Traits Association in Durum Wheat Genotypes under Optimum and Low Nitrogen Conditions

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Abstract

Realizing the nature and degree of association between yield and yield related traits under various environment and conditions is a pre-requisite in any crop improvement. A total of 200 durum wheat genotypes obtained from different sources were tested at Debre-Zeit, Chefe-Donsa and Minjar under optimum and low nitrogen in 2020 season. The objectives were to assess the relationship between grain yield and other important traits, and to determine relationships among the various traits and their direct and indirect effects on durum wheat grain yield under optimum and low nitrogen (N) conditions. The Phenotypic and genotypic association of grain yield with grain filling period, number of seed per spike, biomass yield, harvest index, normalized difference vegetative index, hectoliter weight, and chlorophyll contents were significant and positive under both optimum and low N conditions. Biomass yield, number of seed per spike, normalized difference vegetative index, harvest index, and hectoliter weight were direct contributors to grain yield under both N conditions. Thus, these traits can be used as the primary selection criteria for grain yield in durum wheat under optimum and low Nitrogen.

Keywords: correlation analysis, durum wheat, optimum nitrogen, path analysis

Introduction

Durum wheat (*Triticum turgidum* var. *durum Desf*) is one of the oldest cultivated cereal species in the world (Royo *et al.* 2009). It has significant economic value and provides the raw materials for food industries in the nutrition of the global population (Sissons *et al.* 2005) and suitable for preparing traditional recipes in Ethiopia (Belay *et al.* 2013). Currently, durum wheat has become a major cash crop, with pasta, burghul, and couscous industries paying 10 to 20% more for durum grain than for bread wheat (Sall *et al.*, 2019). Nutritionally, 100 gram of durum wheat contains 339 calories, 13.7 g of protein, 2.5 g of fat, 3.5 g iron, 34 mg calcium, 144 mg magnesium, and 508 g of phosphorus, as well as significant amounts of vitamins, lutein, and fiber for better health (Dan Brennan, 2021). Despite its importance, grain yield is a complex quantitative trait and is governed by many minor genes and confounded by interactions of various traits due to the effect of environments and growing conditions (Singh and Diwivedi 2002).Use of primary and its related traits in phenotypic and genotypic correlations analysis would be important to select the right genotypes through indirect methods (Baye *et al.*, 2020). A correlation coefficient can be used to express how much and in what direction different variables influence the primary characteristics, but it does not indicate the relative importance of direct and indirect effects of yield components (Silva *et al.*, 2009). Path analysis, which involves the unfolding of correlation coefficients for analyzed traits, can be used to determine the direct and indirect effects of yield components (Baye *et al.*, 2020). In order to provide information regarding the proper cause and effect relationship between yield and other traits, correlation and path coefficient analysis could be employed as important tools. Plant breeders can increase the effectiveness and success of selection through better understanding of the genetic relationship between grain yield and its components, which helps identify traits to be used in the future breeding (Wolde and Eticha, 2016) and (Yagdi and Sozen, 2009). Thus, information on the nature and magnitude of character associations between yield and yield related traits is a pre-requisite in improving durum wheat under optimum and low nitrogen. Therefore, the objectives of this study was to estimate phenotypic and genotypic coefficient of correlations and to determine their interrelationships among various traits and their direct and indirect effects on durum wheat grain yield under optimum and low N conditions.

Materials and Methods

Description of the study area

The experiments were carried out at Debre-Zeit, Chefe-Donsa and Minjar experimental stations in 2020 growing season (Table 1).

Table 1. Geographical locations and climatic conditions description of the experimental sites

Descriptions		Locations		
		Debre Zeit	Chefe Donsa	Minjar
Altitude (m.a.s.l)		1900	2435	2257
Latitude and longitude		8^{o} 44’ N, 38^{o} 58’E	8o 57’, 39o 16’E	8°46′ N , 39°16′ E
Mean annual rainfall (mm)		984	1020	865
Temperature	Max. (^{o}C)	26.84	20	28.77
	Min (^{o}C)	11.39	8	12.3
Soil types		Black vertisol	Black vertisol	Vertisol
Agro-/ ecology		Mid altitude	Highland	Mid altitude

Source: DZARC, 2020

Experimental plant materials, design and layout

A total of 200 durum wheat genotypes were used in this study, of which 67 genotypes were obtained from Ethiopian Biodiversity Institute (EBI), 83 from International Maize and wheat Improvement Centre (CIMMYT), 13 from International Center for Agricultural Research in the Dry Areas (ICARDA), and 37 from Debre-Zeit Agricultural Research Center (DZARC) durum wheat breeding program (Appendix Table 1). A composite soil sample was taken from each site, and soil nitrogen analysis was done following standard procedures before planting. The fields that are low/very low in total nitrogen (TN) content were selected to establish the experiments following (Tadesse *et al.*, 1991) soil rating based on TN. Two sets of experiments (Set-I and Set-II) were conducted at each location, and the same genotypes were used for both sets of experiments. The plot size was 1 m x 1 m and the distance between rows, plots, blocks and replications was 0.2, 0.4, 0.5, and 1 meter, respectively. The genotypes were arranged in an alpha lattice design with two replications. The genotypes were assigned to plots at random within each block during planting. The optimum N environment received 92 kg/ha N in split applications at the time of sowing and tillering stage as top-dressing whereas none was applied to Low N environment. A recommended 10 kg/ha phosphorous in the form of triple super phosphate (TSP) was applied under both optimum and low environments. Weeding was done manually, thus, the test fields were weed-free. The fungicide Nativo 300SC (200g/l Tebuconazole + 100g/l Trifloxystrobin) was used to control stem, leaf and yellow rust infestations, and all other crop management techniques were uniformly applied to all genotypes in accordance with the crop's recommendations.

Data collection

The data were collected for phenological, agronomic, physiological and quality traits. Days to heading (DH) was recorded by counting the number of days from sowing to the stage when 50% of the heads emerged within a plot and days to 90% physiological maturity (DM) was recorded by counting the number of days from sowing to physiological maturity on plot basis. Grain filling period (GFP) was obtained by subtracting DH from DM. Plant height (PH), number of fertile tillers per plant (NFT), spike length (SL), spikelet per spike (SPS), and number of seeds per spike (NSPS) were recorded from ten randomly sampled plants from the four central rows and their average data was taken. After the plants were mechanically harvested, data on above ground biomass yield (BM, t/ha^{-1}) and grain yield (GY, t/ha^{-1}) were collected and converted to a hectare basis. BM was measured in the field using a hanging balance during harvesting, whereas GY was calculated by weighing the threshed grain on an analytical sensitive balance and adjusted to 12.5 percent moisture content. Harvest index (HI) was determined from the ratio of GY to BM. Thousand seed weight (TSW) was obtained by counting thousand grains using seed counter and weighing using analytical balance. A handheld green seeker was used to measure Normalized difference vegetative index (NDVI) during heading stage, and it was taken 50-60 cm above the canopy. Random plants were considered to record chlorophyll content (CHO) using SPAD-502 plus chlorophyll analyzer at flag leaf stage Grain protein content (PC) was analyzed using Pertien protein analyzer and hectoliter weight (HLW) was measured by a portable hectoliter test weight kit(model).

Data analysis

The F-max ratio for homogeneity of variance was carried out to determine the validity of the experiment and to combine the data over locations (Domangue, 2015). Since the error variances for all traits were homogeneous, the data was pooled and analyzed across locations. Genotypic and phenotypic correlations between the traits were calculated from the mean of data over locations and replications using variances and covariance's matrix for the association of traits while path analysis was carried out for the traits that had significant correlations with grain yield both at the genotypic and phenotypic levels to determine the direct and indirect contribution of the traits on grain yield following the procedures suggested by (Singh and Chaudhary 1977) and (Dewey and Lu, 1959) using R-software version 4.1.3 (R Core team, 2013). $\mathrm{rij} = pij + \sum_{ik} r\ P\ kj$ Where, rij=mutual association between the independent variable 'i' and the dependent variable 'j' as measured by correlation coefficient. Pij=component of direct effects of the independent variable (i) on dependent variable (j) as measured by the path coefficients. $\sum_{\mathrm{ik}} \mathrm{r}\ \ pkj$=summation of components of indirect effects of independent trait (i) on the given dependent trait (j) through all other independent variables (k).

The influence of the remaining unknown factor was measured as the residual effect. It was calculated as; $\sqrt{1 - \mathrm{R2}}$ where, $\mathrm{R}^2 = \sum_{\mathrm{pij}} \mathrm{rij}$.

