RESEARCH ARTICLE

EVALUATION OF DURUM WHEAT GENOTYPES PERFORMANCE ACROSS LOCATIONS OVER YEARS UNDER ETHIOPIAN CONDITION

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ARTICLE INFO	ABSTRACT
	Ethiopia is the major wheat producer in sub-Saharan African countries and durum wheat is one of the two common wheat species. In Ethiopia, durum wheat production is declining due to different problem such as Lack of widely adaptable, stable, and durable resistant genotypes, Hence, evaluation of genotypes in multi-locations over several cropping season is required. Therefore, the objective of this study was to develop Durum Wheat genotypes that are high yielding, stable, adaptable across years and locations with acceptable industrial quality. 37 genotypes were tested with the two checks at three locations for two cropping seasons with row-column design in two replications. Data were conducted for all traits of interest. The data have been checked for the required assumptions of normality; homogeneity of variance and ANOVA, mean separation, GXE and AMMI analysis have been performed using R-software using different packages. The combined ANOVA shown significant variation among testing environments for all traits of interest ($P < 0.01$, $P < 0.05$) except grain filling period. Trait correlation analysis showed positive relationship of grain yield with thousand kernel weight and days to maturity with days to heading at all locations. Among the tested durum wheat genotypes, six genotypes, namely, G29, G37, G31, G19, G15 and G24 were found to be the top high yielding genotypes across all locations as the mean grain yield of tested genotypes showed. The genotypes G29 and G1 were identified as high yielding and stable across all six environments. Therefore, these lines can be included in the national testing program, to be released as a variety and recommending as good parent for crossing.

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INTRODUCTION

Wheat is the most widely grown cereal crop globally. Ethiopia is the major wheat producer in sub-Saharan African countries. It cultivated on a total area of 2.1 million hectares annually with a total production of 6.7 million tons, is also one of the most important food security crops in Ethiopia. However, the gap between production and supply is high due to urban population food preference transform to bread, pasta, noodle, and porridge which is easily cooked and prepared. Hence Ethiopia import about 1.2 million tons of wheat annually to fill the gap (Tadesse *et al*., 2022). Durum wheat is one of the two common wheat species, which can adapt in different Argo-ecology (Hussain. M *et al*., 2022 and Negisho K *et al*., 2021). Ethiopia is also the center of diversity for tetraploid wheat including durum wheat, although recent genetic analysis indicated that Ethiopia might represent a second center of origin for durum wheat. Durum wheat (*Triticum durum* L.) is a tetraploid (two genomes: AABB) with a total of 28 chromosomes ($2n = 4x = 28$). It is believed to be originated thousands of years ago from hybridization between the wild diploid *T. monococcum* L. subsp. *Boeoticum* (Boiss.) (A genome donor) (Synonym: *Triticum urartu*: AA) and the donor of the B genome which, according to morphological, geographical, and cytological evidence, has been recognized as *T. speltoides* (Tauschi) Gren (Negisho *et al*., 2021). Durum wheat is primarily used for pasta production, but in addition it is used to make flour for leavened biscuits, cookies, biofuel, and for fermentation to make alcoholic beverages such as beer and liquors. In Ethiopia, durum wheat nearly accounts for 15–20% of wheat production and 30% of the whole acreage. Hence, it contributes about 18 to 20% to the national wheat production. In Ethiopia, wheat (both bread and durum) is produced by around 4.62 million households with an estimated land area of 1.7 million ha and mean national yield of 2.97 t/ha. Traditionally, in Ethiopia wheat straw is used as animal feed and as roof thatching material (Negisho K *et al*., 2021). No official national statistics are maintained on the proportion of bread and durum wheat in Ethiopia, but expert opinion and survey data indicates a significant shift towards bread wheat in recent decades. Until the mid-1980s, durum wheat dominated the wheat production in Ethiopia. Estimated that 60–70% of the total wheat area was planted to durum wheat and traditional landraces dominated. Improved durum wheat varieties were estimated to only account for (D. P. Hodson., *et al* 2020). Currently nearly 80% of the wheat production area in Ethiopia is covered by bread wheat, indicating that less than 20% of the wheat production area is covered by improved durum wheat varieties. This is happened due to different problems from this, evolving of new rust races especially stem rust, climate change, Lack of widely adaptable, stable and durable resistant genotypes.

