

Research Article

Variation and Relationships among Agronomic Traits in Durum Wheat [*Triticum turgidum* (L.) Thell. ssp. *turgidum* conv. *durum* (Desf.) MacKey] under South Mediterranean Growth Conditions: Stepwise and Path Analyses

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Relationships among agronomic traits and grain yield were investigated in 56 genotypes of durum wheat (*Triticum durum* Desf.). The results indicated the presence of sufficient variability nearly for all measured traits. Heritability and expected genetic gain varied among traits. Aboveground biomass, harvest index, and spike number were the most grain yield-influencing traits. Early genotypes showed above-average grain and biological yields, spike number, and lower canopy temperature. Assessed genotypes were clustered into three groups which differed mainly for biological, economical, straw, and grain yields, on the one hand, and plant height, chlorophyll content, and canopy temperature, on the other hand. Selection for direct use from clusters carrying best combinations of yield-related traits and crosses to be made between genotypes belonging to contrasted clusters were suggested to generate more variability. Selection preferentially for spike number, biological yield, harvest index, and canopy temperature to accumulate favorable alleles in the selected entries for future uses is suggested.

1. Introduction

Durum wheat (*Triticum turgidum* L. var. *durum*) is grown on around 17 million hectares worldwide, representing 8% of the world's wheat area [1]. It is among the most cultivated crops in the Mediterranean basin, where approximately 75% of the world's durum wheat area is still grown, which contributes to 50% of the worldwide production [2]. In the Mediterranean basin (characterized by highly variable environments), wheat is mainly grown under rainfed conditions, and yield is often constrained by water and heat stresses that are common during the grain-filling period,

which is due to the low and unpredictable seasonal rainfalls and high temperatures during the last stages of its development cycle [3]. Terminal drought and heat stresses negatively affect wheat grain weight and yield [4, 5].

Breeders, all over the world, are trying through wheat breeding programs to develop productive and adapted cultivars to their specific environments. This was resulted in the release of several commercial varieties. However, obtaining high-yielding genotypes of durum wheat, especially for Mediterranean rainfed areas, is considered difficult due to high genotype × environment interaction [6, 7]. In Mediterranean rainfed areas, genetic improvement of

durum wheat for drought and heat stresses can be achieved by direct or indirect selection for yield. Direct selection involves selecting for yield, whereas indirect selection, that is, physiological breeding, involves selecting for yield components or other associated traits.

Information on the extent of variation and character association is useful for selection purposes to improve durum wheat (*Triticum durum* Desf.) grain yield. Evaluation of breeding populations is made to determine variability, character association, heritability, and genetic advance, which are needed to measure the genetic gain that can be expected through selection for a given trait. Wheat grain yield improvement was achieved through selection of closely yield-related characters. Sign and strength of correlations of these traits, with each other and with grain yield, depend on the type of plant material assessed and the environment test. It is, therefore, useful to target traits having the greatest influence on grain yield, to maximize yield genetic gain.

Yield components are agronomic traits that provide an opportunity to improve yield under water stress, along with morphological and physiological traits. Among the phenological, morphological, and physiological traits reported in the literature with high heritability and used in breeding programs, we discuss the following ones.

Early flowering, which positively affects yield, provides the ability to escape to terminal drought stress. The reduced number of days to heading and also days to maturity are important when breeding for terminal drought stress tolerance since they allow for drought escape [2, 8–11].

Plant heights, which have permitted the important improvements in grain yield in wheat in the last years, according to Fisher [12], have been achieved through the deployment of major genes such as the *Rht* reducing plant height genes (dwarf and semidwarf, the main drivers of the Green Revolution). However, there is a minimum height below which yield limitation is evident [5]. In addition, it has been found that greater plant height has a positive effect on yield in dry Mediterranean rainfed conditions; for this reason, it is desirable that the genotypes maintain their height in arid rainfed areas [13], compared to irrigated areas [14]. However, plant cycle and size should not be too short and too small since such traits will compromise yields under both stressed and optimum conditions. This may be attributed to low capacity to accumulate sufficient stem reserves for subsequent partitioning to the grain.

Hence, high yield under stressed conditions of some earliest and shortest genotypes is due to their ability to maintain a high number of productive tillers and a relatively high thousand kernel weight. This could have resulted from a lengthy grain-filling period [14, 15].

Drought increases senescence, by accelerating chlorophyll degradation, leading to a decrease in leaf area and canopy photosynthesis. There is evidence that stay-green phenotypes with delayed leaf senescence can improve their performance under drought conditions [10].

In wheat, leaf chlorophyll content (as a proxy of leaf photosynthesis) and stomatal conductance were proposed as proper criteria for identifying drought-tolerant genotypes under field conditions [16]. These two traits allow as well as

the identification of germplasm combining improved water use efficiency and productivity under both well-watered or water-limited conditions [17].

Canopy temperature can be used as a tool to indirectly evaluate the transpiration rate of a plant [18]. Olivares-Villegas et al. [19] reported that, under drought, canopy temperature is the most drought-adaptive trait contributing to a higher performance. This trait is highly heritable and consistently associated with yield phenotypically and genetically. It can be utilized as a selection criterion to identify high-yielding wheat genotypes or as an important predictor of yield performance under drought since it epitomizes a mechanism of dehydration avoidance.

