

Table S1: Origin and year of release of the 16 genotypes of spring wheat used in the study.

Genotype	Genotypic type	Breeder/ Source	Year released or introduced
Heshangtou	Landrace	Landraces	Before 1900
Jinbaoyin	Landrace	Landraces	Before 1900
Gansu96	Cultivar	GAAS	1944
Dingxi24	Cultivar	DXAAS	1971
Longchun8275	Cultivar	GAAS	1982
021-128	Line	GAAS	1990
Dingxi35	Cultivar	DXAAS	1996
Longchun23	Cultivar	GAAS	2004
Xihan2	Cultivar	GAAS	2007
Longchun26	Cultivar	GAAS	2010
Dingxi43-4	Line	DXAAS	2011
NABUQ-6	Unknown	ICARDA	2012
DURRA-5	Cultivar	ICARDA	2012
Ganhan3	Line	GAAS	2013
Longchun30	Cultivar	GAAS	2013
Ganchun27	Cultivar	GAU	2016

DXAAS, Dingxi Academy of Agricultural Sciences; GAAS, Gansu Academy of Agricultural Sciences; GAU, Gansu Agricultural University; ICARDA, International Center for Agricultural Research in the Dry Areas.



Table S2. Grain yield (GY), spike number (SN), grain number (GN) per spike, 1000-kernel weight (KW), pre-anthesis biomass accumulation (Pre-ABA), post-anthesis biomass accumulation (Post-ABA), and harvest index (HI) of 16 genotypes of spring wheat at YZ and DX. The genotypes are ranked from lowest to highest according to the grain yield at YZ. Statistical significance: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. The values before the asterisks are the least significance differences (LSD) at $P = 0.05$.

Genotypes	GY (g m ⁻²)		SN (m ⁻²)		GN (spike ⁻¹)		1000-KW (g)		Pre-ABA(g m ⁻²)		Post-ABA (g m ⁻²)		HI	
	YZ	DX	YZ	DX	YZ	DX	YZ	DX	YZ	DX	YZ	DX	YZ	DX
Heshangtou	201.5	196.6	225.5	224.7	22.2	24.6	41.1	35.7	627.7	499.3	52.7	32.1	0.30	0.37
Ganhan3	210.3	195.4	198.5	154.0	24.1	30.2	45.6	41.9	481.7	433.3	60.5	65.6	0.39	0.39
021-128	234.1	182.8	239.7	184.5	29.0	33.1	34.1	32.2	474.3	285.2	71.7	116.1	0.42	0.43
Dingxi24	254.4	215.0	281.7	214.3	24.7	28.5	36.6	35.5	695.0	532.3	64.0	80.0	0.36	0.35
Gansu96	268.9	232.2	347.5	245.0	25.4	32.8	31.0	29.0	722.1	540.3	57.4	160.5	0.34	0.34
Longchun8275	279.8	264.6	235.0	200.5	24.6	30.8	49.2	43.1	678.8	426.6	111.6	236.3	0.35	0.40
Xihan2	292.3	232.6	222.3	163.5	30.2	36.5	43.6	39.0	643.4	445.5	98.2	164.1	0.38	0.37
Ganchun27	317.7	238.9	272.0	201.0	26.2	32.6	43.5	36.7	541.6	376.4	186.8	239.9	0.44	0.40
Jinbaoyin	326.2	195.2	361.0	238.0	28.0	26.5	33.3	27.7	778.6	455.2	180.5	95.0	0.34	0.32
Dingxi35	340.7	231.5	347.5	141.3	23.0	41.7	42.6	39.2	749.1	510.7	152.1	230.1	0.38	0.31
NABUQ-6	343.7	209.1	328.3	188.5	25.6	27.6	40.9	40.3	570.1	352.2	180.4	145.9	0.46	0.42
Longchun26	351.4	239.5	294.3	188.0	29.7	42.3	40.4	32.2	554.2	329.9	183.9	197.3	0.45	0.45
Dingxi43-4	375.9	267.6	464.5	237.0	25.4	35.6	34.0	31.7	596.6	376.5	217.6	248.5	0.46	0.43
Longchun23	390.3	269.6	298.3	226.7	33.2	36.0	40.3	32.9	514.2	354.1	260.9	267.2	0.50	0.43
Longchun30	431.6	274.1	300.0	226.7	31.7	33.8	45.7	35.8	592.2	376.3	274.5	245.3	0.50	0.44
DURRA-5	436.6	286.3	328.3	236.0	29.4	33.5	45.3	36.5	623.1	412.4	323.0	296.0	0.46	0.40
LSD _{P=0.05} :														
Genotype (G)	38.82***		46.61***		3.63***		2.03***		53.12***		46.59***		0.035***	
Environment (E)	13.73***		16.48***		1.28***		0.72***		18.78***		16.47*		0.012**	
G×E	54.90***		65.92**		5.13***		2.86***		75.12**		65.89**		0.049**	