Hence, evaluation of genotypes in multi-locations over several cropping season is required to selected and recommend the genotypes which are widely adaptable and stable one as a new varieties (Ayed *et al*., 2021). Therefore, the objective of this study was to develop Durum Wheat genotypes that are high yielding, stable, adaptable across years and locations and disease resistant with acceptable industrial quality.

MATERIALS AND METHODS

Experimental Site Descriptions: In this study 37 genotypes were tested with the two checks (Alem Tena and Quamy). The experiment was carried out at three locations viz. Alem tena, Minjar and Dhera for two cropping seasons during 2020/2021. These locations represent major wheat growing areas for low moisture stress area. The descriptions of the locations are listed in Table 1.

Table 1.The descriptions of the locations

Location	Altitude	Geographical position		Rainfall (mm)	Soil type/texture	Temprature (^{0}C)	
		latitude	Londtude			Min	Max
Alem Tena	1611	$08^0 30'$N	$38^0 95'$E	728	Haplic andosol	NA	NA
Asasa	2340	$07°07'09''$N	$39°11'50''$E	640	Andosol	6.9^0C	18.1^0C
Minjar	1810	$08^0 55'$N	$39^0 45'$E	867		10^0C	28^0C
Dhera	1660	$08^0 19'10''$N	$39^0 19'$E	680	Andosol	14^0C	27.8^0C

Experimental Design and Data collection: Thirty-seven elite durum wheat genotypes originated from various sources, 12 genotypes from ICARDA, 12 From CIMMYT, three from Debre Zeit Agricultural Research Center (DZARC) local cross and one from other country along with the two checks (Alem Tena and Quamy) were evaluated in row- column design with three replications. Each experimental plot conducted in six rows of 2.5 m length with 20 cm spacing between rows. All target trait data based on the plan has been collected (days to heading, days to maturity, grain yield, 1000 kernel weight, hectoliter weight, protein, plant height and stem rust diseases). The seed rate was 125kg/ha at all locations for both years. Fertilizer rate applications have been added based on the specific location recommendations and other agronomic practices including weeding were applied as recommendation uniformly to all plots in each location as necessary.

Statistical Analyses: Grain yield data was recorded on plot basis and converted to Kg ha-1 for analysis. The data have been checked for the required assumptions of normality; homogeneity of variance before further analysis is done. ANOVA, mean separation, GXE and AMMI analysis have been performed using R-software using different packages.

RESULT AND DISCUSSION

As showed in the table 2 the analysis has made for grain yield and its related traits and the genotypes showed a highly significant difference for days to heading, days to maturity, hectoliter weight, thousand kernel weight and plant height, however there is not any significant variation for grain yield and grain filling period. Replication didn't have any impact for all traits of the tested genotypes because it doesn't show any significant difference for any traits. Environment showed a highly significant variation for all traits (DTH, DTM, GFP, HLW, TKW, GYLD and PHT). GXE interaction couldn't show a significant variation for any of the tested traits. The coefficient of variation is seen on table3. Generally, the combined ANOVA shown significant variation among testing environments for all traits of interest (P < 0.01, P < 0.05) and highly significant variations (P < 0.01, P < 0.05) were recorded among the tested genotypes for all considered traits except grain filling period (GFP).

