



# Dissecting drought tolerance for Syria rehabilitation

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**Introduction:**

Wheat *Triticum* spp. is the most widely grown cereal crop in the world and one of the central pillars of global food security (Rosegrant *et al.*, 2001), about 728 million metric tons of wheat was produced on 208 million hectares in 2013 (FAO, 2015).

By the year 2050, the world population is estimated to be 9 billion and the demand for wheat will exceed 900 million tons. Fulfilling this demand is very challenging in the face of climate change, increasing drought, heat stress, and emergence of new virulent diseases and pests. Offsetting these challenges requires designing an effective wheat breeding strategy with the application of new technologies and tools in order to develop varieties with high yield potential and resistance/tolerance to abiotic and biotic stresses, and with acceptable end-use qualities. (Tadesse *et al.*, 2013).

Durum wheat (*Triticum turgidum* L. var. *durum*) is a self-pollinated tetraploid cereal crop (Soiano *et al.*, 2018) grown in a range of climatic zones varying from warm and dry to cool and wet environments (Giraldo *et al.*, 2016). The Mediterranean Basin is the largest durum producing area worldwide (Bonjean *et al.*, 2016). Drought is the main environmental stress that determines its productivity (Mardeha *et al.*, 2006), and often exacerbated by the incidence of extreme temperature during the grain filling period causing high losses in production (Rajaram *et al.*, 2006).

Drought is arguably the most important abiotic stress that affects wheat productivity in the world and affects both source and sink strengths, leading to yield reduction up to 92% in wheat, depending on the crop growth stage, duration and intensity of drought stress (Semenov *et al.*, 2014). The drought stress particularly during reproductive development reduces grain number and grain size in wheat (Dolferus *et al.*, 2011; Dong *et al.*, 2017; Ma *et al.*, 2017). Developing wheat cultivar tolerant to drought stress occurring during reproductive phase is currently a big challenge to wheat breeders (Cattivelli *et al.*, 2008; Mwadzingeni *et al.*, 2016).

Drought tolerance is not a qualitative trait, but a complex quantitative plant trait, that is controlled by numerous genes and plant traits, with minor individual contributions (Blum, 2010; Dolferus *et al.*, 2013; Hu and Xiong, 2014; Serba and Yadav, 2016). Breeding for drought tolerant wheat cultivar is made especially challenging due to the network of traits involved and their polygenic control. This in turn results in high genotype by environment (G×E) interactions, low heritability, and difficulty to conduct mass screening of plant traits and genes (Cattivelli *et al.*, 2008; Fleury *et al.*, 2010; Hu and Xiong 2014). On the other hand, the narrow genetic base of many durum wheat varieties ((Makai *et al.*, 2016) selected under strong breeding pressure for identical target objectives, does not seem to provide the amount of plasticity necessary to target such a complex trait (Jing *et al.*, 2013).

Compared with domesticated varieties, crop wild relatives and primitive wheat have been challenged in natural environments for thousands of years and maintain a much higher level of diversity (Zhang *et al.*, 2016). Hence, interspecific hybridization between durum elite lines and

wild relatives of the Gramineae family is a promising method to restore variability to the modern breeding germplasm (Rajaram and Hettel, 1994).

For instance, Sall *et al* (2018) tested 24 durum wheat genotypes for tolerance to extreme heat along the Senegal River, to reveal that the top and stable yielders were derived from interspecific hybridizations with *Triticum dicoccum* and *Aegilops speltoides*. Similarly, Zaim *et al* (2017) was able to confirm that crop-wild relatives crosses (CWR) out-yielded the best elites and cultivars when tested across drought-prone environments in North Africa, and even showed better quality characteristics.

### Selection Durum Primitive Wheat Genotypes Tolerant to Drought Stress

#### Material and Methods:

A set of 22 durum wheat primitives, including 10 genotypes classified as *Triticum polonicum*, 7 genotypes classified as *Triticum carthilicum*, 4 genotypes classified as *Triticum dicoccom*, one landraces, and in addition 2 cultivar as checks (**Table 1**) were planted in the experimental station in Aleppo, Syria following a randomized complete block design (RCBD) with two replications, two irrigation treatments (well-watering; WW) and (water-stress; WS).