Results and Discussions

Genotypic and phenotypic correlation coefficients under optimum N

Genotypic and phenotypic correlation coefficients of the characters are presented in Table 2. In this study, majority of the genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients demonstrating strong inherent association between the characters, and the environment that modify the phenotypic expression of the characters. However, the phenotypic correlation coefficients of some traits were equal and/or more than its equivalent genotypic correlation coefficients indicating that environmental and genotypic effects were similar. Tsegaye *et al*. (2012) also reported high genotypic than phenotypic correlation in durum wheat.

Correlation of grain yield with other traits under optimum N

GY had positive and significant correlation with GFP, NSPS, BM, HI, NDVI, HLW, TSW, and CHO at both genotypic and phenotypic level; and NFT correlated at phenotypic level (Table 2). This implies that, selection for these characters would leads to simultaneous improvement of GY in durum wheat. The results were comparable with the work of (Kumar *et al*. 2016); *(Singh et al.* 2012) and (Zerga *et al.* 2016) on bread wheat; and (Alemu *et al*. 2020) and (Baye *et al.*, 2020) on durum wheat on different characters. In contrast, DH, DM, PH, SL and PC where DH showed a negative genotypic and phenotypic association with GY and PC and DH had significant correlation at genotypic and phenotypic level in respective order. Meles *et al*. (2017) found negative genotypic and phenotypic correlation coefficients of GY with DH, DM and PC and Surma et al. (2015) with PC. Negative correlation of GY with important traits, which is major limitation in plant breeding leads to undesirable selection probably associated to linkage or pleiotropic gene effect. Abinasa *et al*. (2011) emphasized the biparental mating, mutation breeding and diallele mating in breaking undesirable linkages to improve yield components with negative associations. On the other hand, an inverse association of DH and DM with grain yield is sometimes desirable when terminal heat and drought are anticipated (Mohammadi, 2019).

Correlation among yield related traits under optimum N

DH and DM revealed positive and significant correlation with PH, NFT, SL, SPS, BM and NDVI whereas they showed negative and significant correlation with GFP, NSPS, HI, and CHO at genotypic and phenotypic levels (Table 2). DM was negatively and non-significantly correlated to PC and HLW at both phenotypic and genotypic levels and the former had positively and negatively correlated with DH at genotypic and phenotypic levels respectively. DH was negative and significantly correlation with HLW and DM had positive significant correlation with TSW at both levels.

Table 2. Genotypic (upper diagonal) and phenotypic (below diagonal) correlation coefficients among sixteen variables of durum wheat genotypes under optimum N

Variables	DH	DM	GFP	PH	NFT	SL	SPS	NSPS
DH	**1.00**	0.88**	-0.76**	0.47**	0.46**	0.61**	0.40**	-0.62**
DM	0.83**	**1.00**	-0.36**	0.38**	0.22**	0.38**	0.37**	-0.40**
GFP	-0.69**	-0.19**	**1.00**	-0.41**	-0.61**	-0.68**	-0.29**	0.68**
PH	0.41**	0.32**	-0.32**	**1.00**	0.58**	0.70**	0.45**	-0.68**
NFT	0.38**	0.18**	-0.41**	0.48**	**1.00**	0.68**	0.18*	-0.78**
SL	0.55**	0.34**	-0.54**	0.65**	0.56**	**1.00**	0.59**	-0.70**
SPS	0.29**	0.26**	-0.17**	0.37**	0.14**	0.54**	**1.00**	-0.09ns
NSPS	-0.59**	-0.35**	0.59**	-0.59**	-0.60**	-0.60**	0.04ns	**1.00**
BM	0.40**	-0.32**	-0.29**	0.43**	0.53**	0.52**	0.29**	-0.40**
HI	-0.64**	-0.45**	0.55**	-0.52**	-0.41**	-0.57**	-0.25**	0.64**
NDVI	0.35**	0.24**	-0.31**	0.54**	0.47**	0.54**	0.33**	-0.44**
PC	-0.02ns	-0.01ns	0.01ns	0.13**	0.10*	0.06ns	-0.06ns	-0.09ns
HLW	-0.14**	-0.06ns	0.19**	0.02ns	0.11*	0.02ns	0.03ns	0.07ns
TSW	-0.002ns	0.18**	0.23**	0.35**	0.04ns	0.06ns	0.02ns	-0.19**
CHO	-0.52**	-0.32**	0.51**	-0.39**	-0.41**	-0.48**	-0.12*	0.65**
GY	-0.17*	-0.09ns	0.19**	-0.05ns	0.13**	-0.01ns	0.06ns	0.16**

***=Significant at 1% level, *=Significant at 5%level, ns=non-significant*

Table 2.Continued

Variables	BM	HI	NDVI	PC	HLW	TSW	CHO	GY
DH	0.51**	-0.75**	0.53**	0.001ns	-0.17*	0.01ns	-0.59**	-0.17*
DM	0.39**	-0.57**	0.37**	-0.05ns	-0.12ns	0.19**	-0.40**	-0.14ns
GFP	-0.47**	0.70**	-0.55**	-0.08ns	0.17*	0.24**	0.63**	0.16*
PH	0.49**	-0.68**	0.67**	0.18**	-0.07ns	0.38**	-0.53**	-0.12ns
NFT	0.64**	-0.57**	0.65**	0.07ns	0.11ns	0.02ns	-0.62**	0.11ns
SL	0.61**	-0.70**	0.70**	0.07ns	-0.005ns	0.07ns	-0.62**	-0.04ns
SPS	0.35**	-0.41**	0.43**	-0.11ns	-0.07ns	-0.01ns	-0.27**	-0.01ns
NSPS	-0.53**	0.75**	-0.66**	-0.15*	0.06ns	-0.24**	0.75**	0.16*
BM	**1.00**	-0.41**	0.90**	-0.01ns	0.67**	0.12ns	-0.41**	0.60**
HI	-0.29**	**1.00**	-0.54**	-0.25**	0.44**	0.05ns	0.73**	0.48**
NDVI	0.75**	-0.32**	**1.00**	0.14*	0.40**	0.26**	-0.57**	0.39**
PC	0.07ns	-0.15**	0.16**	**1.00**	-0.17*	0.17*	0.16*	-0.22**
HLW	0.56**	0.39**	0.39**	0.02ns	**1.00**	0.21**	0.20**	0.96**
TSW	0.14**	0.06ns	0.23**	0.12*	0.19**	**1.00**	0.13ns	0.15*
CHO	-0.23**	0.55**	-0.26**	0.18**	0.19**	0.13*	**1.00**	0.26**
GY	0.64**	0.53**	0.40**	-0.06ns	0.79**	0.17**	0.25**	**1.00**

***=Significant at 1% level, *=Significant at 5%level, ns=non-significant*

DH had non-significant positive correlation with TSW at genotypic and negative at phenotypic level (Table 2). The results were in agreement with (Baye *et al.*, 2020) who reported that, the correlations of DH and DM were positive and significant with PH, SPS and BM. Similarly, (Mecha *et al.*, 2017) described that GFP, TSW, HLW and HI showed a negative and significant association with DH and DM.

GFP showed negative and significant correlation with PH, NFT, SL, SPS, BM and NDVI at phenotypic level and a significant positive correlation for the same traits at genotypic level but the correlation was significant and positive with NSPS, HI, TSW, HLW, and CHO at both levels suggesting that longer interval between DH to DM contributed for the increments of these traits. It had negative at genotypic and positive at phenotypic level but non-significant correlation with PC (Table 2).

Similarly, (Dabi *et al*. 2016) stated that highly significant and positive correlation of GFP with HLW and TSW at both genotypic and phenotypic levels. PH showed highly significant positive correlation with NFT, SL, SPS, BM, NDVI and PC and highly significant negative correlation with NSPS, HI and CHO at both genotypic and phenotypic level. The finding was in agreement with Tabassum *et al*. (2017) for HI in bread wheat. Moreover, PH had positive and negative non-significant correlation with HLW at phenotypic and genotypic level, respectively. Birkneh (2021) reported positive significant correlation of PH with SL and SPS. NFT had positive and significant correlation with SL, SPS, BM and NDVI and highly significant negative correlation with NSPS, HI and CHO at both level. Moreover, NFT had positive significant correlation with PC and HLW at phenotypic level and positive non-significant correlation at genotypic level (Table 2). Similarly, NFT showed a non-significant but positive correlation with TSW at both levels. The result was in line with (Meles *et al*. 2017) that showed negative correlation of NFT with NSPS.