Table 2. Analysis source of variance across locations over years

Source	Df	DTH	DTM	GFP	HLW		TKW	GYLD	PHT
Entry	38	7.57E-33***	1.60E-16***	0.109665	8.93E-11***		2.79E-10***	0.999989	2.40E-10***
Rep	2	0.276143	0.0251792	0.275275	0.27458		0.177647	0.340543	0.796078
Location	2	1.97E-68***	6.66E-129***	6.53E-56***	3.72E- 26***		3.51E-13***	2.83E-30***	1.43E-12***
Entry: loc	76	0.998257	0.8478529	0.931858	0.959002		0.96093	1	0.999653
Residuals	783								
LSD		3.01	2.46	2.05	4.57	4.10			6.84
CV		4.34	3.79	12.8	14.06	3.18		21.57	16.38

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ',' 1. Df = degree of freedom, DTH = days to heading, DTM = days to maturity, GFP = grain filling period, HLW = hectoliter weight, TKW = thousand kernel weight, GYLD = grain yield and PHT = plant height

At Alem Tena site the tested genotypes showed a strong positive correlation of grain yield with HLW and days to heading with days to maturity. Some traits such as grain yield and HLW showed a strong negative correlation with stem rust coefficient of infection (CI). The tested genotypes at Dhera and Minjar sites showed similar positive correlation as Alem Tena site for grain yield with HLW and days to heading with days to maturity, however any trait couldn't show negative correlation with coefficient of infection for stem rust diseases Fig1.

Table 3. Mean performance for grain yield (kg ha-1) of 39 Durum wheat genotypes including the 2 checks tested across 6 environments (2020–2021 cropping seasons)

Genotype	AT_20	AT_21	DR_20	DR_21	MJ_20	MJ_21	Mean
G1	1685.0	2320.0	5341.5	2520.0	4487.5	4216.7	3428.4
G2	2057.5	2268.9	5347.0	1595.5	3005.0	3871.7	3024.3
G3	2180.0	1888.9	5328.0	2091.1	4155.0	4255.0	3316.3
G4	1550.0	2102.2	5813.5	1905.5	4077.5	2631.7	3013.4
G5	2707.5	2194.4	4950.0	1371.1	3687.8	2451.7	2893.7
G6	2382.5	2246.7	5510.0	1765.5	3325.0	2410.0	2940.0
G7	1967.5	2315.6	5768.5	2060.0	3610.0	3658.3	3230.0
G8	2947.5	1813.3	5940.0	1814.5	3057.5	3636.7	3201.6

G9	2577.5	1878.9	5333.5	1957.8	2775.0	3301.7	2970.7
G10	2032.5	2380.0	6212.0	1558.9	3810.0	3741.7	3289.2
G11	2480.0	2185.5	6037.0	1392.2	3795.0	3176.7	3177.7
G12	1762.5	1595.5	5589.0	2185.6	3307.5	3675.0	3019.2
G13	1927.5	2098.9	5819.0	2553.3	3247.5	3165.0	3135.2
G14	1902.5	2193.4	5820.0	2014.4	2875.0	3765.0	3095.1
G15	2235.0	1887.8	6583.0	2450.0	3247.5	5350.0	3625.5
G16	2525.0	2406.7	4958.5	1856.6	3405.0	2681.7	2972.2
G17	2432.5	2384.4	6103.5	2213.3	2902.5	4243.3	3379.9
G18	2187.5	2581.1	4375.5	2707.8	3837.5	3181.7	3145.2
G19	2847.5	2166.7	6636.5	2436.6	3267.5	3945.0	3550.0
G20	2602.5	1878.9	5846.5	1854.4	3182.5	3163.3	3088.0
G21	3155.0	2103.3	5295.0	1508.9	3455.0	3051.7	3094.8
G22	2150.0	2765.6	5943.5	2571.1	2545.0	2820.0	3132.5
G23	3197.5	1633.3	5900.0	2265.6	4095.0	3205.0	3382.7
G24	3087.5	2156.7	5217.0	2270.0	4260.0	3766.7	3459.6
G25	2467.5	1518.9	5627.0	2012.2	3907.5	2828.3	3060.2
G26	2315.0	1813.4	6405.0	1607.8	3710.0	2993.3	3140.8
G27	2430.0	2081.1	6017.0	1604.5	4335.0	3471.7	3323.2
G28	2227.5	1985.5	5646.5	2240.0	3820.0	3198.3	3186.3
G29	3185.0	1261.1	6505.0	2477.8	4182.5	3317.5	3488.1
G30	2277.5	1927.8	5028.5	2160.0	4345.0	3155.0	3149.0
G31	2367.5	3245.0	5117.3	2301.1	4282.5	3643.3	3492.8
G32	2045.0	2613.3	5695.0	1680.0	2620.0	4110.0	3127.2
G33	3032.5	1720.0	5555.0	1440.0	2967.5	4106.7	3136.9
G34	2645.0	2700.0	6400.0	1733.4	2600.0	3120.0	3199.7
G35	2390.0	2465.6	7218.0	1774.5	3092.5	3565.0	3417.6
G36	2515.0	3043.4	5068.5	2140.0	3061.3	2636.7	3077.5
G37	2327.5	2856.7	5910.0	2176.7	3718.8	3940.0	3488.3
G38	2180.0	2812.2	5740.5	2015.6	3180.0	2171.7	3016.7
G39	1910.0	2320.0	3750.3	2463.4	3527.5	3761.7	2955.5