**Table 1. List of primitive genotypes**

Genotype	Origin	Genotype	Origin
1 <i>T. polonicum</i>	Italy	13 <i>T.dicoccum</i>	Ethiopia
2 <i>T. polonicum</i>	Italy	14 <i>T.dicoccum</i>	Syria
3 <i>T. polonicum</i>	Italy	15 <i>T.dicoccum</i>	Syria
4 <i>T. polonicum</i>	Italy	16 <i>T. durum</i>	Greece
5 <i>T. polonicum</i>	Italy	17 <i>T.carthilicum</i>	Turkey
6 <i>T. polonicum</i>	Italy	18 <i>T.carthilicum</i>	Turkey
7 <i>T. polonicum</i>	Italy	19 <i>T.dicoccum</i>	CIMMYT
8 <i>T. polonicum</i>	Italy	20 <i>T.carthilicum</i>	Syria
9 <i>T.carthilicum</i>	Italy	21 <i>T. polonicum</i>	CIMMYT
10 <i>T.carthilicum</i>	Italy	22 <i>T. polonicum</i>	CIMMYT
11 <i>T.carthilicum</i>	France	23 Bohouth7	Chick
12 <i>T.carthilicum</i>	Italy	24 Cham5	Chick



**This study aim to:**

Selection the best drought tolerant genotype using Drought Index.

**Data were collected for:**

Phenological Traits (Number of Days to Heading, Number of Days to Physiological Maturity, and Grain Filling Period).

Morphological traits (Plant Height, Spike Length, Peduncle Length, and Awns Length)

Yield Components (Thousand Kernels Weight, Number of Grain per Spike, Grain Weight / Spike, Grain Yield).

Physiological Traits (Flag Leaf Area (FLA), Chlorophyll Content (SPAD index) (CHL C)).

Disease were recorded by visual selection.



For estimating the tolerance and susceptibility of genotypes the following indices were used:

Stress Susceptibility Index (SSI), Tolerance (TOL), Mean Productivity (MP) Geometric Mean Productivity (GMP) and Stress Tolerance Index (STI), Yield Stability index (YSI):

**a-**  $YSI = Y_s/Y_p$  (Bouslama and Schapaugh 1984)

**b-**  $TOL = Y_p - Y_s$  (Rosielle and Hamblin, 1981)

**c-**  $MP = (Y_p + Y_s)/2$  (Rosielle and Hamblin, 1981)

**d-**  $GMP = \sqrt{(Y_p \times Y_s)}$  (Fernandez, 1992)

**f-**  $SSI = [1 - (Y_s/Y_p)] / SI$   $SI = 1 - (\underline{Y}_s/\underline{Y}_p)$  (Fisher and Maurer, 1978)

**g -**  $STI = (YP) \times (YS) / (\underline{YP})^2$  (Fernandez, 1992)

Where:  $Y_p$  =Mean yield of the genotype under non-stress conditions,  $Y_s$  =Mean yield of the genotype under stress conditions,  $\underline{Y}_p$  =Mean yield of all genotypes under non-stress conditions and  $\underline{Y}_s$  = Mean yield of all genotypes under stress conditions.

### Results:

Analysis of variance showed significant differences for the genotype effect, and also between treatments and GxT (**Table 2**).

**Table 2. Mean squares for grain yield**

Source of variation	d.f	MS
R	1	171.4
G	23	37568.4**
T	1	875183.3**
GxT	23	6094.6**
Error	47	464.8

### Effect of Drought on Yield:

The drought treatment significantly reduced the yield for all genotypes (**Table 3**). The lowest decreases was recorded for a landrace from Greece, with 21.44% reduction, followed by a *T. dicoccum* obtained from the CIMMYT genebank with 27.97%. The top yielding line under irrigated conditions was *T. polonicum* from Italy (number 4), which was also among the best ones under drought. The top yielder under drought was *T. carthilicum* from Syria. Interestingly, the two cultivars included in this screening were not among the best for drought nor irrigated conditions.

**Table 3. Yield performances under two treatments and percentage of yield reduction of genotypes**

G	Irrigated	Drought	Losses %	G	Irrigated	Drought	Losses %
1	328.0	112.5	65.70*	13	341.2	176.2	48.36*
2	503.6	217.8	56.75*	14	297.8	178.9	39.93*
3	229.9	59.3	74.21*	15	233.6	127.1	45.59*
4	611.2	217.9	64.35*	16	483.7	380.0	21.44*
5	197.5	82.4	58.28*	17	211.2	95.1	54.97*
6	391.8	154.4	60.59*	18	268.0	160.6	40.07*
7	383.2	154.2	59.76*	19	414.4	298.5	27.97*
8	290.0	81.7	71.83*	20	578.4	307.7	46.80*
9	220.3	75.6	65.68*	21	431.2	225.5	47.70
10	242.4	106.2	56.19*	22	462.0	161.1	65.13*
11	176.0	52.3	70.28*	Bohouth7	425.0	127.9	69.91*
12	339.5	149	56.11*	Cham5	445.0	220.0	50.56*
L.S.D 43.37							
C.V 8.3							

**Correlation between grain yield and drought tolerance indices:**

Grain yield in the two environments that were tested had positive significant correlation (**Table 4**), in addition to high significant correlations with MP, GMP and STI indices. Generally, those indices having high correlation with performance in different conditions, were introduced as the best indices because they separated and identified genotypes with high production in diverse environments. So, MP, GMP and STI indices were identified as the best indices for screening and identification of superior genotypes in various environments with different levels of stress.