SL had highly significant positive correlation with, SPS, BM and NDVI and highly significant negative correlation with NSPS, HI and CHO at both levels whereas, it had positive non-significant correlation with PC, HLW and TSW at phenotypic level (Table 2). The results of this study are in agreement with (Seyoum *et al*. 2021) who reported a significant and positive correlation of SL with spikelet per spike. A contrasting finding was reported by (Zecevic *et al*. 2004) on the correlation of SL and NSPS in wheat.

SPS showed significant positive correlation with BM and NDVI and highly significant negative correlation with HI and CHO at both levels. NSPS exhibited significant positive correlation with HI and CHO, whereas BM, NDVI and TSW associated highly significantly and negatively with NSPS at both levels. It was observed that, negative significant and non-significant correlation of PC with NSPS at genotypic and phenotypic level, respectively, and had also positive non-significant correlation with HLW at both level (Table 2).

BM had significant positive correlation with NDVI, HLW and TSW at phenotypic level, and NDVI and HLW traits showed significant positive correlation at genotypic level. However, HI and CHO were highly significant negative correlation with BM at both levels which is in line with the work of (Kumar *et al.*, 2018) who reported negative association of biomass and HI. HI showed highly significant positive correlation with HLW and CHO, highly significant negative correlation with NDVI and PC at phenotypic and genotypic level. NDVI revealed highly significant positive correlation with PC, HLW and TSW but negative significant correlation with CHO at both levels. PC had significant positive correlation with TSW and CHO at both levels. HLW had significant positive correlation with TSW and CHO at both levels.

Correlation coefficient under low N

Table 3 presents the genotypic and phenotypic correlation coefficient of GY, yield components and physiological traits for diverse durum wheat genotypes. Genotypic correlation coefficients were found higher than the phenotypic correlation coefficients for majority of the traits suggesting that characters association had not been mainly influenced by environmental dynamics.

Correlation between grain yields with other traits under low N

The correlations of GY with GFP, NSPS, BM, HI, NDVI, HLW and CHO were significant and positive at both genotypic and phenotypic levels. Similarly, TSW showed highly significant correlation with GY at phenotypic level, demonstrating the importance of these traits for yield improvement. DH and DM showed negative and significant correlation with GY at both levels, this could be attributed to the high influences of environment and inherent variations among genotypes. Similarly, PH and SL negatively and significantly correlated with GY at genotypic level but non-significant at phenotypic level. NFT, SPS and PC were positively and non-significantly correlated with GY at phenotypic level.

Ivić *et al.* (2021) stated similar findings on the correlation of GY with HI, PH and PC under low nitrogen treatments. Talebi *et al.* (2010) indicated similar results for PH, BM, NSPS and SL but under low water regime the result was contrary in the HI of durum wheat landraces. The correlation of GY and PC was negative as it illustrated by various studies in durum wheat under drought environment. According to (Salsman *et al.*, 2021) and (Guttieri *et al.*, 2017) GY correlated negatively with DH, PH and grain PC. Moreover, (Khayatnezhad *et al.*, 2010) reported positive and significant correlations of GY with TSW, total plant weight and HI among durum wheat genotypes under dry conditions. Contrary to this result, (Russell, 2020) reported non-significant correlation of GY with all traits except number of spikes in spring wheat grown under low N conditions.

Table 3. Genotypic (upper diagonal) and phenotypic (below diagonal) correlation coefficients among sixteen variables of durum wheat genotypes under low N

Variables	DH	DM	GFP	PH	NFT	SL	SPS	NSPS
DH	1	0.97**	-0.91**	0.53**	0.68**	0.73**	0.61**	-0.71**
DM	0.91**	1	-0.77**	0.53**	0.62**	0.68**	0.59**	-0.69**
GFP	-0.80**	-0.49**	1	-0.44**	-0.66**	-0.72**	-0.59**	0.63**
PH	0.41**	0.43**	-0.24**	1	0.54**	0.65**	0.53**	-0.64**
NFT	0.49**	0.45**	-0.38**	0.47**	1	0.78**	0.54**	-0.69**
SL	0.67**	0.62**	-0.53**	0.57**	0.58**	1	0.70**	-0.73**
SPS	0.42**	0.42**	-0.29**	0.43**	0.34**	0.63**	1	-0.27**
NSPS	-0.64**	-0.58**	0.51**	-0.42**	-0.45**	-0.56**	-0.001ns	1
BM	0.35**	0.39**	-0.17**	0.26**	0.39**	0.37**	0.22**	-0.28**
HI	-0.66**	-0.58**	0.54**	-0.36**	-0.24**	-0.42**	-0.18**	0.56**
NDVI	0.35**	0.34**	-0.24**	0.35**	0.39**	0.44**	0.31**	-0.34**
PC	0.16*	0.19**	-0.06ns	0.21**	0.10*	0.29**	0.01ns	-0.28**
HLW	-0.19**	-0.19**	0.14**	-0.11**	-0.01ns	-0.11**	-0.12**	0.06ns
TSW	0.08ns	0.20**	0.11*	0.40**	0.14**	0.19**	0.03ns	-0.41**
CHO	-0.34**	-0.26**	0.33**	-0.17**	-0.26**	-0.21**	-0.03ns	0.41**
YD	-0.22**	-0.14**	0.25**	-0.09ns	0.09ns	-0.06ns	0.01ns	0.19**

***=Significant at 1% level, *=Significant at 5%level, ns=non-significant*

Table 3 Continued

Variables	BM	HI	NDVI	PC	HLW	TSW	CHO	YD
DH	0.48**	-0.79**	0.58**	0.20**	-0.43**	0.13ns	-0.43**	-0.22**
DM	0.51**	-0.74**	0.60**	0.23**	-0.40**	0.22**	-0.37**	-0.16*
GFP	-0.36**	0.76**	-0.50**	-0.13ns	0.42**	0.06ns	0.49**	0.27**
PH	0.26**	-0.61**	0.50**	0.29**	-0.34**	0.49**	-0.38**	-0.26**
NFT	0.57**	-0.47**	0.75**	0.29**	0.001ns	0.16*	-0.49**	0.08ns
SL	0.42**	-0.61**	0.60**	0.35**	-0.32**	0.20**	-0.37**	-0.14*
SPS	0.26**	-0.44**	0.31**	0.04ns	-0.53**	0.005ns	-0.21**	-0.13ns
NSPS	-0.47**	0.69**	-0.64**	-0.43**	0.08ns	-0.53**	0.51**	0.16*
BM	1	-0.16*	0.75**	0.29**	0.66**	0.21**	-0.21**	0.66**
HI	0.01ns	1	-0.35**	-0.32**	0.84**	-0.06ns	0.53**	0.62**
NDVI	0.53**	-0.01ns	1	0.34**	0.16*	0.40**	-0.38**	0.34**
PC	0.24**	-0.16**	0.25**	1	-0.02ns	0.21**	-0.02ns	-0.01ns
HLW	0.31**	0.41**	0.18**	0.05ns	1	0.29**	0.09ns	0.85**
TSW	0.24**	0.06ns	0.31**	0.20**	0.18**	1	-0.06ns	0.09ns
CHO	0.02ns	0.40**	-0.09ns	0.03ns	0.07ns	0.01ns	1	0.20**
YD	0.71**	0.69**	0.32**	0.05ns	0.54**	0.19**	0.28**	1

***=Significant at 1% level, *=Significant at 5%level, ns=non-significant*

Correlation among yield related traits under low N

The present study showed negative and significant correlation of DH and DM with GFP, NSPS, HI, HLW and CHO at genotypic and phenotypic levels (Table 3). These traits had positive and significant correlation with other characters at both genotypic and phenotypic level except TSW with DH. GFP had positive and significant correlation with NSPS, HI, HLW, TSW and CHO, while the other characters showed negative and significant correlation with GFP.

Similarly, (Mwadzingeni *et al.*, 2016) stated that DH and DM had positive and significant correlation with PH, SL, SPS, NSPS and TSW under drought stress condition. Yield contributing traits such as PH, NFT, SL, SPS, BM and TSW showed significant and positive correlation with each other at genotypic and phenotypic levels except SPS and TSW which showed non-significantly correlated to each other at both levels. Similarly, Lupini *et al*. (2021) reported negative correlation among PH and TSW with HI and positive correlation between PH and TSW in durum wheat evaluated under different nitrogen and water regimes. (Khayatnezhad *et al.*, 2010) also stated positive and significant correlation between PH and NFT, total plant weight and thousand seed weight, number of fertile tiller and total plant weight, and SL and grain per spike among durum wheat genotypes under water and dry conditions.

