determined that there was a positive correlation between CM-1000 measurement data during the heading period and grain yield.

CONCLUSION

The recorded findings remained in line with the postulated hypothesis as bread wheat genotypes under investigation varied significantly in terms of yield attributes and nutritional quality traits. It was concluded that the SPAD meter effectively determined the yield and quality characteristics of bread wheat genotypes at varying development periods in semi-arid conditions. Additionally, the NDVI value viably differentiated bread wheat genotypes during the stem elongation, anthesis and milky stage. Moreover, it was inferred that CM-1000 can be used to determine the grain yield of bread wheat during the heading period. At the same time, it has been concluded that these spectral reflection devices can be used as a selection tool in breeding studies, considering the plant development period. Overall, G-41 genotype surpassed rest of bread wheat genotypes under investigation by recording the maximum grain yield that might be recommended to wheat growers for general adaptation under semi-arid climate. Moreover, the GreenSeeker device provided more reliable and accurate winter wheat yield prediction data along with being lesser expensive and simpler device for farmers to use on a large scale.

Compliance with Ethical Standards

Peer-review

Externally peer-reviewed.

Conflict of interest

The authors declare no conflict of interest.

Author contribution

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