However, not all studies have demonstrated correlated benefits of canopy temperature and grain yield in wheat [20]. Further, the study of Giunta et al. [21] on durum wheat has indicated that genotypes with warmer canopy temperature, implying more closed stomata, produced the highest yields. Rebetzke et al. [17] found that preflowering canopy temperature increases were associated with reduced final plant height and increased harvest index and grain yield but were uncorrelated with aerial biomass. In contrast, postflowering, cooler canopies were associated with greater aerial biomass and increased grain number and yield.

Grain yield of cereals is the result of the development and growth of yield components during the life of the crop. The most popular approach to attempt understanding wheat yield is that dividing it into numerical components (i.e., plants per unit land area, spikes per plant, spikelets per spike, grains per spikelet, resulting in the number of grains per m^2 , and average individual grain weight). This approach is simple to understand and easy to do. It only requires one sample at maturity and a minimum process of the sample to divide the components in the sample, and by multiplying these components, one can obtain the yield [22]. Grain number and grain weight are the main components affecting grain yield and are negatively correlated [23–25]. Graziani et al. [2] reported that, among yield components, number of grains m^{-2} showed the strongest correlation with grain yield.

In his study, Mohsin et al. [26] found that grain yield correlated positively with flag leaf area, plant height, biomass, number of spikes, spike length, number of spikelets per spike, number of grains per spike, 1000-grain weight, and harvest index.

Fellahi et al. [27] reported for bread wheat a positive and significant correlation of seed yield with biological yield, spike weight, and spike number. Aboveground biomass had the highest effect, explaining more than 83.0% of grain yield variation. This suggested that any increase in biological yield, particularly the spike weight fraction, affected positively grain yield. Aboveground biomass was largely determined by spike number, which explained 85.20% of total variation in biological yield. Kandel et al. [28] reported similar results for these traits. In addition, moderate to high positive and significant correlations of grain yield with number of spikes, grains per spike, and 1000-grain weight under both stressed and optimum conditions imply the direct contribution of these yield components to yield and should be considered as important target traits during selection [14, 15], and it can be

confirmed that maintenance of a high number of productive tillers and kernels per spike contributes more to the grain yield when compared to the other yield components under stress because the number of grains produced per plant will compensate better for the reduction in seed weight [23]. However, under optimum conditions, all the yield components have considerable contribution to grain yield, implying that selection for any of the yield components could significantly improve the yields [18]. Straw yield was positively related to spike number while thousand kernel weight and plant height exhibited significant and negative correlations with seed number per spike [5]. This suggested that compensation effect was operating among traits, lessening the overall effect on grain yield. Fellahi et al. [29] reported that any increase in spike number improved both aboveground biomass and grain yield. As selection criteria, spike number could be easily appreciated visually, in the field. Furthermore, according to Royo et al. [30], grain yield increases have been mostly based on increases in harvest index and number of grains per unit area through an enhanced number of spikes and grain set.

Salmi et al. [31] found appreciable variability for several durum wheat traits such as days to heading, plant height, aboveground biomass, grain yield, and yield components. Broad-sense heritability was high for days to heading and plant height, intermediate for spike number and number of kernels per spike, and low for grain yield and aboveground biomass.

On the other hand, Graziani et al. [2] found high broad-sense heritability for yield, in contrast with González-Ribot et al. [25]. For the yield components (spike number, grain number, and grain number per spike) and harvest index, broad-sense heritability was low to moderate [2, 25]. Mohsin et al. [26] and Arya et al. [32] found high broad-sense heritability for harvest index. Heritability was, respectively, high to moderate for the physiological traits chlorophyll content and canopy temperature [2, 10].

Expected genetic gain, expressed as % of trait mean, varied from 4.8% for days to head to 45.9% for grain yield. Relatively to check the cultivar, the best selected entries, for the grain yield, were taller and had an above average biological yield; the harvest index and spike number were below the average thousand kernel weight [31]. In the same context, Arya et al. [32] found the lowest value for days to maturity (9.44%) while the highest gain for number of grains per spike (36.88%). For grain yield, expected genetic gain was 31.98%.

Hannachi et al. [33] reported that both additive and dominance gene actions were implicated in the expression of durum wheat traits, *H1* component was larger than *D* component for days to heading, spike number, kernel per spike, and grain yield and smaller for plant height and thousand kernel weight. This indicated the complex inheritance pattern of yield and yield components, suggesting that selection to improve these traits should be conducted on nonsegregating plant material [33]. Results of several research indicated that effective progress could be made through selection of morphological characters to enhance grain yield potential [27, 34–37].

The objectives of this study were to evaluate phenotypic variability, heritability, and genetic advance, to analyze relationships existing among yield and morphophysiological traits of 56 genotypes of durum wheat (*Triticum durum* Desf.) grown under south Mediterranean conditions, and to determine the direct and indirect contributions of the important traits with the aim to select the more desirable traits which may contribute to the improvement of durum wheat and identify the characters of utmost importance which may be used as selection criteria in a wheat breeding program.

2. Materials and Methods

2.1. Site, Plant Material, and Experimental Design. Plant material under study consisted of 56 genotypes of durum wheat (*Triticum durum* Desf.) (Table 1). These genotypes were evaluated in a randomized complete block design with two replications at the Field Crop Institute Agricultural Research Station (ITGC-ARS), El-Khroub, Algeria (36°17'N, 6°38'E, and 640 m above sea level), during the 2014–2015 cropping season. Plot dimensions were 4 rows, 5 m long, and 20 cm apart. Land preparation, sowing date, fertilizer application, and weed control were as recommended for the local area. The seeds were sown in early January 2015, 100 kg/ha of 46% triple superphosphate was applied at sowing and at jointing, and 130 kg/ha of 46% urea was broadcasted. Weeds were controlled chemically with Cossack® OD (mesosulfuron-methyl(mesomaxx) + iodosulfuron-methyl-sodium + mefenpyr-diethyl) at 1 l/ha rate.