Most yield component traits showed positive significant correlation with NDVI and PC at both levels where SPS had non-significant correlation with PC. Yield component traits excluding NSPS and HI showed negative correlation but significant with CHO at genotypic level; and SPS and BM were non-significant at phenotypic level. PH, SL and SPS revealed negative while NSPS, BM and HI showed positive correlation with HLW at both levels. In line with this study (Ivić *et al*. 2021) reported negative correlation of HI with PC under low N for winter wheat cultivars but in contrast to this result, (Kubota *et al.*, 2018) found positive correlation of HI with PC of spring wheat cultivars only under low N but negative correlation under high N condition for the same traits. NDVI had positive and significant correlation with grain PC and HLW at both levels. Moreover, this trait exhibited negative significant at genotypic while positive and non-significant correlation at phenotypic level with CHO.

Path Coefficient analysis under optimum N

Path analysis partitions correlation coefficients in to direct and indirect effects which examines the cause and effect relationship between GY and other yield attributes and it provides clear picture of character associations for formulating efficient selection strategy. In this experiment, ten independent characters were selected as causal variables when GY is designated as dependent variable at genotypic and phenotypic level (Table 4 and 5).

Path analysis revealed that DH, GFP, BM, HI, NDVI, HLW and CHO had a positive direct effects with GY while NSPS, PC and TSW exerted negative and weak direct effect on GY at genotypic level. The maximum positive direct effect was observed for NDVI followed by HI, HLW and CHO (Table 4). Hence, direct selection based on these traits could be more effective for the improvement of GY in durum wheat. These findings were in agreement with the result of (Tsegaye *et al.*, 2012) who stated small direct effect of BM on GY at genotypic level, and (Kumari *et al.*, 2020) who reported positive direct effect of HI and negative direct effect of NSPS and TSW on GY of bread wheat. In another study, (Nukasani *et al.*, 2013) described TSW had a direct but negative direct effect on GY. Bhushan *et al.* (2013) stated that positive direct effect of HI and biological yield. In contrary, (Bhushan *et al.*, 2013) reported negative direct effect of DH on GY. The indirect effects of DH, BM and NDVI on GY via HI were negative. However, positive indirect effects of GFP, NSPS, HLW and CHO on GY were exerted through HI. On the other hand, DH, BM and HLW were showed positive indirect effects on yield through NDVI (Table 4).

Table 4. Estimates of direct (bold and diagonal) and indirect effects at genotypic level for durum wheat genotypes tested at the three locations under optimum N

Variables	DH	GFP	NSPS	BM	HI	NDVI	PC	HLW	TSW	CHO	Rg
DH	**0.11**	-0.08	0.06	0.05	-0.36	0.31	0.00	-0.07	0.00	-0.19	-0.17*
GFP	-0.09	**0.11**	-0.06	-0.04	0.34	-0.32	0.01	0.07	-0.05	0.20	0.16*
NSPS	-0.07	0.07	**-0.09**	-0.05	0.36	-0.39	0.02	0.03	0.05	0.24	0.16*
BM	0.06	-0.05	0.05	**0.09**	-0.20	0.52	0.00	0.28	-0.02	-0.13	0.60**
HI	-0.08	0.07	-0.07	-0.04	**0.48**	-0.32	0.03	0.18	-0.01	0.23	0.48**
NDVI	0.06	-0.06	0.06	0.08	-0.26	**0.59**	-0.02	0.17	-0.05	-0.18	0.39**
PC	0.00	-0.01	0.01	0.00	-0.12	0.08	**-0.13**	-0.07	-0.03	0.05	-0.22**
HLW	-0.02	0.02	-0.01	0.06	0.21	0.24	0.02	**0.41**	-0.04	0.06	0.96**
TSW	0.00	0.03	0.02	0.01	0.02	0.15	-0.02	0.09	**-0.19**	0.04	0.15*
CHO	-0.07	0.07	-0.07	-0.04	0.35	-0.33	-0.02	0.08	-0.02	**0.31**	0.26**

Residual effect =0.27, R-square=0.93, **, * significant at 1% and at 5% probability levels respectively, rg: genotypic correlations of variables with the GY.

At phenotypic level, BM and HI had high direct effect on GY (Table 5). Therefore, these traits could be considered as important selection criterion in durum wheat improvement program hence direct selection of these traits for yield improvement would be effective under optimum nitrogen conditions. However, the other traits exerted weak and insignificant direct and indirect effect on GY in the present findings (Table 5). Similar results were reported by (Seyoum *et al.* 2021) and (Baye *et al.*, 2020). In this study, DH, NFT, HLW and NDVI exerted moderate to high positive indirect effect on GY while GFP, NSPS, HI and CHO showed moderate negative indirect effect on GY through BM. Moreover, GFP, NSPS, HLW and CHO exerted moderate positive indirect effect but DH, NFT, BM and NDVI exhibited moderately negative indirect effect on GY via HI (Table 5). Although, the correlation between HLW and GY was strong and highly significant its direct effect was negative and had low magnitude indicating its indirect contribution to GY via BM and HI. The result also revealed that residual effect was 0.270 for genotypic and 0.174 for phenotypic path coefficients, demonstrating all traits evaluated in the present result explained about 73 and 82.6 percent of the variability in GY, respectively (Table 4 and 5).

Table 5. Estimates of phenotypic direct (bold diagonal) and indirect effects of different variables on GY of durum wheat genotypes tested at three locations under optimum N conditions

variables	DH	GFP	NFT	NSPS	BM	HI	NDVI	HLW	TSW	CHO	rp
DH	**-0.026**	-0.002	-0.005	0.010	0.353	-0.488	0.001	0.001	0.00001	-0.014	-0.17*
GFP	0.018	**0.003**	0.005	-0.010	-0.256	0.419	-0.001	-0.001	-0.001	0.014	0.19**
NFT	-0.010	-0.001	**-0.013**	0.010	0.467	-0.313	0.001	-0.001	0.000	-0.011	0.13ns
NSPS	0.015	0.002	0.008	**-0.017**	-0.353	0.488	-0.001	-0.001	0.001	0.018	0.16*
BM	-0.010	-0.001	-0.007	0.007	**0.882**	-0.221	0.002	-0.004	-0.001	-0.006	0.64**
HI	0.016	0.002	0.005	-0.011	-0.256	**0.762**	-0.001	-0.003	0.000	0.015	0.53**
NDVI	-0.009	-0.001	-0.006	0.007	0.661	-0.244	**0.002**	-0.003	-0.001	-0.007	0.40**
HLW	0.004	0.001	-0.001	-0.001	0.494	0.297	0.001	**-0.008**	-0.001	0.005	0.79**
TSW	0.000	0.001	-0.001	0.003	0.123	0.046	0.001	-0.001	**-0.005**	0.004	0.17*
CHO	0.013	0.002	0.005	-0.011	-0.203	0.419	-0.001	-0.001	-0.001	**0.027**	0.25**

Residual effect =0.174, R-square value= 0.97, **, * significant at 1% and at 5% probability levels respectively, rg: genotypic correlations of variables with the GY.

Path coefficient analysis under low N

Yield is a complex resultant character and influenced by several components and the environment. Due to internal modifications among the components, increase in one component results in a decrease in other component(s) and hence does not affect the resultant trait, yield. The results of genotypic and phenotypic path analysis under low N were presented in Table 6 and 7. Genotypic path analysis revealed the highest positive direct effect on GY observed in HLW followed by NSPS, BM and NDVI indicating, the importance of direct selection of these traits to identify high yielding genotypes. The higher positive direct effect has been reported for NSPS (Khan and Naqvi, 2012); (Oliveira *et al.*, 2021) and BM (Talebi *et al.*, 2010). All traits applied positive direct effect on GY except DM and PH had negative direct effect with significant genetic correlations. Alternatively, DH, DM, PH, SL and NDVI had negative indirect effect on GY through NSPS whereas GFP, HI and CHO exerted positive indirect effect through this trait. The indirect effects of NDVI, HLW, DH and DM on GY through BM were positive. NSPS had negative indirect effect while DH, DM, SL and BM had positive direct effect on GY through NDVI. Positive indirect effect was exerted on GY by BM and HI through HLW while the indirect effects of the other traits were weak and insignificant (Table 6). The residual effect was 0.367, indicating that about 63.3 percent of variability in GY might be contributed by these eleven traits examined in the path analysis. This gives an impression that some other factors which have not been measured also contributed to the variability in GY.