Trait Correlation: In this experiment association of grain yield and its yield components among 37 tested elite durum wheat genotypes with the two checks were exploited to verify the association of considered traits. Correlation analysis showed that grain yield at all tested sites had a highly significant ($P<0.01$) positive associations with hectoliter weight (HLW) and negative correlation with coefficient of infection (CI) for stem rust disease. Days to heading (DTH) at all tested sites had also a highly significant ($P<0.01$) positive associations with days to maturity (DTM).
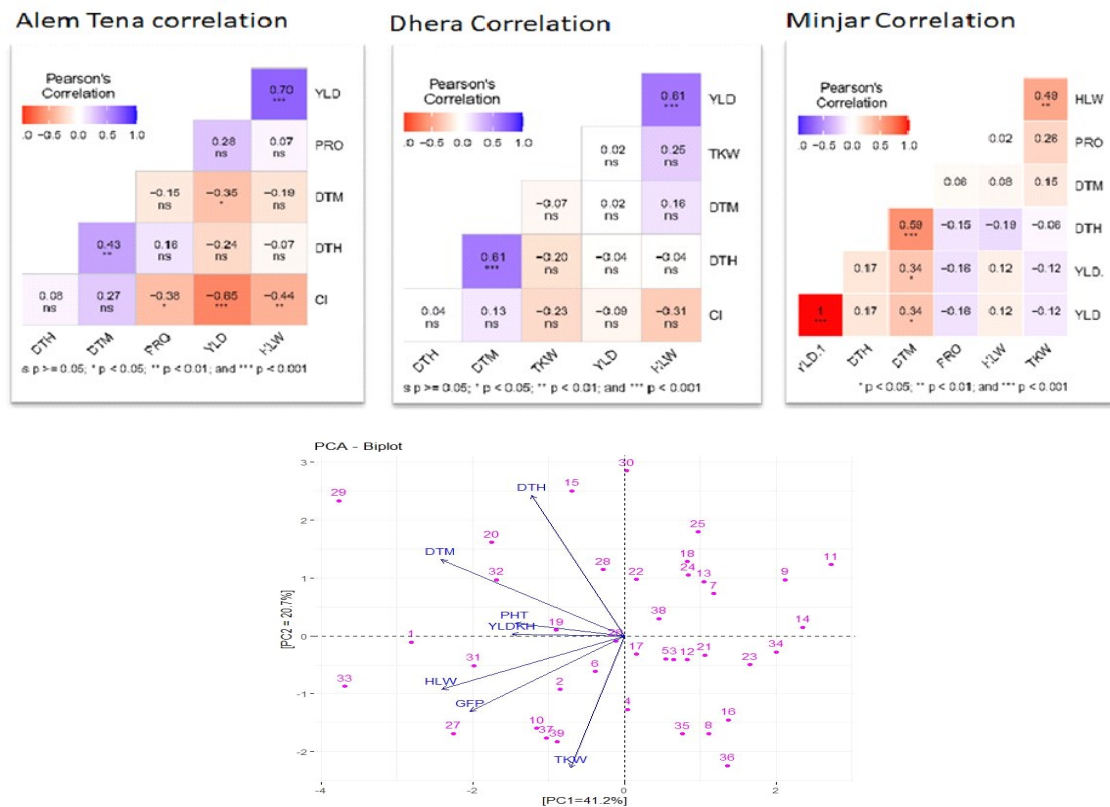