2.2. Notations and Measurements. The following morphological traits were measured. Number of days to heading (DHE, days) was counted as number of calendar days from the date of sowing to the time when 50% of the spikes were half way out from the flag leaf. Plant height (PHT, cm) was measured at maturity from the soil surface up to the tip of the spike, excluding awns. Aboveground biomass (BIO, g/m), spike number (SN, #/m), straw yield (STW, g/m), and grain yield (GY, g/m) were recorded from a vegetative sample harvested from one row, 1.0 m long per plot. Harvest index (HI, %) was derived as 100 times the ratio of grain yield to aboveground biomass:

$$HI (\%) = 100 \times \frac{GY}{BIO} \quad (1)$$

Economical yield (Y_{eco}) was deduced as grain yield plus 0.3 times straw yield, according to Annicchiarico et al. [38]: $Y_{eco} = GY + 0.3STW$. At heading stage, chlorophyll content and canopy temperature were read with a chlorophyll meter type Yara N-Tester (Yara GmbH & Co. KG, Dülmen, Germany) and an infrared thermometer model Fluke 62 Max+ (Fluke Corporation, Everett, WA, USA), respectively.

2.3. Data Analysis. Collected data were subjected to an analysis of variance according to the additive model in a complete block design with two replicates, as per Steel and Torrie [39] (Table 2) as follows: $Y_{ij} = \mu + g_i + b_j + e_{ij}$, where

TABLE 1: List of the 56 genotypes of durum wheat evaluated in 2014-2015 at the INRAA-ITGC-ARS, El-Khroub, Algeria.

Number	Name, cross, pedigree
1	Chacan
2	Capeiti8
3	Waha
4	Fg/Palest20C/606//Mexi/3/Rabi
5	Mrb5
6	Tez/Fri//Wulp
7	Kamillaroi
8	Chen "S"
9	TP/Zb//Gdo578/3/Swan
10	Omsinina-1
11	Camadi Abou 73 N°7510
12	JoriC96
13	Omruft2
14	Hoggar (=Vitron)
15	Granizo
16	Tell76
17	Inrat 69
18	M1084
19	Daki
20	Jordan collect 8"S"N°42
21	Cocorit C71
22	Kyperounda
23	Str/AA//21563
24	Araldur
25	Belikh2
26	Sahel
27	Langdon
28	Occotillo
29	Durell
30	Ardente
31	Zb/Fg
32	Kebir
33	Gta dur
34	Simeto
35	Kucuk
36	Gidara-2
37	Sooty9/Rascon-37
38	Yavaro79
39	Ajaia-12/F3Locl (sel.ethio.135)//Plata13
40	Barba de lobo
41	Neodur
42	Bousselam
43	Ahlal
44	Ofanto
45	Acsad1103
46	Beltagy-2
47	Geruftel
48	F413/3/Arthur71/Lahn//Blk2/ Lahn/4/Quarmal/Icamor
49	Azeghar-1//1Blrn/Mrf-2
50	Mrf-2/Stj2//Gdr2/Mgnl1 Oss1/Sij5/Bid1/4/
51	Bezaiz-Shfiisd-19539/Waha/3/Stj
52	Ter-1/3/Stj3//Bcr/Lks4
53	F413/3/Arthur71/Lahn//Blk2/ Lahn/4/Quarmal/Icamor
54	Beltagy-3
55	Beltagy-2
56	Mgnl3/Ainzen-1

TABLE 2: Skeleton of the analysis of variance.

Source	df	Mean square	F test ratio	Expected mean square (EMS)
Block	1	MS _b	MS _b /MS _e	—
Genotype	55	MS _g	MS _g /MS _e	$\sigma_e^2 + b\sigma_g^2$
Residual	55	MS _e	—	σ_e^2

Y_{ij} is the observed value of the measured trait for i th genotype and j th block, μ is the overall mean for the measured trait, g_i is the i th genotype effect, b_j is the j th block effect, and e_{ij} is the residual associated with i th genotype and j th block.

Genotypic (σ_g^2) and phenotypic (σ_p^2) variance components were derived from the expected mean square according to Aquaah [40] as follows:

$$\sigma_g^2 = \frac{MS_g - MS_e}{b}, \quad (2)$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2.$$

The least significance difference at 5% probability (LSD_{5%}) was derived according to Steel and Torrie [39] as follows:

$$LSD_{5\%} = t_{5\%} \sqrt{\frac{2\sigma_e^2}{b}}, \quad (3)$$

where t is the tabulated t value at 5% probability with $(b-1)$ ($g-1$) df of the residual, b is the number of blocks, and σ_e^2 is the residual mean square. Based on the estimates of phenotypic (σ_p^2), genotypic (σ_g^2), and environmental (σ_e^2) variances, phenotypic (PCV) and genotypic coefficients of variation (GCV) were obtained according to the method outlined by Cruz et al. [41]:

$$PCV(\%) = \frac{100\sigma_p}{\bar{X}}, \quad (4)$$

$$GCV(\%) = \frac{100\sigma_g}{\bar{X}},$$

where σ_p and σ_g are the phenotypic and genotypic standard deviations and \bar{X} is the grand mean of the trait of interest. Broad-sense heritability (h_{bs}^2) was calculated using variance components according to Aquaah [40]:

$$h_{bs}^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2} \times 100, \quad (5)$$

where σ_g^2 is the genotypic variance and σ_e^2 is the environmental variance. Selection differential (S), the expected response to selection (RS), absolute value expressed as % of the grand mean (%RS) were calculated according to Cruz et al. [41] as follows:

$$S = X_s - X_0,$$

$$RS = Sh_{bs}^2 = ih_{bs}^2\sigma_p, \quad (6)$$

$$RS(\%) = 100 \left(\frac{RS}{X_0} \right),$$

TABLE 3: Analysis of variance mean squares for 10 characters of 56 durum wheat genotypes.

Source	Block	Genotype	Residual
DF	1	55	55
DHE	1.75	8.71**	0.64
BIO	3960.32	2865.79**	558.85
SN	405.08	207.87**	67.43
GY	987.70	375.11**	130.60
Y_{eco}	1671.07	805.83**	148.48
PHT	0.65	111.84**	1.71
STW	992.46	1507.05**	526.67
HI	24.78	64.79**	11.55
CHL	493.08	8323.08**	598.81
CT	0.10	7.39**	0.35

DHE = days to head, BIO = aboveground biomass, SN = spike number, GY = grain yield, Y_{eco} = economical yield, PHT = plant height, STW = straw yield, HI = harvest index, CHL = chlorophyll content, and CT = canopy temperature.

where X_0 is the grand mean of the trait of interest, X_s is the mean of the selected individuals ($X_0 \pm LSD_{5\%}$), i is the selection intensity ($S/\sigma_p = 2.06$) at 5% probability level, and σ_p is the phenotypic standard deviation of the trait of interest.

Trait relationship was inspected through phenotypic (r_p) and genotypic (r_g) correlation coefficients, stepwise regression, and path analyses. Phenotypic (r_p) and genotypic (r_g) correlation coefficients were calculated as ratios of covariance to root square of the product of corresponding variances, as follows:

$$r_p = \frac{Cov_p(xy)}{\sqrt{\sigma_p^2(x) * \sigma_p^2(y)}} \quad (7)$$

$$r_g = \frac{Cov_g(xy)}{\sqrt{\sigma_g^2(x) * \sigma_g^2(y)}}$$

The genotypic covariance was derived using the property of the sum of two variables, x and y , whose expected mean square is as follows:

$$\sigma(x + y) = \sigma_g(x) + \sigma_g(y) + 2\sigma_g(xy). \quad (8)$$

This can be rewritten as follows:

$$Cov_g(xy) = \sigma_g(xy) = \frac{\sigma(x + y) - \sigma_g(x) - \sigma_g(y)}{2}. \quad (9)$$

Direct and indirect effects of independent variables (i) on dependent variable (j) were obtained by decomposing correlation coefficients between dependent (j) and independent variables (i) according to Singh and Chaudhary [42]. Statistical analyses were performed with LazStats [43], Past [44], and Cropstat [45] software.

3. Results and Discussion

3.1. Variability, Performance, Heritability, and Expected Response to Selection. Results of the analysis of variance indicated significant genotype effect, suggesting the presence of sizeable variation among genotypes for all measured traits (Table 3). Days to heading varied from a minimum of 117.5 to 125.0 days, with a range of 7.5 days, a value statistically

significant compared to $LSD_{5\%}$. Phenotypic and genotypic coefficients of variation were very low in magnitude, suggesting little variability for this trait within the set of studied genotypes. Low variability was reported by Oulmi et al. [46] and Hannachi et al. [34] in durum wheat and by Fellahi et al. [47] in bread wheat, for this trait. Earliness is controlled by various genes related to vernalization, photoperiod, and earliness per se [5]. When grown under heat and drought terminal stresses, plant materials drastically reduced growth cycle, minimizing variability of this trait [47].

Based on a single-year data, broad-sense heritability of days to heading this trait was high, suggesting minor environmental effect, since genotypic variance was almost equal to phenotypic counterpart (Table 4). To minimize the effect of terminal heat and drought stresses, selection favored early heading genotypes; at the same time, the selection material must be late enough to avoid late spring frost [5, 48]. However, due to its low genotypic coefficient of variation, there is little scope to improve this trait through selection. Undoubtedly, earliness has been the predominant trait improved for Mediterranean conditions and may not be a prospective trait for future breeding [5].

Aboveground biomass, measured at maturity, varied from 81.0 to 313.5 g/m. The range of this trait was 232.4 g/m, value significantly greater than the minimum mean of 81.0 g/m, measured for the least aboveground biomass performing genotype. Both phenotypic and genotypic coefficients of variation were high, taking values of 24.11 and 19.79%, respectively.

Broad-sense heritability was just medium, being less than 70% (Table 4). Based on genotypic coefficient of variation and broad-sense heritability, aboveground biomass appeared to be amenable to improvement, within the set of studied genotypes. González-Ribot et al. [25] reported a very low heritability of 9% for aboveground biomass.