**Table (4) correlation coefficients between Yp, Ys and drought tolerance indices.**

Yp	1	-							
Ys	2	<0.001	-						
GMP	3	<0.001	<0.001	-					
MP	4	<0.001	<0.001	<0.001	-				
SSI	5	0.2096	<0.001	<0.001	0.002	-			
STI	6	<0.001	<0.001	<0.001	<0.001	<0.001	-		
TOL	7	<0.001	0.2979	0.002	<0.001	<0.001	0.0074	-	
YSI	8	0.2096	<0.001	<0.001	0.002	<0.001	<0.001	<0.001	-
		1	2	3	4	5	6	7	8

**Drought Index:**

Maximum grain yield in drought condition was recorded for genotypes G 16 and G (19, 20) respectively, which showed significant preference compared to other genotypes. In supplemental irrigation condition, G13 and G29 had significant preference other genotypes.

According to the TOL, records showed that G (5, 11, 14, 15, 16, 17, 18, 19) had the most tolerance and G (22, Bohouth7) had the least tolerance. In terms of SSI, G (16, 19) showed the least susceptibility. Based on the MP index, G (19, 20, 4) were identified as the most tolerant genotypes and G (11) with lower values on this index were the most susceptible genotypes. Using STI and GMP indices it can be deduced that G (16, 20) were the most tolerant genotypes in contrast genotypes G (3, 11) showed high sensitivity. The highest values of YSI were observed for G (16, 19) and the genotypes with a high YSI were expected to have high yield under both stressed and non-stressed Condition. Ranking of grain yield for genotype in two environments and different indices for each genotype showed that genotypes G (16, 19, and 20) had the best ranking with low standard deviation of rank.

**Table (5) Values of Drought Tolerance Indices from the Potential Yield and the Stress Yield**

G	GMP		MP		SSI		TOL		STI		YSI		YS		YP	
1	192.1	hi	220.3	fg	1.1704	ghijk	215.5	def	0.2766	ghij	0.3432	ghijk	112.5	fgh	328	fgh
2	331.1	cd	360.7	b	1.0092	cdefg	285.8	gh	0.8219	cd	0.4337	cdefg	217.8	c	503.6	b
3	116.7	mn	144.6	jkl	1.3203	k	170.6	abcd	0.102	k	0.2591	k	59.3	jk	229.9	jkl
4	364.8	b	414.6	a	1.1473	ghijk	393.3	i	0.9992	b	0.3562	ghijk	217.9	c	611.2	a
5	127.6	lm	139.9	kl	1.0377	defgh	115.1	a	0.1219	jk	0.4177	defgh	82.4	i	197.5	l
6	245.7	ef	273.1	de	1.0782	fghij	237.4	efgh	0.4523	ef	0.3949	fghij	154.4	e	391.8	ef
7	243.1	ef	268.7	de	1.0649	efghi	229	defg	0.4427	efg	0.4024	efghi	154.2	e	383.2	ef
8	153.8	jkl	185.8	ghi	1.279	jk	208.3	cdef	0.1773	ijk	0.2823	jk	81.7	i	290	ghij
9	128.6	klm	147.9	jkl	1.1688	ghijk	144.7	abc	0.1244	jk	0.3441	ghijk	75.6	ij	220.3	kl
10	160.5	jk	174.3	ijk	1.0011	cdefg	136.2	ab	0.1931	ijk	0.4382	cdefg	106.2	gh	242.4	ijkl
11	95.4	n	114.1	l	1.2381	hijk	123.7	a	0.0683	k	0.3052	hijk	52.3	k	176	l
12	224.6	fg	244.2	def	0.997	cdefg	190.5	bcde	0.3779	fgh	0.4405	cdefg	149	e	339.5	fg
13	245.2	ef	258.7	de	0.8619	bcde	165	abcd	0.4506	ef	0.5163	bcde	176.2	d	341.2	fg
14	230.8	fg	238.4	ef	0.7117	b	119	a	0.3991	efg	0.6006	b	178.9	d	297.8	ghi
15	172.2	ij	180.3	hij	0.807	bc	106.5	a	0.2224	hijk	0.5471	bc	127.1	fg	233.6	ijkl
16	428.7	a	431.9	a	0.3792	a	103.7	a	1.3788	a	0.7872	a	380	a	483.7	bc
17	141.7	ijklm	153.1	ijk	0.9788	cdefg	116.1	a	0.1507	jk	0.4507	cdefg	95.1	hi	211.2	kl