Figure 1. correlation between traits on different locations

This finding was in agreement with associations of yield and yield components studies caried out in durum wheats (Shimelis, 2006) which indicated that thousand kernel weight had significant direct role to enhance grain yield among durum genotypes. Among the tested durum wheat genotypes, six genotypes, namely, G29, G37, G31, G19, G15 and G24 were found to be the top high yielding genotypes across all locations as

the mean grain yield of tested genotypes showed. At Alem Tena site genotype G23, G29, G21, G24 and G33 performed well in the first year and G31, G36, G37 and G38 performed well in the second year in term of grain yield potential. For the case of Dhera site in the 1st year evaluation all genotypes showed a good performance, the top 5 genotypes were G35, G19, G15, G29 and G26, in the 2nd year top the top 5 were G18, G22, G13, G1 and G26, Luckly G29 perform well for both years. At Minjar site, G1, G30, G27, G31, G24 and G29 in the 1st season and G15, G3, G17, G1, G32 and G33 in the 2nd season performed good for grain yield. Generally, G29 is the widely adaptable genotype which performs well at most testing locations is followed by G1 see table 3. The average mean yield of the tested genotypes across locations ranged from 2893.7kg ha-1 (DW184086) to 3625.5 kg ha-1 (DW184058) in ascending order. The rank of the tested genotypes mostly changed from location to location.

Genotype-by-trait (GT) biplots and trait relationship analyses: Fig. 2 shows a GT-biplot which was used to study relationships among multiple traits and to identify genotypes that were particularly desirable relative to specific (several) trait(s). The proportion of total variation explained by the first two PC axes was 61.9%. There is a strong positive relationship revealed between PHT and YLDKH, between HLW and GFP, and positive correlation between Four traits (YLDKH, PHT, DTH and DTM). These four traits (YLDKH, PHT, DTH and DTM) have near-zero correlation with HLW and GFP). There is no negative association between traits. The GT-biplot can help to compare genotypes based on multiple traits and to identify genotypes that are particularly good for certain trait(s). The GT-biplot also can be used to discriminate genotypes based on each trait (Mohammadi *et al*., 2011). The best genotypes based on grain yield and PHT were G1 followed by G19, whereas G32 had the highest DTM, Genotype 33 showed lowest HLW as G27 showed poor GFP. The genotypes near to origin of the biplot had an average performance based on multiple traits. Similar reports on GT biplots ((Mohammadi *et al*., 2011)) demonstrated that the GT biplot is an tremendous tool for visualizing genotype-by-trait data and revealing the interrelationships among the traits.