Spike number varied from 31.0 to 86.0, with a range value of 55.0 spikes/m. Both phenotypic and genotypic coefficients of variation were appreciably high, taking values of 23.44 and 16.74%, respectively. Broad-sense heritability was low to medium, (51.02%), suggesting a sizeable environmental effect on the expression of this trait. In their studies, Graziani et al. [2] and González-Ribot et al. [25] found a low heritability of 27% for spike number. Similarly, grain and straw yields expressed low broad-sense heritability, high phenotypic and genotypic coefficients of variation, and significant ranges.

Plant height, chlorophyll content, and canopy temperature had high broad-sense heritability and relatively low phenotypic and genotypic coefficients of variation. The same results have been reported by Graziani et al. [2] and Lopes et al. [10], except for canopy temperature which has a moderate heritability value. Harvest index and economical yield have medium broad-sense heritability and medium to high coefficients of variation (Table 4).

Expected response to selection was relatively low for the number of days to heading (3.17%) and high for the remaining traits. The observed values were over 30.0% for biological and economical yields, over 25.00% for grain yield, plant height, and straw yield, over 20.00% for spike number and harvest index, and over 15.0% for canopy temperature and chlorophyll content (Table 4).

TABLE 4: Arithmetic mean, minimum and maximum values, range, least significant difference, phenotypic and genotypic coefficients of variation, phenotypic and genotypic variances, broad-sense heritability, and expected response to selection for 10 morphological and agronomic traits of 56 durum wheat genotypes evaluated in 2014-2015.

Traits	Mean	Min	Max	Range	LSD _{5%}	C _{Vp} (%)	C _{Vg} (%)	σ_p^2	σ_g^2	h_{bs}^2	RS (%)
DHE	121.48	117.50	125.00	7.50*	1.60	1.78	1.65	4.68	4.03	86.29	3.17
BIO	171.64	81.00	313.50	232.50*	47.37	24.11	19.79	1712.32	1153.47	67.36	33.45
SN	50.06	31.00	86.00	55.00*	16.45	23.44	16.74	137.65	70.22	51.02	24.63
GY	60.72	37.35	108.15	70.80*	22.90	26.19	18.21	252.86	122.25	48.35	26.08
Y _{eco}	94.00	59.33	169.76	110.43*	24.42	23.24	19.29	477.15	328.68	68.88	32.97
PHT	56.07	39.50	75.75	36.25*	2.62	13.44	13.24	56.77	55.07	96.99	26.85
STW	110.92	27.75	205.35	177.60*	45.99	28.75	19.96	1016.86	490.19	48.21	28.55
HI	35.94	26.57	65.74	39.18*	4.91	17.19	14.36	38.17	26.62	69.74	24.70
CHL	638.60	493.50	830.50	337.00*	49.04	10.46	9.73	4460.94	3862.14	86.58	18.65
CT	23.57	21.45	27.80	6.35*	1.19	8.35	7.96	3.87	3.52	90.84	15.62

DHE = days to head, BIO = aboveground biomass, SN = spike number, GY = grain yield, Y_{eco} = economical yield, PHT = plant height, STW = straw yield, HI = harvest index, CHL = chlorophyll content, and CT = canopy temperature.

Similar findings have been reported by Ghaed-Rahimi and Heidari [49] who observed 3.10% of expected response to selection for canopy temperature, 23.93% for harvest index, and 4.18% for days to heading. However, these authors reported low values of expected response to selection for biological yield (4.68%) and grain yield (6.95%) compared to what was found in the present study.

Expected genetic gain, expressed as % of trait mean, found by Salmi et al. [31] varied from 4.8% for days to heading to 45.9% for grain yield. High genetic advance coupled with high heritability estimates offers the most effective condition for selection. The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure [32].

3.2. Trait Relationship. Study of the relationships between traits indicated that number of days to heading exhibited negative and significant phenotypic correlations with aboveground biomass (-0.273^*), spike number (-0.266^*), grain yield (-0.339^{**}), and canopy temperature (0.388^{**}). The corresponding genetic correlations were high in magnitude, except the one relating days to head to canopy temperature (Table 5).

The weakness of the phenotypic correlations is imputable to the modifying effect of the environment which reduced the genotypic variation of the number of days to heading. Despite this, the results suggested that early genotypes tended to be more performing in terms of grain yield, aboveground biomass, and spike number and avoided terminal stresses. Low canopy temperature is associated with the ability to extract water from deeper in the soil profile [10]. This encourages selection of early plant material.

Aboveground biomass exhibited significant and positive correlation coefficients with spike number (0.709^{**}), grain yield (0.836^{**}), economical yield (0.965^{**}), straw yield (0.962^{**}), and plant height (0.272^*), and negative correlation coefficients with harvest index (-0.309^*). Aboveground biomass, grain yield, spike number, economical yield, and straw yield were highly interrelated, at both phenotypic and genetic levels. These results suggested aboveground biomass as an indirect selection criterion to improve grain yield, along

with spike number and straw and economical yields. Phenotypic correlation indicated that plant height was significantly and positively correlated with economical yield (0.300^*), but not with straw yield. The genetic correlations indicated that this trait had high negative correlations with canopy temperature (-4.281) and with harvest index (-1.569). Thus, plant height is usually negatively related to the HI [50].