18	207.4	gh	214.3	fgh	0.7132	b	107.4	a	0.3222	fghi	0.5998	b	160.6	de	268	hijk
19	350.9	bc	356.4	b	0.4707	a	115.9	a	0.9302	bc	0.7359	a	298.5	b	414.4	de
20	421.9	a	443.1	a	0.8338	bcd	270.7	fgh	1.3331	a	0.5321	bcd	307.7	b	578.4	a
21	311.8	d	328.3	bc	0.8481	bcd	205.7	cdef	0.7305	d	0.524	bcd	225.5	c	431.2	cde
22	272.7	e	311.6	c	1.159	ghijk	300.9	h	0.5569	e	0.3496	ghijk	161.1	de	462	bcd
Bohouth7	233.1	fg	276.4	d	1.2455	ijk	297.1	h	0.4075	efg	0.3011	ijk	127.9	f	425	cde
Cham5	312.6	d	332.5	bc	0.8974	bcdef	225	defg	0.7318	d	0.4964	bcdef	220	c	445	bcde

### Multivariate Analysis:

Principal component analysis (PCA) Table (6) revealed that the first PCA (PC1) explained 86.35% of the variation and had positive correlation with Ys, Yp, MP, GMP, TOL, YSI and STI but negative correlation with SSI. The second PCA (PC2) explained 13.63% of the total variability and correlated positively with YS, YSI, GMP, MP, and STI.

**Table (6) Principal component analysis for potential yield (YP), stress yield (YS) and drought tolerance indices**

Principal component	YP	YS	YSI	GMP	MP	SSI	STI	TOL
1	0.60188	0.36214	0.00027	0.4655	0.48212	-0.00048	0.00179	0.23973
2	-0.2762	0.49792	0.00151	0.25361	0.11083	-0.00269	0.00125	-0.77407

Genotypes possessed high values of PC1, PC2 could be high yielding under stressed and non-stressed environments and according to that values this genotypes (16, 19, 20, 21 and Cham 5) are the best genotypes under stressed and non-stressed environments Table (7).

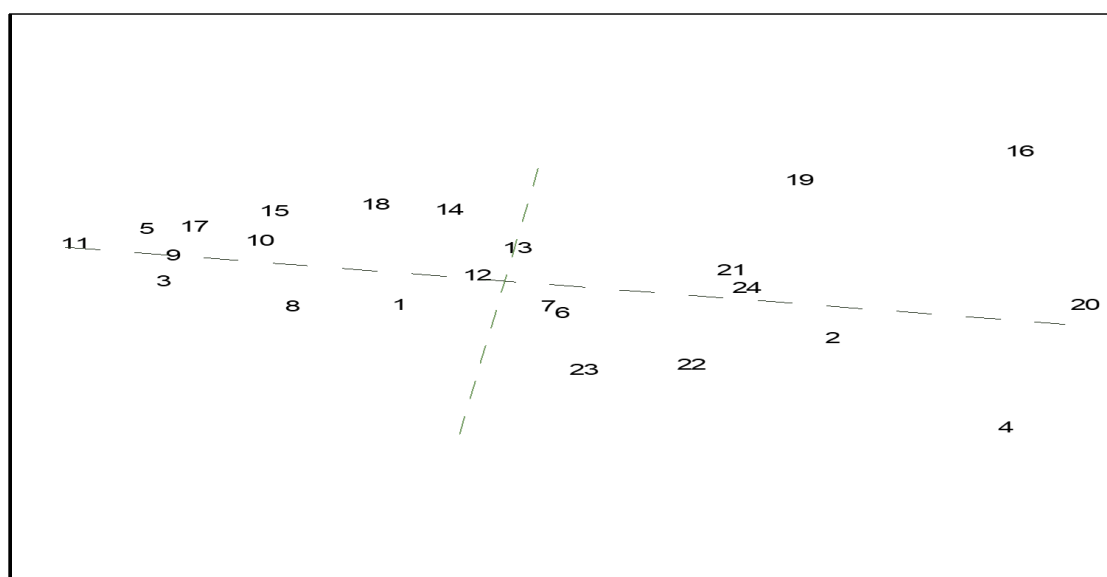
**Table (7) Principal component analysis for Yp, Ys and drought tolerance indices on 24 Durum wheat genotypes**



Genotupes	1	2	Genotupes	1	2
1	-68.4	-53	13	-6.3	31.9
2	224.7	-52.7	14	-58.9	74.9
3	-229.1	-45.1	15	-174.6	55.2
4	356.9	-151	16	307.5	207.2
5	-250.7	20.5	17	-224.7	27.3
6	40.8	-47.3	18	-108.8	74.4
7	30.2	-39.6	19	166.6	148.2
8	-138.6	-65.8	20	380.6	15.3
9	-228	-10.9	21	140.1	24.7
10	-178.1	15.8	22	131.8	-101.3
11	-299.9	-6.2	Bohouth7	61.2	-118.7
12	-27.6	-7.7	Cham5	153.4	3.9

Biplot graph based on drought tolerance indices had characteristics of grouping the genotypes into four distinct groups:

Group-1 included 5 genotypes (16, 19, 20, 21, and 24) which are the best genotypes under two conditions, Group-2 included 6 genotypes (2, 4, 6, 7, 22, and 23) which have better performance under normal condition and poor performance under stress conditions. Whereas Group-3 categorized as having the genotypes (5, 10, 11, 12, 13, 14, 15, 18) with better performance under stress conditions and relatively poor performance under normal water conditions. Finally Group-4 was categorized as having the genotypes () with poor performance under normal and stress



conditions.