Genotype and genotype by environment interaction (gge) biplot analysis: The visualization of a 'which-won-where' pattern in multi-environment trials is essential to study the possible existence of different mega-environments in a region ((Singh *et al*., 2019). The peak genotypes were the most responsive for being located at the greatest distance from the biplot origin. The genotypes with either the best or poorest performance in one or all environments were considered responsive falling within the sectors (Singh *et al*., 2019). In this biplot, the equality line divides the graph into eight sectors and six environments were retained in two sectors (Figure 3). G35, G27 and G29 were the winning durum wheat genotypes. There were strong correlations between environments located within the same sector. The genotype G39 was the poorest yielding, as it was located farthest from all location markers. The biplot showed that the three different climate locations can be differentiated from each other and that they can discriminate genotypes in opposite directions(Mohammadi *et al*., 2011).
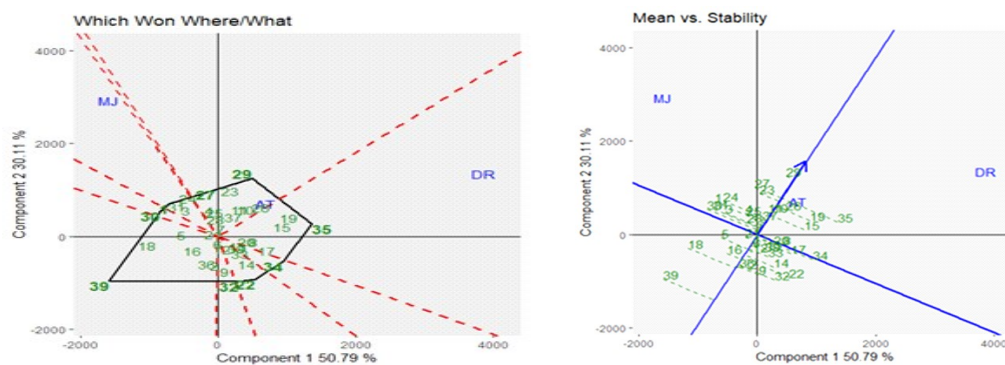

Figure 2. GGE Biplot shows components1 and 2 explaining 80.9% of the total variation using column Metric preserving SVP and Tester-Centered G+GE with no scaling.
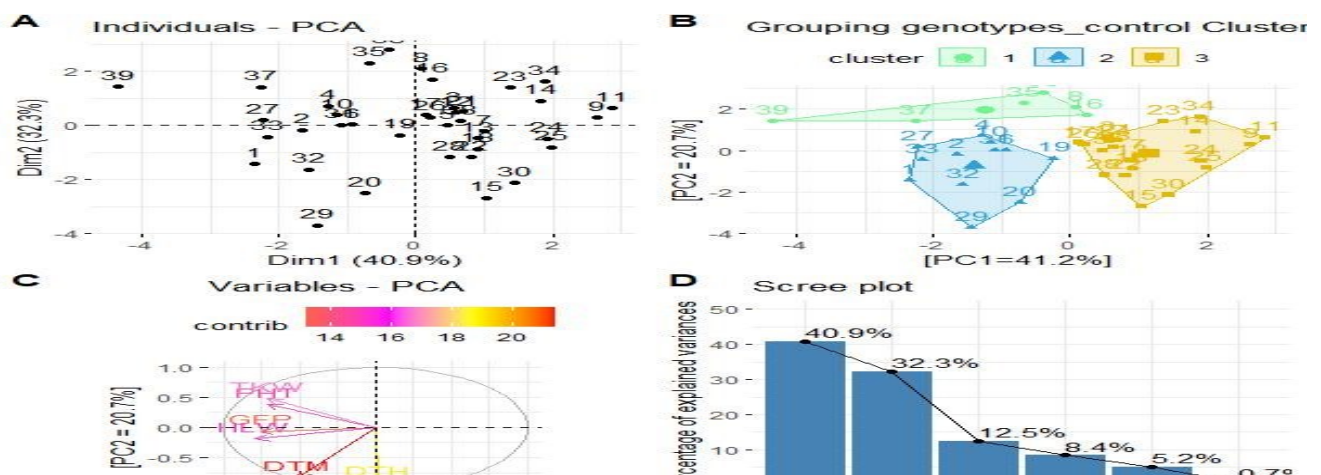