Table 6. Estimates of direct (bold and diagonal) and indirect effects at genotypic level for durum wheat genotypes tested at the three locations under low N

Traits	DH	DM	GFP	PH	SL	NSPS	BM	HI	NDVI	HLW	CHO	rg
DH	**0.12**	-0.01	-0.15	-0.05	0.10	-0.26	0.17	-0.12	0.18	-0.17	-0.03	-0.22**
DM	0.12	**-0.01**	-0.13	-0.05	0.09	-0.25	0.18	-0.12	0.19	-0.16	-0.03	-0.16*
GFP	-0.11	0.01	**0.16**	0.04	-0.10	0.23	-0.13	0.12	-0.16	0.17	0.04	0.27**
PH	0.07	-0.01	-0.07	**-0.09**	0.09	-0.23	0.09	-0.09	0.16	-0.13	-0.03	-0.26**
SL	0.09	-0.01	-0.12	-0.06	**0.14**	-0.27	0.15	-0.09	0.19	-0.13	-0.03	-0.14*
NSPS	-0.09	0.01	0.10	0.06	-0.10	**0.36**	-0.17	0.11	-0.20	0.03	0.04	0.16*
BM	0.06	-0.01	-0.06	-0.02	0.06	-0.17	**0.35**	-0.02	0.23	0.26	-0.02	0.66**
HI	-0.10	0.01	0.12	0.06	-0.08	0.25	-0.06	**0.16**	-0.11	0.33	0.04	0.62**
NDVI	0.07	-0.01	-0.08	-0.05	0.08	-0.23	0.26	-0.05	**0.31**	0.06	-0.03	0.34**
HLW	-0.05	0.01	0.07	0.03	-0.04	0.03	0.23	0.13	0.05	**0.39**	0.01	0.85**
CHO	-0.05	0.00	0.08	0.04	-0.05	0.19	-0.07	0.08	-0.12	0.04	**0.07**	0.20**

**, * significant at 1% and at 5% probability levels respectively, rg: genotypic correlations with the GY and Residual effect =0.367, R-square=86.5

The phenotypic path analysis result revealed direct and positive effects of DM, BM, HI and HLW whereas; DH, GFP, NSPS, NDVI, TSW and CHO were found to be negative direct effect on GY (Table 7). Chowdhry *et al.* (2000) and (Hussain *et al.*2012) reported similar observations in agreement with the current study results for some of the traits. NSPS via HI and NDVI via BM exerted moderately positive indirect effect on GY. DH and DM were moderate indirect positive effect via BM and negative indirect effect via HI on GY. On the other hand, GFP, NSPS, HLW and CHO had moderate positive indirect effect on GY through HI (Table 7). As the indirect contribution of various characters were low in magnitude, not considered worthy to be described. The residual effect was 0.148, indicating about 85 percent of the variation in yield was due to these ten characters examined even though there are some other factors, which were not measured in the present study.

Table 7. Estimates of phenotypic direct (bold diagonal) and indirect effects of different variables on GY of durum wheat genotypes tested at three locations under low N conditions

Variables	DH	DM	GFP	NSPS	BM	HI	NDVI	HLW	TSW	CHO	rp
DH	**-0.496**	0.289	0.182	0.011	0.254	-0.430	-0.021	-0.012	-0.002	0.003	-0.22**
DM	-0.451	**0.318**	0.112	0.010	0.284	-0.378	-0.020	-0.012	-0.004	0.002	-0.14*
GFP	0.396	-0.156	**-0.228**	-0.009	-0.124	0.352	0.014	0.009	-0.002	-0.003	0.25**
NSPS	0.317	-0.184	-0.116	**-0.018**	-0.204	0.365	0.020	0.004	0.009	-0.003	0.19**
BM	-0.173	0.124	0.039	0.005	**0.727**	0.007	-0.031	0.019	-0.005	0.000	0.71**
HI	0.327	-0.184	-0.123	-0.010	0.007	**0.651**	0.001	0.025	-0.001	-0.003	0.69**
NDVI	-0.173	0.108	0.055	0.006	0.385	-0.007	**-0.059**	0.011	-0.007	0.001	0.32**
HLW	0.094	-0.060	-0.032	-0.001	0.225	0.267	-0.011	**0.062**	-0.004	-0.001	0.54**
TSW	-0.040	0.064	-0.025	0.007	0.174	0.039	-0.018	0.011	**-0.022**	0.000	0.19**
CHO	0.168	-0.083	-0.075	-0.007	0.015	0.260	0.005	0.004	0.000	**-0.008**	0.28**

Residual effect =0.148, R-square value= 0.98, **, * significant at 1% and at 5% probability levels respectively, rp: genotypic correlations with the GY

Conclusion

In present study, majority of the genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients, demonstrating strong inherent association between the measured characters and less influenced by environmental dynamics. Correlation coefficient analysis revealed that durum GY had a positive and significant association with GFP, NSPS, BM, HI, NDVI, HLW, and CHO at genotypic and phenotypic levels under both optimum and low N conditions. This showed that the traits were effective for direct selection of genotypes to improve grain yield.

Similarly, NFT identified as an important trait under optimum and TSW was under low nitrogen based on phenotypic correlation analysis to improve grain yield. In contrast, GY had a negative association with DH, DM, PH, SL, and PC at the genotypic and phenotypic levels under both optimum and low N conditions.

NDVI had the greatest positive direct effect on GY at the genotypic level, followed by HI, HLW, and CHO, while at the phenotypic level, BM and HI had the greatest positive direct effect on GY under optimum N. Indirect effects of BM via NDVI at the genotypic level and NDVI via BM at the phenotypic level, as well as NSPS via HI at the genotypic and phenotypic levels, were observed on GY under optimum N conditions. Under low N conditions, HLW, NSPS, BM, and NDVI had the highest positive direct effect on GY at the genotypic level. Moreover, at the phenotypic level, DM, BM, HI, and HLW had a positive direct effect on GY. As a result of the strong correlation and positive direct and indirect effects of BM, NSPS, NDVI HI, and HLW on GY, breeders need to apply direct selection of these traits during breeding stages to develop new durum wheat varieties with improved yield under low N conditions.

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Appendices

Appendix Table 1 Durum wheat genotypes used for the experiment

NO	**GENOTYPES**	**SOURCE**	**PEDIGREE/ ID/ACCESSIONS**
1	FIGSDRYWET016	ICARDA	RUSS199/ID-82244
2	FIGSDRYWET078	ICARDA	AFG68::77/ID-90233
3	FIGSDWHOTCLD015	ICARDA	ETH732::91/ID-81510
4	FIGSDRYWET028	ICARDA	ETH64:112/ID-83807
5	DURUM_PANEL_UNIBO-054	ICARDA	D333/GAVIOIA/4/AVETORO//ALUINCO/D/EIOD/ID-MARJANA MOROCCO
6	FIGSDRYWET001	ICARDA	OMN87:113/ID-43315
7	DURUM_PANEL_UNIBO-048	ICARDA	INRA1807 /ID-CHAOUI MOROCCO
8	Land race	EBI	ETH CHEFE-9
9	Land race	EBI	ETH 208474
10	Land race	EBI	ETH 2368039
11	Land race	EBI	ETH 222796
12	FIGSDWHOTCLD009	ICARDA	ETH74::56/ID-79653
13	Land race	EBI	ETH 203762
14	FIGSDRYWET0144	ICARDA	IRNS382/ID-119026
15	DURUM_PANEL_UNIBO-081	ICARDA	ID-BRAVADUR,SW USA
16	FIGSDRYWET091	ICARDA	ETH731::112/ID-90482
17	FIGSDRYWET108	ICARDA	IRNS294/ID-98797
18	Land race	EBI	ETH 226804
19	ICARASHA2	ICARDA	Stj3/Ber/Lks4/3/Ter3
20	Land race	EBI	238498
21	Land race	EBI	ID-MU350/238498
22	Land race	EBI	ID-MU386/208215
23	Land race	EBI	ID-MU369/215411
24	Land race	EBI	ID-MU71/222859
25	Land race	EBI	ID-MU46/208746
26	Foka	DZARC	COCORIT-71/CANDEAL-II**[1551][2837]**
27	Bichena	DZARC	IUMILLO/COCORIT-71**[1551]**
28	Land race	EBI	ID-MU367/208316
29	Land race	EBI	ID-MU282/222408
30	Denbi	DZARC	AJAIA/BAUSHEN**[3589]**
31	Land race	EBI	ID-MU398/236988
32	Land race	EBI	ID-MU193/238531
33	Land race	EBI	ID-MU389/202012
34	Land race	EBI	ID-MU329/208162
35	Land race	EBI	ID-MU19/228862