This suggested that dwarf genes are linked to genes controlling high harvest index and sensitivity to high temperatures. This is suggested also by the genetic correlations of straw yield and harvest index (0.554) and straw yield and canopy temperature (2.302) (Table 5). Phenotypic correlations indicated that chlorophyll content and canopy temperature had no effect on morphological traits except that early genotypes exhibited low canopy temperature than late ones. This could be explained by the selection history of the studied genotypes, as chlorophyll content and canopy temperature were not used apart or along with grain yield and morphological traits in the selection process. But the genetic correlation indicated that genes controlling high chlorophyll content tended to be linked to those controlling high temperature tolerance. Findings about relationships between morphological and yield-related traits were in accordance with results of Leilah and Al-Khateeb [51] who reported that wheat grain yield was positively correlated with plant height, spike number, harvest index, and biological yield.

When subjecting the measured traits to regression analysis, the full model captured 94.58% of the total variation in grain yield and indicated that only aboveground biomass and harvest index had highly significant effect on the dependent variable. With the same set of traits, stepwise regression retained aboveground biomass and harvest index which explained 94.90% of the total variation observed in grain yield (Table 6). These results corroborated with those of Fellahi et al. [27] who reported that stepwise regression model retained biological yield and harvest index, which explained 99.7% of grain yield variation. In the same context, Leilah and Al-Khateeb [51] found that stepwise regression analysis identified spike yield, harvest index, spike number, and biological yield as the most important grain yield predictors.

TABLE 5: Phenotypic (below diagonal) and genotypic (above diagonal) correlation coefficients for ten characters of 56 genotypes of durum wheat.

	DHE	BIO	SN	GY	Y_{eco}	PHT	STW	HI	CHL	CT
DHE	—	-0.334	-0.303	-0.402	-0.359	-0.180	-0.311	-1.008	-0.919	-0.096
BIO	-0.273**	—	0.925	1.046	1.009	0.315	1.012	-0.239	-0.119	-0.134
SN	-0.266**	0.709**	—	0.955	0.927	0.143	0.942	-0.345	-0.049	-0.102
GY	-0.339**	0.836**	0.758**	—	1.015	0.401	1.105	-0.402	-0.382	-0.160
Y_{eco}	-0.316*	0.965**	0.763**	0.951**	—	0.348	1.040	-0.306	-0.230	-0.144
PHT	-0.175 ns	0.272*	0.130 ns	0.307*	0.300*	—	-0.225	-1.569	-0.230	-4.281
STW	-0.207 ns	0.962**	0.599**	0.654**	0.857**	0.222 ns	—	0.554	-0.021	2.302
HI	-0.091 ns	-0.309*	0.069 ns	0.219 ns	-0.070 ns	-0.011 ns	-0.535**	—	-0.596	-1.205
CHL	-0.029 ns	-0.067 ns	0.135 ns	-0.179 ns	-0.123 ns	0.024 ns	-0.003 ns	-0.192 ns	—	-1.080
CT	0.388**	-0.143 ns	-0.001 ns	-0.187 ns	-0.170 ns	-0.091 ns	-0.103 ns	-0.067 ns	0.107 ns	—

DHE = days to head, BIO = aboveground biomass, SN = spike number, GY = grain yield, Y_{eco} = economical yield, PHT = plant height, STW = straw yield, HI = harvest index, CHL = chlorophyll content, and CT = canopy temperature.

TABLE 6: Full and stepwise regression models and direct and indirect effects of independent variables on grain yield.

Full regression model							
	b	t	Prob	R^2 mult			
Constant	41.742 ± 47.85	0.872	0.392	—			
DHE	-0.630 ± 0.39	-1.613	0.121	—			
BIO	0.328 ± 0.04	9.382	0.000	—			
SN	0.126 ± 0.12	1.065	0.299	—			
PHT	0.071 ± 0.08	0.903	0.376	—			
HI	0.934 ± 0.13	7.049	0.000	—			
CHL	-0.013 ± 0.01	-1.140	0.267	—			
CT	0.173 ± 0.41	0.419	0.679	0.9458			
Stepwise regression model							
Variables available: BIO, SN, PHT, HI, CHL, and CT							
	β	$b \pm SE_b$	t	a	R^2 mult		
BIO	0.999	0.361 ± 0.012	31.22**	—	—		
HI	0.528	1.271 ± 0.077	16.49**	-46.954	0.949		
Variables available: SN, PHT, HI, CHL, and CT							
SN	0.769	1.033 ± 0.104	9.95**	—	—		
CHL	-0.287	-0.061 ± -0.016	3.75**	—	—		
PHT	0.231	0.319 ± 0.0140	2.79**	26.08	0.683		
Path analysis							
Variable	DHE	BIO	SN	PHT	HI	CHL	CT
Direct effect	-0.014	0.918	0.068	0.050	0.490	-0.033	-0.010
Indirect effects	-0.325	-0.082	0.690	0.257	-0.271	-0.146	-0.177
r_{ij}	-0.339	0.836	0.758	0.307	0.219	-0.179	-0.187

DHE = days to head, BIO = aboveground biomass, SN = spike number, GY = grain yield, Y_{eco} = economical yield, PHT = plant height, STW = straw yield, HI = harvest index, CHL = chlorophyll content, and CT = canopy temperature.

Path analysis results indicated that the negative and significant correlation coefficients, relating grain yield to the number of days to heading (-0.339**), were made of sizeable negative indirect effects (-0.325) via other traits and an almost nil direct effect (-0.014). The high and significant correlation coefficients relating grain yield to aboveground biomass (0.836**) and to spike number (0.758**) were made of high direct effect for biological yield (0.918) and indirect effects for spike number (0.690). Indirect effects of biological yield (-0.082) and direct effect of spike number (0.068), on grain yield, were too small to be of interest. The significant correlation coefficient of plant with grain yield had greater indirect effects (0.27) than direct effect (0.050). Interestingly, the nonsignificant correlation coefficient relating grain yield to harvest index was made of sizeable positive direct (0.490) and negative indirect effects (-0.271). Chlorophyll and

canopy temperature had no significant direct or indirect effects on grain yield (Table 6).