Fig (1) Principal Components with rotated axe

**Conclusion:**

Based on the results of this research, G (16, 19, and 20) maintained preference in both environments tested in the experiment. They also had high values for STI, GMP and MP indices. These genotypes had the best ranking.

These Genotypes are capable of producing high yields when water is in adequate supply, and only suffer a minimum loss during droughts.

In addition this genotypes were the best in the most of studied traits, Table (8) and Table (9)

**Table (8) Morphological and Physiological Traits For genotypes**

Genotypes	PL		AWL		SL		PH		CHL-C		FLA	
1	34.88	bcd	9.21	hi	15.668	a	120.25	a	35.4	bcde	26.24	def
2	37.04	a	9.69	fgh	7.98	hij	112.75	c	31.85	cdef	29.17	abcde
3	32.85	defg	6.07	k	11.525	d	113.5	c	34.88	bcde	29.74	abcd
4	31.1	fg	11.03	e	7.763	hijk	108.75	d	33.08	bcdef	31.72	a
5	33.75	cde	9.67	fgh	9.31	g	113	c	36.25	bcd	31.69	ab
6	31.82	efg	9.97	fg	8.2	hi	107.5	de	35	bcde	31.73	a
7	35.63	abc	13.99	ab	7.733	hijk	116.25	b	35.13	bcde	23.82	fghi
8	33.55	cde	10.97	e	11.75	cd	114.5	bc	30	defg	24.18	fghi
9	25.63	h	9.79	fgh	10.32	e	97.5	f	23.88	gi	16.41	kl
10	27.83	h	9.43	gh	9.5	fg	98.5	f	36.73	bc	19	jk
11	21.91	i	7.92	j	10.03	ef	89.5	i	33.43	bcdef	13.59	l
12	33.31	def	9.19	hi	9.668	fg	109	d	29.88	defgh	30.33	abc
13	32.1	efg	11.92	d	9.218	g	105.75	e	38.63	b	21.97	ghij
14	27.79	h	9.75	fgh	7.443	jk	80.75	k	27.38	fghi	25.14	fgh
15	30.83	g	13.92	b	11.418	d	93.75	g	35.28	bcde	21.66	ghij
16	36.51	ab	14.62	a	8.398	h	99	f	38.28	bc	30.01	abcd
17	27.15	h	9.74	fgh	12.193	bc	85	j	35.9	bcd	19.66	jk
18	33.7	cde	7.57	j	10.558	e	91.25	hi	28.88	efghi	20.95	ij
19	32.44	efg	11.86	d	6.638	l	77.75	l	45.83	a	27.76	acdef
20	27.11	h	12.96	c	7.85	hijk	85.5	j	35.93	bcd	27.43	cdef
21	26.33	h	10.26	f	7.908	hijk	92	gh	32.73	bcdef	23.94	fghi
22	27.09	h	14.04	ab	12.393	b	93	gh	36.93	bc	25.66	efg
23	26.97	h	8.6	i	7.213	kl	80.75	k	33.25	bcdef	21.2	hij
24	27.8	h	9.87	fgh	7.625	ijk	85.75	j	33.23	bcdef	24.49	fghi
l.s.d.	2.773		0.8948		0.8623		3.116		7.808		4.895	
C.V	4.5		4.2		4.5		1.6		11.4		9.8	