NO	GENOTYPES	SOURCE	PEDIGREE/ ID/ACCESSIONS
36	Land race	EBI	ID-MU397/236269
37	Boohai	DZARC	COOT(SIB)/CANDEAL-II**[40][115][1551][2837]**
38	Land race	EBI	ID-MU375/222414
39	Land race	EBI	ID-MU274/210817
40	Land race	EBI	ID-MU320/222655
41	Quamy	DZARC	FLAMINGO,MEX/CRANE//FLAMINGO/3/HUIT
42	Land race	EBI	ID-MU295/8034
43	Land race	EBI	ID-MU56/238555
44	Land race	EBI	ID-MU77/222856
45	Land race	EBI	222413
46	Land race	EBI	222298
47	Land race	EBI	236987
48	Land race	EBI	222191
49	Land race	EBI	238133
50	Land race	EBI	7960
51	Land race	EBI	231538
52	Land race	EBI	138130
53	Land race	EBI	231541
54	Land race	EBI	231594
55	Land race	EBI	226958
56	Land race	EBI	204563
57	Land race	EBI	222415
58	Land race	EBI	8175
59	Land race	EBI	231573
60	Land race	EBI	222629
61	Land race	EBI	226963
62	Land race	EBI	231499
63	Land race	EBI	238138
64	Land race	EBI	238122
65	Land race	EBI	231597
66	Land race	EBI	208931
67	Land race	EBI	204573-1
68	Land race	EBI	222387
69	Land race	EBI	227009
70	Land race	EBI	226971-2
71	Land race	EBI	208261
72	Land race	EBI	7961
73	Land race	EBI	222568

NO	GENOTYPES	SOURCE	PEDIGREE/ ID/ACCESSIONS
74	Land race	EBI	231536-1
75	Land race	EBI	236974-1
76	Land race	EBI	222198
77	Land race	EBI	222382
78	Land race	EBI	238135
79	Land race	EBI	231584
80	Land race	EBI	204485
81	Land race	EBI	8356
82	Land race	EBI	231585
83	Land race	EBI	227007
84	Land race	EBI	238134
85	Land race	EBI	8333-2
86	CD15DZ_ELT/off/1084/2015	CIMMYT	CMH83.2578/4/D88059//WARD/YAV 79/3/ACO89/5/2*SOOTY.9/RASCON-37/6/1A.1D 5+1-6/…
87	CD15DZ_ELT/off/1024/2015	CIMMYT	JUPAREC2001*2/1M/10/KOFA/9/USDA595 /3/D67.3/RABI//CRA/4/ALD/5/HUI/YAV-1/16/…
88	CD15DZ_ELT/off/994/2015	CIMMYT	JUPAREC2001*2/RBC/5/MOHAWK/3/GUANAY//TILD-1LDTUS-4/4/ARMENT //SRN- 3/…
89	CD15DZ_ELT/off/253/2015	CIMMYT	BHA/5/MOHAWK/4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7/YAZI-1/6/CF4205/4/YAZI-1…
90	CD15DZ_ELT/off/943/2015	CIMMYT	LILE/6/CF4205/4/YAZI-1AKAKI4//SOMAT3/3AUK/GUIL//GREEN /5/CANELD-9.1//…
91	CD15DZ_ELT/off/950/2015	CIMMYT	YAVA 79/9/ USDA 595/3 /D67.3 /RABI/ /CRA/4/ALO/5/HUI/YAV-1/6/ARDENTE /7/HUI/YAV 79/8/…
92	CD15DZ_ELT/off//248/2015	CIMMYT	CF420S/4/YAZI-1AKAKI-4//SOMAT 3/3/AUK/GUIL//GREEN/5/CANELD-9.1//SHAKE-3/…
93	CD15DZ_ELT/off/275/2015	CIMMYT	CF420S/4/YAZI-1/AKAKI-4//SOMAT-3/3/AUK/GUIL//GREEN/5/CANELD-9.1//SHAKE-3/…
94	CD15DZ_ELT/off/982/2015	CIMMYT	ALTAR 84/STINT//SILVER-45/3/GUANAY/4/GREEN-14//YAV-10/AUK/10/CMH79.959/CHEN//…
95	CD15DZ_ELT/off/1029/2015	CIMMYT	JUPAREC2001*2/KHAPLI/4/INRAM-1805//SOMAT-4/INTER-8/3/SOOTY-9/RASCON-37//…
96	CDSS09B00191T-099Y-020M-6Y00M	CIMMYT	RBC/7/CMH83.2578/4/D88059//WARD/YAV79/3/ACO89/5/2*S00TY-9/RASCON-37/6/…
97	CDSS09B00067S-099Y-035M-3Y-0M	CIMMYT	STORLOM/3/RASCON-37//TARRO-2//RASCON-37/4/D00003A/5/1A.1D5+1-06/3*Mojo/3/AJAIA-12/…
98	CDSS09B00203T-099Y-066M-2Y-0M	CIMMYT	CIT71/5/MOHAWK/4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7/YAZI-1/7/CMH83. 2578/4/D88059//…
99	ICD08-291-0AP	CIMMYT	otb4/3/HFN94N-8/Mrb5//Zna-1/4/5+j3//Dra2/Bcr/3/Ter-3
100	CDSS09B00190T-099Y-036M-18Y-0M	CIMMYT	RBC/HUALITA/5/MOHAWK/3/GUANAY//TILO-1/LOTUS-4/4/ARMENT//SRN-3/NIGRIS-4/3/…
101	CD15DZ_ELT/off/1103/2015	CIMMYT	KOFA/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV-1/6/ARDENTE/7/HUI/YAV79/8/…
102	CD15DZ_ELT/off/1116/2015	CIMMYT	JUPAREC2001*2/IM/5/KOFA/4/DUKEM-1//PATAK-7YAZI-1/3/PATKA/7/YAZI-1/6/ALAS/…
103	CD15DZ_ELT/Off/1102/2015	CIMMYT	KOFA/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV-1/6/ARDENTE/7/HUI/YAV79/8/…
104	CD15DZ_ELT/off//1057/2015	CIMMYT	KRON05/10/KOFA/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/HAV-1/6/RADENTE/7/HUI/…
105	CD15DZ_ELT/off/999/2015	CIMMYT	JUPAREC2001*2/RBC/11/PLATA-10/6/MQUE/4/USDA/573//QFN/AA-7/3/ALBA/D/5/AVO/HUI/7/…
106	CD15DZ_ELT/off/1112/2015	CIMMYT	JURAREC2001*2/IM/7/CMH83.2578/4/D88059//WARD/YAV79/3/AC089/5/2*S00TY-9/…
107	CD15DZ_ELT/off/1067/2015	CIMMYT	CHAM1/5/MOHAWK/3/GUANAY//TILO-1/LOTUS-4/4/ARMENT//SRN-3/NIGRIS-4/3/CANELO-9.1/6/…
108	CD15DZ_ELT/off/1094/2015	CIMMYT	STORLOM/3/RASCON-37/TARRO-2//RASCON-37/4/D00003A/5/1A.1D5+1-06/3*MOJO/3/AJAIA-12/…
109	CD13DZOS F6SR 2013 MS DZLS/22	CIMMYT	CF420S/4/YAZI-1/AKAKI-4//S0MAT-3/3/AUK/GUIL//GREEN/5/CANEL0-9.1//SHAKE-3/…
110	CD13DZOS F6SR 2013 MS DZLS/93	CIMMYT	K0FA/9/USDA595/3/D67.3/RABI//CRA/4/AL0/5/HUI/YAV-1/6/ARDENTE/7/HUI/YAV79/8/…