Figure 3. Individual PCA, Genotype clustering, trait contribution and Scree plot

The partitioning of GGE through GGE biplot analysis showed that PCA1 and PCA2 accounted for 50.79% and 30.11% of the GGE sum of squares respectively for grain yield. The first two principal components for this model explained a proportion as high as 80.90% of the data variability as shown in Figure 3. The polygon is drawn by joining the genotypes (G29 (DW184057), G35 (DW183152), G39 (Quamy), G22 (DW183102) and G32 (DW183136) that are located farthest from the biplot origin so that all other genotypes are contained in the polygon. The genotypes at the corner of the polygon can be called the vertex genotypes. The vertex genotypes are either the best or poorest in one or more environments. The genotype at the vertex of the polygon performs best in the environment falling within the sectors ((Dabi, 2023)).

Individual PCA, Genotype clustering, trait contribution and Scree plot: As the individual PCA explained most of the variation explained by dimension1 (PCA1) followed by the dimension2 (PCA2) the rest of the dimension have few roles to create a variation (from dimension3 to dimension6). As the scree plot showed 59.6% of the variation explained via the first two principal components (PCA1=35.1% and PCA2=24.5%). The genotype grouping cluster indicated that these tested genotypes grouped into three, mostly our genotype source is from CIMMYT, ICARDA and some from our local crosses, that may be the case it is grouped in to three. As indicated from the figure4 (C) the contribution of TKW and HLW are good as compared to the other traits such as DTH, DTM, PHT and YLD.

CONCLUSION

The genotypes tested across locations for two years showed performance variation for yield and yield related trait. There was a highly significant variation between genotypes and environment, while no variation Genotype by environment observed for yield and yield related traits. Using approaches such as ANOVA, trait correlations, mean performance and GGE biplot. The genotypes G29 and G1 were identified as high yielding and stable across all six environments. Therefore, these lines can be included in the national testing program, to be released as a variety and recommending as good parent for crossing.

Author Contributions: Yewubdar Shewaye carried out the experimental data analysis and written the manuscript. Shitaye Homa give comment on the manuscript.

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Competing Interests: The author declares that there is no opposing interest.

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Table 4. List of durum wheat genotypes with checks evaluated across locations

Code	Genotype	Pedigree
G1	DW171222	DW171222
G2	DW171230	DW171230
G3	DW171246	DW171246
G4	DW184065	Ter1//mrf1/stj2/3/Icasyr1
G5	DW184086	Icasyr1/3/Bcr/SbI5//Turartu/4/13376/Bcrch1//Ossl 1/Stj5
G6	DW184089	Icarasha1//Quabrach3/RedseedTer109
G7	DW183149	ARMENT // SRN_3/NIGRIS_4/3/CANELO_9.1/4/ TOSKA_26/RASCON_37 // SNITAN/5/PLAYERO/11/ï¿½ CDSS12Y00440S_069Y_050M_23Y_0M
G8	DW184085	Ter1//mrf1/stj2/3/Icasyr1
G9	DW183117	AG 1-22/2*AC089//2*UC1113/3/5*SOOTY_9/ RASCON _37/5/SILK_3/DIPPER_6/3/AC089/ï¿½ CDSS09Y00657S_013Y_08M_16Y_0M_04Y_0B
G10	DW184062	IcamorTA471//IcamoreTA459/Ammar8/4/Stj3//Dra2/Bcr/3/Ter3
G11	DW184055	Atlast 1/961081//Icasyr1/3/Zegrenses1
G12	DW184050	Jk/Ch1604//Ysf1/Otb6/3/Adnan2/Berghouata1
G13	DW183123	E90040 / MFOWL _13// LOTAIL_6/3/PROZANA / ARLIN // MUSK_6/ 9/ USDA 595/3/ D67.3 /RABI // CRA /4/ï¿½
G14	DW184071	Waha (plc/Ruff//Gta/Rtte)
G15	DW184058	Waha (plc/Ruff//Gta/Rtte)
G16	DW184028	Icamor TA041/IcamorTA0469/3/Bcr/Gro1/Mgn11/5/MIK12