**Table (9) Yield Components and Phenological Traits**

Genotypes	GW/S		GN/s		TKW		DH		DM		GFP	
1	1.377	def	27.15	n	47.58	e	134	n	164.5	i	30.5	l
2	2.779	a	44.3	c	58.77	a	134.8	o	166.8	kl	32	j
3	0.904	jk	22	o	37.43	l	141.5	t	170.2	p	28.5	o
4	2.591	a	44	c	56.59	b	138	r	168.8	mn	30.5	l
5	0.715	k	22	o	40.93	ij	132.8	l	170.2	p	37.5	c
6	2.115	b	37.5	fg	52.37	c	132	k	166.5	k	34.5	g
7	1.679	c	35.8	ghi	45.07	f	140	s	169	n	29	n
8	1.161	fgh	21.3	o	50.02	d	139.8	s	168.5	m	28.75	no
9	0.925	ijk	33.35	jkl	29.35	n	134.5	o	162.5	f	28	p
10	1.025	hij	30.08	m	32.69	m	135.5	p	163.5	h	28	p
11	0.713	k	31.75	lm	21.79	p	133.5	m	163	g	29.5	m
12	1.526	cde	44.55	c	33.4	m	127.5	g	163.5	h	36	d
13	1.617	c	40.75	d	38.7	kl	123.8	d	161.5	d	37.75	c
14	1.329	efg	30.15	m	42.95	gh	117.5	a	153	a	35.5	e
15	1.127	ghi	34.1	ijk	32.34	m	128.5	h	169.5	o	41	a
16	2.699	a	59.2	a	45.47	f	123	c	162	e	39	b
17	0.957	hij	36.1	gh	25.65	o	130.5	j	162	e	31.5	k
18	1.339	efg	34.75	hij	37.98	kl	124.5	e	159.5	c	35	f
19	2.1	b	46.65	b	44.51	fg	121	b	157	b	36	d
20	2.696	a	46.73	b	57.08	ab	136	q	166.5	k	30.5	l
21	2.052	b	38.65	ef	51.74	cd	133	l	165.5	j	32.5	i
22	1.947	b	32.2	kl	57.1	ab	127	f	161.5	d	34.5	g
23	1.59	cd	39.73	de	39.62	jk	134.5	o	167	l	32.5	i
24	1.583	cd	40.31	de	42.15	hi	130	i	163.8	h	33.75	h
l.s.d.	0.283		2.585		2.476		1.85		2.119		2.57	
C.V	8.8		3.5		2.9		0.7		0.6		3.9	

### Estimating of Genetic variance heritability and genetic advance in Interspecific Hybrids in durum wheat

Nine parents were planted in the first season 2016/2017 in AL-sofera location



4 Female: 3 cultivated variety and one line from ICARDA was emasculated



Five Primitive wheat (2) Genotypes *T.dicoccum* (2) Genotypes *T.carthlicum* and one Genotype (*T.polonicum*) used as a Male Parents the crossing was done using North Carolina II design at the end 20 hybrids groups were obtained (5×4).





Table (1) Plane of Crossing

	Male					Female
<i>T. dicoccum</i> Syria	<i>T. polonicum</i> CIMMYT	<i>T. carthlicum</i> Italy	<i>T. carthlicum</i> Italy	<i>T. dicoccum</i> Ethiopia		
X	X	X	X	X		
X	X	X	X	X	CandocrossH25/Bicredera1/3/ICAMORTA0463//Lah/Ch12504/4/Bcrch1//Ossl1/Stj5/5/Ysf1/Otb6	
X	X	X	X	X	Cham9	
X	X	X	X	X	Cham7	
X	X	X	X	X	Cham5	

**Next season 2017/2018:**

The twenty hybrids groups and their parents were planted in a Randomized Complete Block Design (RCBD) with two replications in Hemaima Station under drought stress.





Data were collected for:

Phenological traits (Number of Days to Heading, Number of Days to Physiological Maturity, and Grain Filling Period).

Morphological traits (Plant Height, Spike Length, Peduncle Length, and Awns Length)  
Yield Components (Thousand Kernels Weight, Number of Grain per Spike, Grain Weight / Spike).



### **This study aim to:**

Estimating Heritability in narrow and board sense, Additive and Dominance Variance, Dominance degree, expected genetic advance for some Interspecific Hybrids under drought stress.

### **Biometrical and genetic analyses:**

#### **Heritability:**

Heritability in the broad ( $h^2b$ ) and narrow ( $h^2n$ ) sense were estimated from the following formulae (Warner, 1952):

$$h^2b = 100 (\delta^2G/\delta^2ph)$$

$$h^2n = 100 (\delta^2A/\delta^2ph)$$

$\delta^2G$ = Genotypic variances,  $\delta^2A$ = additive variances,  $\delta^2D$ = dominance variances

$\delta^2ph$ = phenotypic variances,  $\delta^2E$ = Environmental Variance

$$\delta^2G = \delta^2A + \delta^2D$$



$$\delta^2\text{ph} = \delta^2\text{G} (\delta^2\text{A} + \delta^2\text{D}) + \delta^2\text{E}$$

**Expected genetic advance:** (Allard, 1960):

$$\text{EGA} = (h^2n) (\sigma\text{P}) (i)$$

$\sigma\text{P}$  = Phenotypic standard deviation.

$i$  = Selection differential (the  $k$  value for 1 % selection intensity) equals (2.64).

$$\text{EGA \%} = (\text{EGA}/\text{X}) * 100$$

$\text{X}$  = Mean of the respective cross.