NO	**GENOTYPES**	**SOURCE**	**PEDIGREE/ ID/ACCESSIONS**
111	CD13DZOS F6SR 2013 MS DZLS/106	CIMMYT	RBC/HULITA/5/M0HAWK/3/GUANAY//TIL0-1/L0TUS-4/4/ARMENT//SRN-3/NIGRIS-4/3/…
112	CD13DZOS F6SR 2013 MS DZLS/81	CIMMYT	CF420S/4/YAZI-1/AKAKI-4//S0MAT-3/3/AUK/GUIL//GREEN/5/CANEL0-9.1//SHAKE-3/…
113	CD13DZOS F6SR 2013 MS DZLS/105	CIMMYT	RBC/HULITA/5/M0HAWK/3/GUANAY//TIL0-1/L0TUS-4/4/ARMENT//SRN-3/NIGRIS-4/3/…
114	CD13DZOS F6SR 2013 MS DZLS/84	CIMMYT	CF420S/4/YAZI-1/AKAKI-4//S0MAT-3/3/AUK/GUIL//GREEN/5/CANEL0-9.1//SHAKE-3/…
115	CD13DZOS F6SR 2013 MS DZLS/111	CIMMYT	RBC/5/ARMENT//SRN-3/NIGRIS-4/3/CANEL0-9.1/4/LIR0-3/L0TAIL-6/6/C F4 20S/4/YAZI-1/…
116	CD13DZOS F6SR 2013 MS DZLS/83	CIMMYT	CF420S/4/YAZI-1/AKAKI-4//S0MAT-3/3/AUK/GUIL//GREEN/5/CANEL0-9.1//SHAKE-3/…
117	CD13DZOS F6SR 2013 MS DZLS/87	CIMMYT	CF420S/4/YAZI-1/AKAKI-4//S0MAT-3/3/AUK/GUIL//GREEN/5/CANEL0-9.1//SHAKE-3/…
118	CD13DZOS F6SR 2013 MS DZLS/80	CIMMYT	CF420S/4/YAZI-1/AKAKI-4//S0MAT-3/3/AUK/GUIL//GREEN/5/CANEL0-9.1//SHAKE-3/…
119	CD13DZOS F6SR 2013 MS DZLS/97	CIMMYT	K0FA/9/USDA595/3/D67.3/RABI//CRA/4/AL0/5/HUI/YAV-1/6/ARDENTE/7/HUI/YAV79/8/…
120	CD15DZ_ELT/off/251/2015	CIMMYT	CF420S/4/YAZI-1AKAKI-4//SOMAT-3/3/AUK/GUIL//GREEN/5/CANELD-9.1//SHAKE-3/…
121	CD15DZ_ELT/off/1006/2015	CIMMYT	JUPAREC2001*2/RBC/6/STORLOM/3/RASCON-37/TARRD-2//RASCON-37/4/D00003A/5/…
122	CD15DZ_ELT/off/989/2015	CIMMYT	TRIDENT/3*KUCUK/7/CMH83 2578/4/D88059//WARD/YAV 79/3/AC089/5/2*SOOTY-9/RASCON-37/6/…
123	CD15DZ_ELT/off/303/2015	CIMMYT	AGI22/2*ACO89//2*UC1113/3/5*KOFA/5KOFA/4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7/…
124	CD15DZ_ELT/off/1035/2015	CIMMYT	CMH83.2578/4/D88059//WARD/YAV79/3/AC089/5/2*S00TY-9/RASCON-37/6/1A.1D 5+1-06/…
125	CD15DZ_ELT/off/1034/2015	CIMMYT	CMH83.2578/4/D88059//WARD/YAV79/3/AC089/5/2*S00TY-9/RASCON-37/6/1A.1D 5+1-06/…
126	CD15DZ_ELT/off/1038/2015	CIMMYT	WID22289/10/SWAHEN-2/KIRKI-8//PROZANA-1/4/ADAMAR-15//ALBIA-1/LTAR84/3/SNITAN/9/…
127	CD15DZ_ELT/off/1115/2015	CIMMYT	JUPAREC2001*2/IM/5/KOFA/4/DUKEM-1//PATAK-7YAZI-1/3/PATKA/7/YAZI-1/6/ALAS/…
128	CD15DZ_ELT/off/1037/2015	CIMMYT	BOLENGA/10/KOFA/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV-1/6/ARDENTE/7/HUI/…
129	CD15DZ_ELT/off/1069/2015	CIMMYT	CHAM1/4/INRAM-1005//SOMAT-4/INTER/8/3/SOOTY-9/RASOON-37//TILO-1/LOTUS-4/5/…
130	CD15DZ_ELT/off/1079/2015	CIMMYT	CMH83.2578/4/D88059//WARD/YAV79/3/AC089/5/2*S00TY-9/RASCON-37/6/1A.1D 5+1-06/…
131	CD15DZ_ELT/off/998/2015	CIMMYT	JUPAREC2001*2/RBC/11/PLATA-10/6/MQUE/4/USDA573//QFN/AA-7/3/ALBA-D/5/AVO/HUI/7/…
132	CD15DZ_ELT/off/1000/2015	CIMMYT	JUPAREC2001*2/RBC/11/PLATA-10/6/MQUE/4/USDA 573//QFN/AA-7/13/ALBA-D/5/AVO/HUI/7/…
133	CD15DZ_ELT/off/1025/2015	CIMMYT	JUPARE C 2001*2/IM/10/KOFA/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV-1/6/…
134	CD15DZ_ELT/off/980/2015	CIMMYT	ALTAR.84/STINT//SILVER-45/3/GUANAY/4/GREEN-14//YAV-10/AUK/10/CMH79.959/CHEN//…
135	CD15DZELT/off/973/2015	CIMMYT	ALAM0:DR/4/ARMENT//SRN-3/NIGRIS-4/3/CANEL0-9.1/5/PLATA-6/GREEN-17//SNITAN/4/…
136	CD15DZELT/off/1117/2015	CIMMYT	JUPAREC2001*2/IM/5/K0FA/4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7/YAZI-1/6/ALAS/…
137	CD15DZELT/off/849/2015	CIMMYT	NASSIRA/10/PLATA-10/6/MQUE/4/USDA573//QFN/AA-7/3/ALBA-D/5/AV0/HUI/7/PLATA-13/8/…
138	CD15DZELT/off/306/2015	CIMMYT	AG1-22/2*AC089//2*UC1113/3/5*K0FA/5/K0FA/4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7/…
139	CD15DZELT/off/846/2015	CIMMYT	AMRIA/6/ALTAR84/STINT//SILVER-45/3/GUANAY/4/GREEN-14//YAV-10/AUK/5/S0MAT-4/…
140	CD15DZELT/off/1239/2015	CIMMYT	GER0MTEL-3/8/ST0T//ALTAR84/ALD/3/THB /CEP7780//2*MUSK-4/6/EC0/CMH76A.722//…
141	CD15DZELT/off/889/2015	CIMMYT	GEROMTEL-3/7/ALTAR84/BINTEPE85/3/ST0T//ALTAR84/ALD/4/P00-11/YAZI-1/5/…