Khan et al. [52] reported significant and positive direct effect of spike number and large indirect effects of days to heading and plant height on grain yield. The number of spikes and biological yield appeared to be the most effective variables influencing grain yield, in the present study; therefore, it is reasonable to assume that wheat grain yield, under south Mediterranean conditions, could be increased by selecting genotypes with high spike number, biological yield, and harvest index. Classifying the 56 wheat genotypes on the basis of the measured traits yielded three clusters, showing gradation, from cluster XG2 to XG1 to XG3, for biological, economical, grain, and straw yields, spike number, and harvest index. Differences between clusters for canopy temperature and number of days to heading were not

TABLE 7: Cluster means for the 10 measured traits of the 56 durum wheat genotypes.

	BIO	SN	GY	Y_{eco}	STW	PHT	HI	CHL	CT	DHE
XG2	151.1	45.7	54.3	83.3	96.9	53.5	36.8	621.8	23.7	121.8
XG1	178.5	53.9	61.2	96.4	117.3	57.4	34.6	710.8	23.8	121.2
XG3	203.7	53.8	73.0	112.2	130.7	59.5	36.0	577.8	23.1	121.3

DHE = days to head, BIO = aboveground biomass, SN = spike number, GY = grain yield, Y_{eco} = economical yield, PHT = plant height, STW = straw yield, HI = harvest index, CHL = chlorophyll content, and CT = canopy temperature.

large. Chlorophyll content was high in cluster XG1 and low in cluster XG3 (Table 7).

Relative differences among clusters are indicated in Figure 1. Cluster XG3 carried entries having best combinations for biological, economical, grain, and straw yields, spike number, harvest index, and plant height. Therefore, selection of suitable genotypes among the 13 available within this cluster would be beneficial, if the selected genotypes show appreciable gain over currently adopted cultivars or checks. In fact, selection of the best 5 genotypes belonging to cluster XG3 brought appreciable gains, principally for biological (10.4 to 30.3%), economical (10.3 to 31.2%), grain (13.7 to 33.7%), and straw (−2.4 to 39.3%) yields, spike number (9.9 to 20.8%), and canopy temperature (−17.3 to −21.8%). No significant change in the number of days to heading (0.0 to 3.3%) was noted.

Changes in harvest index (−11.9 to 9.7%), chlorophyll content (−9.9 to 2.4%), and plant height (−3.4 to 12.6%) were variable (Figure 2). Furthermore, choosing appropriate parents, for hybridization purposes, is an important step in plant breeding program. In fact, performance of progenies depends on parental genotype. As differences between clusters could be attributed to differences in allelic forms, crosses made between genotypes belonging to different clusters are expected to generate variability within which selection to improve the targeted traits would be more efficient.

Altogether, results of the present study indicated that the existing variability varied among traits, being low for number of days to heading, plant height, chlorophyll content, and canopy temperature and high for biological, grain, economical, and straw yields and harvest index. Heritability was low for grain and straw yields, medium for biological and economical yields, spike number, and harvest index, and high for days to heading, spike number, plant height, chlorophyll content, and canopy temperature. Expected response to selection was relatively low for the number of days to heading and high for the remaining traits. These results corroborate findings reported by Salmi et al. [31] and Ghaed-Rahimi and Heidari [49].

The results of correlation coefficients indicated that early genotypes performed best in terms of grain yield, aboveground biomass, and spike number and avoided terminal heat stress, encouraging selection of early plant material. Correlation coefficient results pointed to aboveground biomass as an indirect selection criterion to improve grain yield, along with spike number, straw yield, economical yield, and harvest index. These findings were in accordance with results of Fellahi et al. [27], Salmi et al. [31], Hannachi et al. [34], and Leilah and Al-Khateeb [51]. Path analysis indicated that days

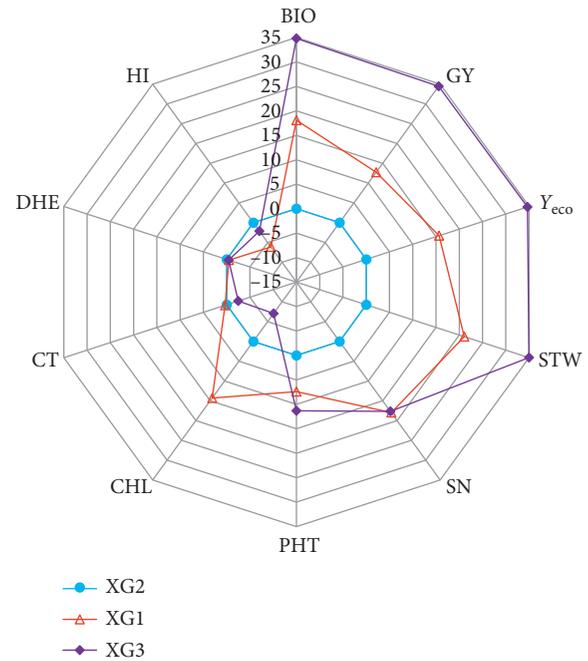


FIGURE 1: Relative deviation of the performances of clusters XG1 and XG3 as percent of mean values of cluster XG2 for the measured traits.

to heading and spike number affected grain yield mainly through indirect effects, while aboveground biomass had high direct effect. Harvest index had both significant positive direct and negative indirect effects. Three contrasted clusters were extracted from the data set.