G17	DW184042	Miki3(stj3//Bcr/Lks4
G18	DW183164	C F4 20 S /4/ YAZI_1/AKAKI-4// SOMAT_3/3/ AUK/GUIL// GREEN/5/ CANELO_9.1//SHAKE-3/
G19	DW183147	P91.272.3.1/3*MEX175//2*JUPARE C 2001/11/ BOOMER_33/ZAR/3/BRAK_2/AJAIA_2//
G20	DW183016	ALTAR 84/STINT//SILVER_45/3/GUANAY/4/ GREEN _14// YAV_10/AUK/10/CMH79.959/CHEN//..
G21	DW184072	Quasloukos 1/5/Azn 1/4/BEZAIZSHF// SD19539/ Waha/3/ Gdr2/6/Azeghar 1/4/Icamor TA0462/3/Maamouri3//Vitron?Bidra1/5/Mgn13?Ainzen1
G22	DW183102	SELIM /10/RCOL/THKNEE_2/9/ USDA595/3/D67.3/ RABI// CRA/4/ALO/5/HUI/YAV_1/6/ ARDENTE/7/
G23	DW184051	Icamilmus1/3/Marsyr3//saadi1989/Chan/4/IcamorTA0471//IcamorTA0459/Waha/3/Mgn13/Ainzen1
G24	DW183138	MOHAWK/3/GUANY//TILO_1/LOTUS_4/4/ARMENT//SRN_3NIGIRIS_4/3/CANELO_9.1/6/YAZI_1/... CDSSB00263T-087Y-044M-12Y-0M
G25	DW183106	ALAMO:DR/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/5/PLATA_6GREEN_17//SNITAN/4/ ï¿½CDSS11Y00076S_099Y_012M_37Y_0M_06Y_0B
G26	DW184013	Icamor TA047/IcamorTA0459/w/
G27	DW184021	Baniswaf6/Miki2
G28	DW184043	Icasyr1/3/Gcn//Stj/Mrb3/4/Mgn13/Ainzen1/3/Bcr/Gro1//Mgn11
G29	DW184057	SWAHEN_2/KIRKI_8//PROZANA_1/4ADMAR_15//ALBIA_1/åŒ"DSS11Y00222S_099Y_050M_15Y_0M_06Y_0B
G30	DW185005	ERPEL(SIB)1(SIB)RUSO
G31	DW183014	ALTAR84/STINT// SILVER_45/3/ GUANAY/4/ GREEN_14 // YAV_10ï¿½ CDSS11Y00213S_099Y_040m_30Y_0M_06Y_0B
G32	DW183136	ALTAR 84/STINT// SILVER_45/3/ GUANAY/4/ GREEN_14 // YAV_10/ AUK/ 10/CMH79.959/ CHEN//
G33	DW184023	Stj3//Bcr/Lks4
G34	DW184031	Mrb3/Mna1//Ter1/3/ IcamorTA459/Ammar7/4/Beltegy2
G35	DW183152	BELLAROI /5/ HUBEI // SOOTY_9 / RASCON_37/3/2* SOOTY-9RASCON_37/4/ SOOTY_9/ Ã¯Â¿Â½ CDSS13 Y0052IT _ 0 9 9 Y030M-12Y_4M_0Y
G36	DW184027	Icamor TA041/IcamorTA0469/3/Bcr/Gro1/Mgn11/5/MIK12
G37	DW184096	IcamrTA0471//IcamorTA0459/Ammar8/4/Stj3//Dra2/Bcr/3/Ter3
G38	Alemtena	Alemtena
G39	Quamy	MEX/CRANE//FLAMINGO/3/HUIT[2837][3589]; TEZONTLE/YAVAROS-79//HUITLE/3/ALTAR-84

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