NO	GENOTYPES	SOURCE	PEDIGREE/ ID/ACCESSIONS
142	CD15DZELT/off/891/2015	CIMMYT	GEROMTEL-3/7/ALTAR84/BINTEPE85/3/ST0T //ALTAR84/ALD/4/P0D-11/YAZI-1/5/…
143	CD15DZELT/off/1235/2015	CIMMYT	TA5057/10/2*CMH85.797//DUKEM-12/2*RASC0N-21/9/USDA595/3/D67.3/RABI//…
144	CD15DZELT/off/1072/2015	CIMMYT	CMH83.2578/4/D88059//WARD/YAV79/3/AC089/5/2*S00TY-9/RASC0N-37/6/1A.1D5+1-06/…
145	CD15DZELT/off/664/2015	CIMMYT	GER0MTEL-3/10/CHEN-1/TEZ/3/GUIL//CIT71/CII/4/ S0RA/PLATA-12/5/ST0T//ALTAR84/…
146	CD15DZELT/off/745/2015	CIMMYT	CND0/VEE//PLATA-8/3/6*PLATA-11/6/PLATA-8/4/GARZA/AFN//CRA/3/GTA/5/RASC0N/9/…
147	CD15DZELT/off/790/2015	CIMMYT	AMRIA/6/ALTAR84/STINT//SILVER-45/3/GUANAY/4/GREEN-14//YAV-10/AUK/5/S0MAT-4/…
148	CD15DZELT/off/792/2015	CIMMYT	AMRIA/8/ST0T//ALTAR84/ALD/3/THBCEP7780//2*MUSK-4/6/EC0/CMH76A.722//BIT/3/…
149	CD15DZELT/off/801/2015	CIMMYT	GER0MTEL-3/6/S0MAT-3/PHAX-1//TIL0-1/L0TUS-4/3/GUANAY/5/NETTA-4/DUKEM-12//…
150	CD15DZELT/off/802/2015	CIMMYT	GER0MTEL-3/9/GUANCAN INIA/GUANAY /8/GEDIZFG0//GTA/3/SRN1/4/T0TUS/5/ENTE/MEXI-2//…
151	CD15DZELT/off/935/2015	CIMMYT	C0RDEIR0/9/GUAYACANINIA/GUANY/8/GEDIZ FG0//GTA/3/SRN-1/4/TOTUS/5/ENTE/MEXI-2//…
152	CD15DZELT/off/981/2015	CIMMYT	ALTAR84/STINT//SILVER-45/3/GUANAY /4/GREEN-14//YAV-10/AUK/10/CMH79.959/CHEN//…
153	CD15DZELT/off/995/2015	CIMMYT	JUPARE C 2001*2/RBC/11/PLATA-10/6/MQUE/4/USDA573 //QFN/AA-7/3/ALBA-D/5/AV0/HUI/7/…
154	CD15DZELT/off/1032/2015	CIMMYT	JUPARE C 2001*2/KHAPLI/5/M0HAWK/4/DUKEM -1//PATKA-7/YAZI-1/3/PATKA-7YAZI-1/11/…
155	CD15DZELT/off/1081/2015	CIMMYT	CMH83.2578/4/D88059//WARD/YAV79/3/AC089/5/2*S00TY-9/RASC0N-37/6/1A.1D5+1-06/…
156	CD15DZ-ELT/off/1082/2015	CIMMYT	CMH83.2578/4/D88059//WARD/YAV79/3/AC089/5/2*S00TY-9/RASC0N-37/6/1A.1D5+1-06/…
157	CD15DZELT/off/1087/2015	CIMMYT	CMH83.2578/4/D88059//WARD/YAV79/3/AC089/5/2*S00TY-9/RASC0N-37/6/1A.1D5+1-06/…
158	CD15DZELT/off/1129/2015	CIMMYT	KR0N0S/10/K0FA/9/USDA595/3/D67.3/RABI//CRA/4/AL0/5/HUI/YAV-1/6/ARDENT/7/HUI/…
159	CD15DZELT/off/1131/2015	CIMMYT	CMH83.2578/4/D88059//WARD/YAV79/3/AC089/5/2*S00TY-9/RASC0N-37/6/1A.1D5+1-06/…
160	CD15DZELT/off/1144/2015	CIMMYT	ST0RL0M/3/RASC0N-37/TARR0-2//RASC0N-37/4/D00003A/5/1A.1D5+1-06/3*M0J0/3/AJAIA-12/…
161	CD15DZELT/off/1152/2015	CIMMYT	K0FA/9/USDA595/3/D67.3/RABI//CRA/4/AL0/5/HUI/YAV-1/6/ARDENT/7/HUI/YAV79/8/…
162	CD15DZELT/off/1159/2015	CIMMYT	T.DIC0CC0NPI164578/10/K0FA/9/USDA595/3/D67.3/RABI//CRA/4/AL0/5/HUI/YAV-1/6/…
163	CD15DZELT/off/1164/2015	CIMMYT	NASSIRA/10/PLATA10/6/MQUE/4/USDA573//QFN/AA-7/3/ALBA-D/5/AV0/HUI/7/PLATA-13/8/…
164	CD15DZELT/off/1176/2015	CIMMYT	CHAM-3/4/N0K-23//PLATA-6/GREEN17/3/S0RA /2*PLATA-12//SRN-3/NIGRIS-4…
165	CD15DZELT/off/1193/2015	CIMMYT	A624/5/S0RA/2*PLATA-12/3/S0RA/2*PLATA-12//S0MAT-3/4/AJAIA-13/YAZI//DIPPER-2/BUSHEN-3
166	CD15DZELT/off/1516/2015	CIMMYT	JUPARE C 2001*2/IM/5/K0FA/4/DUKEM1//PATKA -7/YAZI-1/3/PATKA-7/YAZI-1/6/ALAS/…
167	CD15DZELT/off/1244/2015	CIMMYT	JUPAREC2001*2/IM/5/K0FA/4/DUKEM 1//PATKA-7/YAZI-1/3/PATKA-7/YAZI-1/6/ALAS/…

NO	**GENOTYPES**	**SOURCE**	**PEDIGREE/ ID/ACCESSIONS**
168	CD15DZ-ELT/off/305/2015	CIMMYT	G 122/2*AC089//2*UC1113/3/5 *K0FA/5/K0FA /4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7/…
169	Ude	DZARC	CHEN/ALTAR84//JO69
170	Mangudo	DZARC	MRF1/STJ2|/3/1718/BT//KARIM,TUN
171	Tesfaye	DZARC	ARMENT//SRN-NIGRIS-4/3/CANED-9.1/4/TOSKA-26RASCON-37//SNITSN/5/PLAYERO
172	Alemtena	DZARC	Icasyr-1/3/Gcn//Sti/Mrb3
173	Mukiye	DZARC	STJ3//BICRE/LOUKOS-4/3/TER3
174	Yerer	DZARC	CHEN/TEZONTLE/3/GUILLEMOT//CANDEAL-II
175	D-2018	DZARC	CGS
176	Utuba	DZARC	Icajihan42) Omruf1/Stojocri2/3/1718/BeadWheat24//Karim
177	Werer	DZARC	1346/LAHN//BICRE/LOUKOS-4
178	Asasa	DZARC	chorlito/yavaros//free-gallipoli/3/free-gallipoli/canadian-red/4/free-gallipoli/don-pedro/5/huitle
179	Cocorit 71	DZARC	RASPINEGRO-DE-AGUILASENANO/4*TEHUACAN-60//STEWART-63/3/ANHINGA
180	Dire	DZARC	CHEN/TE3/BUSHEN4/3/
181	Tate	DZARC	CD94523
182	Toltu	DZARC	4/B/R9096#21001(980SN Patho)
183	Bulalla	DZARC	DurumICARDA/Ethiopia
184	Hitosa	DZARC	CHEN/ALTAR-84
185	Obsa	DZARC	ALTAR84/ALTO-1/AJAYA
186	Bakalcha	DZARC	980SN Gedirfa/Gwerou #15 patho
187	Selam	DZARC	GERARDO/3/ND-61-130/LEEDS//COCORIT-71/4/HORA/5/HORA//COCORIT-71/CANDEAL
188	Malefia	DZARC	ALTAR-84/STERNA,MEX/LAHN
189	Breeding pipleline, DWNL p#2	DZARC	C F4 20 S/4/YAZI-1/AKAKI-4//SOMAT-3/3/AUK/GUIL//GREEN/5/CANELO-9.1//SHAKE-3/…
190	Breeding pipleline, DWNL p#5	DZARC	Yerer/UC11132….25Yellow/DZ2013mehF1 P#6/DZ2014meh F2 P#6-1
191	Breeding pipleline, DWNL p#13	DZARC	JUPARE C 2001*2/IM/5/K0FA/4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7/YAZI-1/6/ALAS/…
192	Breeding pipleline, DWNL p#15	DZARC	AG 1-22/2*AC089//2*UC1113/3/5*K0FA/5/K0FA/4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7/…
193	Breeding pipleline, DWNL p#16	DZARC	BHA/15/MOHAWK/4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7/YAZI-1/6/CF4 20S/4/YAZI-1/…
194	Breeding pipleline, DWNL p#18	DZARC	JUPARE C 2001* 2/RBC/5/MOHAWK/3/GUANAY//TILD-1LDTUS-4/4/ARMENT //SRN- 3/…
195	Breeding pipleline, DWNL p#20	DZARC	ALTAR 84/STINT//SILVER-45/3/GUANAY/4/GREEN-14//YAV-10/AUK/10/CMH79.959/CHEN//…
196	Breeding pipleline, DWNL p#21	DZARC	Icasyr-1/3/Gcn//Sti/Mrb3
197	Breeding pipleline, DWNE P#4	DZARC	Yerer/UC1113225Yellow/DZ2013mehF1 P#6/DZ2014meh F2 P#6-1
198	Breeding pipleline, DWNE P#5	DZARC	Yerer/UC 1113GPC Lr 1908001/59/ DZ 2013mehF1P#7/DZ 2014 mehF2 P#7-1
199	Breeding pipleline, DWNE P#6	DZARC	Yerer/UC 1113GPC Lr 1908001/59/ DZ 2013mehF1P#7/DZ 2014 mehF2 P#7-2
200	Breeding pipleline, DWNE P#13	DZARC	otb4/3/HFN94N-8/Mrb5//Zna-1/4/5+j3//Dra2/Bcr/3/Ter-3