Crosses between genotypes belonging to different clusters to generate variability within which selection to improve the targeted traits would be more efficient are proposed. This increases possibilities to improve both yield potential and stress tolerance. Selection should be done, preferentially for spike number, biological yield, harvest index, and canopy temperature to accumulate favorable alleles in the selected entries. Selection of best genotypes, for direct uses as cultivars, from clusters carrying best combinations of yield-related traits is feasible.

4. Conclusion

Sufficient variability was noted for the measured traits in the data set obtained from the 56 assessed genotypes. Heritability

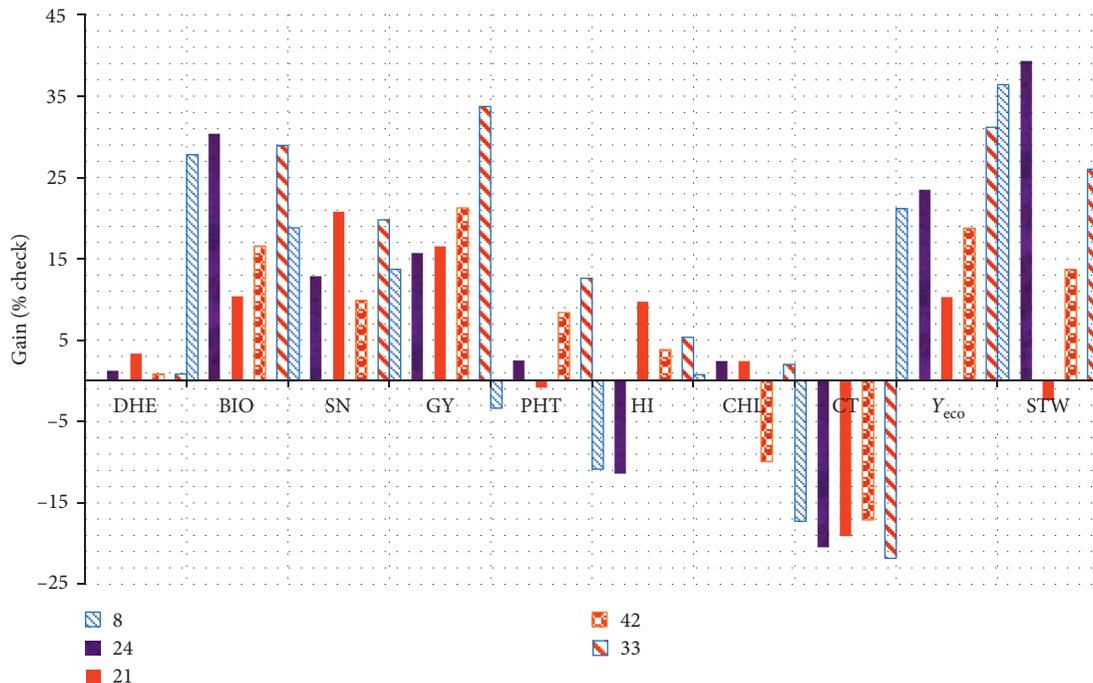


FIGURE 2: Gain (% of check) for the measured traits brought by selection of the 5 best yielding entries from cluster XG3.

and expected genetic gain varied among the measured traits. Relationship analysis designated aboveground biomass, harvest index, and spike number as the most grain yield-influencing traits. High genetic advance coupled with high heritability estimates offers the most effective condition for selection. The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure. Selection for earliness is encouraging since early genotypes exhibited above-average grain and biological yields and spike number and most importantly avoided terminal heat stress. Selection for direct use from cluster carrying best combination of yield-related traits and crosses among genotypes belonging to contrasted clusters were suggested to generate more variability. Selection should be done, preferentially for spike number, biological yield, harvest index, and canopy temperature to accumulate favorable alleles in the selected entries for future uses. The results suggest that genotypes with high expression of biomass (source), good harvest index expression, and other yield components can be used as parents in durum wheat breeding program to boost the genetic gains.

Disclosure

This work is part of the Ph.D. thesis of Ali Mansouri.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this article.

Acknowledgments

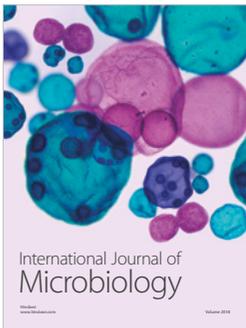
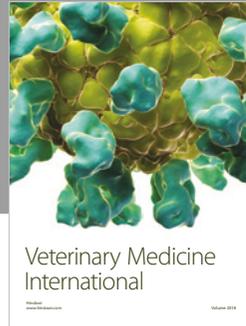
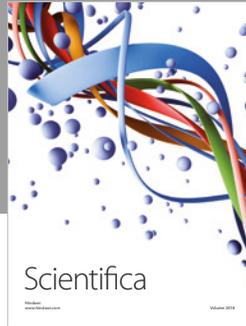
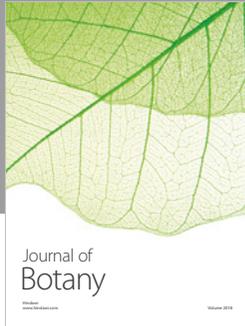
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