**Dominance Degree:** (Mather and Jinks, 1977)

$$\alpha = (\delta^2\text{D}/\delta^2\text{A})^{0.5}$$

The estimates of the average degree of dominance " $\alpha$ " were used to indicate the type of dominance, as follows:

" $\alpha$ " = 0 indicates no dominance,

" $\alpha$ " < 1 indicates partial dominance,

" $\alpha$ " = 1 indicates complete dominance and

" $\alpha$ " > 1 indicates over dominance

**Variance components:** (Comstock and Robinson, 1952) (Lynch and Walsh, 1998):

The genotypic ( $\delta^2\text{G}$ ), additive ( $\delta^2\text{A}$ ), dominance ( $\delta^2\text{D}$ ) and phenotypic ( $\delta^2\text{ph}$ ) variances were calculated as follows:

$$4\delta^2 \text{ gca} = \delta^2\text{A}$$

$$(\sigma^2 \text{ mf}) = 4\delta^2 \text{ sca} = 4 \delta^2\text{D}$$

$$\delta^2\text{E} = \delta^2\text{e}/r$$

## Results:

The results showed significant differences among genotypes for all studied traits, additive gene action controlled all traits, the genes that controlled all traits shown partial dominance, Broad sense heritability was high for all traits, whereas the Heritability in Narrow sense was high for most of the traits except peduncle length, and awns length were mid, a high value for Expected genetic advance associated with high Narrow sense heritability was recorded for (Plant Height, Spike Length, Grain Filling Period, Kernels weight / spike, Thousand Kernels weight.

Table (2) Estimation of components of variance and genetic parameters

variance and genetic parameters	PH	PL	SL	AWL	DH	DM	GFP	TKW	GN	GW/S
$\delta^2A$	64.913	42.194	0.762	3.084	50.28	36.036	39.446	56.201	24.915	0.581
$\delta^2D$	9.415	30.03	0.1004	2.157	2.507	5.415	10.545	20.18	5.941	0.235
$\delta^2E$	1.655	0.423	0.0147	0.089	0.432	0.542	1.116	0.935	0.223	0.009
$h^2b$	0.978	0.99	0.98	0.983	0.992	0.987	0.978	0.987	0.992	0.989
$h^2n$	0.854	0.581	0.869	0.578	0.945	0.858	0.772	0.726	0.802	0.704
$a$	0.381	0.844	0.363	0.836	0.223	0.387	0.517	0.599	0.488	0.635
$X$	75.03	32.5	8.273	13.303	125.4	150.4	25	48.45	49.02	2.97
EGA%	20.45	31.38	20.29	20.683	11.32	7.616	45.467	27.174	18.782	44.49

$\delta^2A$  Additive Variance,  $\delta^2D$  Dominance Variance,  $\delta^2E$  Environmental Variance,  $h^2b$  broad Heritability,  $h^2n$  Narrow Heritability,  $a$  Dominance Degree,  $X$  Mean of the respective cross **EGA%** expected genetic advance

The Data will analyze for estimating the **Heterosis** and **gcs** and **sca** for all the studied traits in all hybrid.

### Syrian Mapping Populations

450 genotypes obtained from the crossing of 3 parental lines were planted in Terbol. These were generated from:

Faraj: (*T. araraticum* F4/3/ARTHUR71/LAHN//BLK2/LAHN/4/QUARMAL) is a Moroccan cultivar released in 2007 for low moisture conditions, with a *T. araraticum* insertion that ensures resistance to Hessian Fly.

Nachit: (Amedakul1/TdicoSyrCol//Loukos) is a new variety from ICARDA also released for low moisture areas of Morocco in 2017. It is generated as a top cross with *T. dicoccum* collected from Syria and it is characterized by a deep root system, early flowering, and large yellow grains.

Jabal (Korifla/AegSpeltoidesSyr//Mrb5) is currently undergoing consideration for release, with the specific target of the Atlas Mountains, where in season rainfall does not exceed the 150 mm - 250 mm and the soil are extremely shallow. It is derived from a top cross with *Ae. Speltoides* and it is characterized by shallow root system adapted to soils with limited depth.

Finally, the elite line DAWRYT110 (Amedakul1/TdicoSyrCol//Cham1) when tested in 0.5 ha trials on farm under high moisture environments in Morocco (Fes and Meknes areas) it reached yields 50-80% superior to the most grown commercial variety, but it performed very poorly under dry conditions.

In 2015, ‘Jabal’, ‘Faraj’, and ‘DAWRYT110’ were cross polinated to ‘Nachit’ to create 3 half-sibs segregating populations.

P1. Nachit/DAWRYT110

P2. Nachit/Faraj

P3. Nachit/Jabal

These populations were advanced to F1 during the Terbol summer season, then during the winter season of Terbol 15 spikes were selected on the basis of fertility, height, and maturity, and bulk harvested to generate F1:3. These were planted under high temperatures and severe droughts during the summer cycle of Terbol, and the best ones bulk harvested. The F1:4 were then grown in Terbol normal season and 150 spikes were harvested from each population. The resulting F5 seeds were planted again in the off-season of Terbol and bulk harvested. Finally, 150 individual spike were collected and planted as F5:6 individuals for each population in 2017-18 season in Terbol for multiplication. The final mapping populations are as follows:

\*150 genotypes F5:6 with pedigree

Amedakul1/TdicoSyrCol//Loukos/3/Amedakul1/TdicoSyrCol//Cham1.

\*150 genotypes F5:6 with pedigree

Amedakul1/TdicoSyrCol//Loukos/3/Faraj.

\*150 genotypes F5:6 with pedigree

Amedakul1/TdicoSyrCol//Loukos/3/Korifla/AegsSpeltoidesSyr//Mrb5.

Several traits were already measured in Terbol season 2017-18:

### **Phonological Traits:**

#### **1. Days to heading (DTH):**

Number of days from germination date to the date at which 50% of main spike / plot will completely be emerged from the flag leaves.

#### **2. Days to physiological maturity (DTM):**

Number of days from germination date to the date at which 50% of main flag leaf and peduncles /plot will be turned to yellow color (physiological maturity).

#### **3-Grain Filling Period (GFP):**

Days to physiological maturity minus Days to heading.

#### **4- Grain Filling Rate (GFR):**

Grain yield/ Grain Filling Period according to (Golparvar, 2011).

### **Morphological Traits:**

#### **1. Plant height (PH) in cm:**

Measured as plant length from the soil surface to the tip of the spikes, excluding awns.

#### **2. Spike length (SL) in cm.**

### **Visual selection**

A score on a scale 1 to 5 was given based on the overall plant ideotype, assuming 3 as the score for the parents.

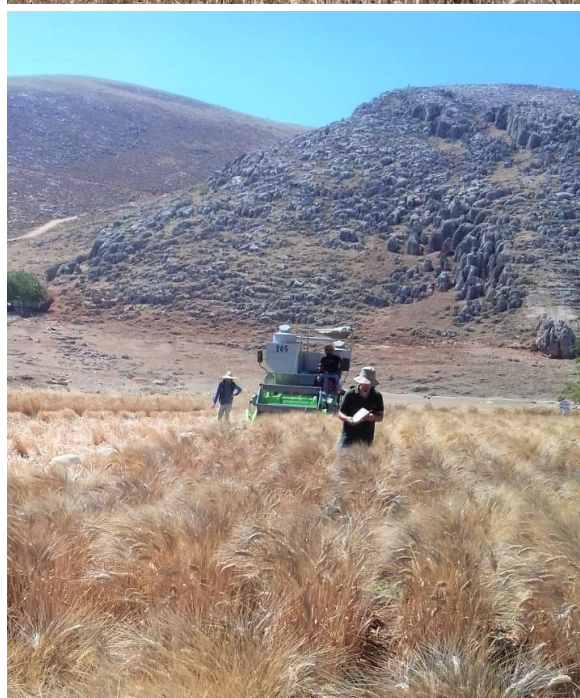
### **Yield components:**

The following traits were measured on 2 spike from each genotype:

Number of kernels per spike (KPS), grain weight of one spike, 1,000-kernels weight (TKW)

### **Harvesting and Grain yield**

Each row was harvested independently and the weight of the grains was measured.



## Results

The preliminary screening conducted in Terbol, reveal that the mapping populations segregated for a maximum of 10 days for flowering time, with only Nachit/Faraj presenting outlayer lines. Similarly, maturity was reached in a range of less than 10 days, with Nachit/Faraj showing the minimum variation. Grain filling period also had limited variation, especially for the Nachit/DAWRYT110 population. Some segregation could still be observed for plant height (PLH), with a range of 20 cm in almost all populations.

Concerning grain yield, transgressive segregation was observed for all three populations, with several entries beating their parents. Furthermore, good segregation for this trait could be observed with ranges from 1,100 Kg ha<sup>-1</sup> up to 10,000 Kg ha<sup>-1</sup>. Similarly, TKW, W.spk and GR.spk all segregated widely, with good transgressive segregations.

All together, these preliminary data suggest that phenology was substantially fixed, height range was limited, but response for grain yield and its components was maximized. As such, it does represent an ideal set of mapping populations for the discovery of yield related QTLs.

**Table 1. Average performances of the mapping populations compared to their parental lines**

MP	DtH	DtM	GFP	PLH	GY	TKW	GW.spk	K.spk	Spk.m
DAWRYT110	125	169	44	87	5,800	50	3.6	72	7.6
Faraj	125	172	47	89	7,150	50	4.1	80	8.1
Nachit	125	169	44	98	6,590	55	3.7	66	8.5
Jabal	127	169	42	84	6,110	53	4.2	78	8.5
Nachit/DAWRYT110	124	171	47	88	5,772	58	4.6	80	9.0
Nachit/Faraj	126	172	46	88	5,682	51	4.3	85	8.9
Nachit/Jabal	125	171	46	86	5,236	58	5.0	83	8.9