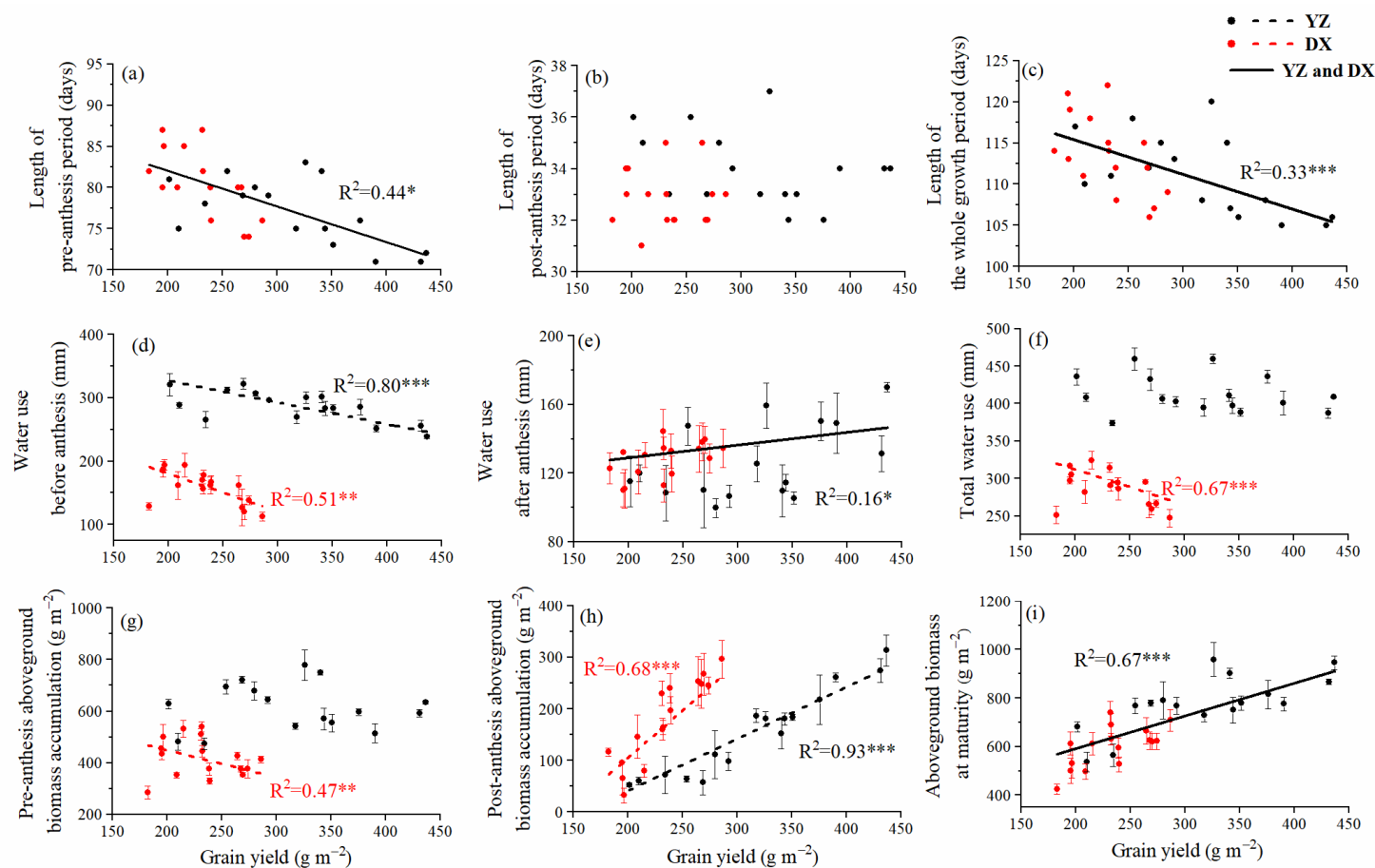


Figure S1. The relationship between grain yield and (a) length of pre-anthesis period, (b) length of post-anthesis period, (c) length of the entire growth period, (d) water use before anthesis, (e) water use after anthesis, (f) total water use from sowing to maturity, (g) accumulation of pre-anthesis aboveground biomass, (h) accumulation of post-anthesis aboveground biomass, and (i) aboveground biomass at maturity. Fitted data are the mean $\pm$ one standard error of the mean of three replications for 16 genotypes; a single regression is fitted where the two sites did not differ significantly and only the statistically significant linear regressions are shown. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

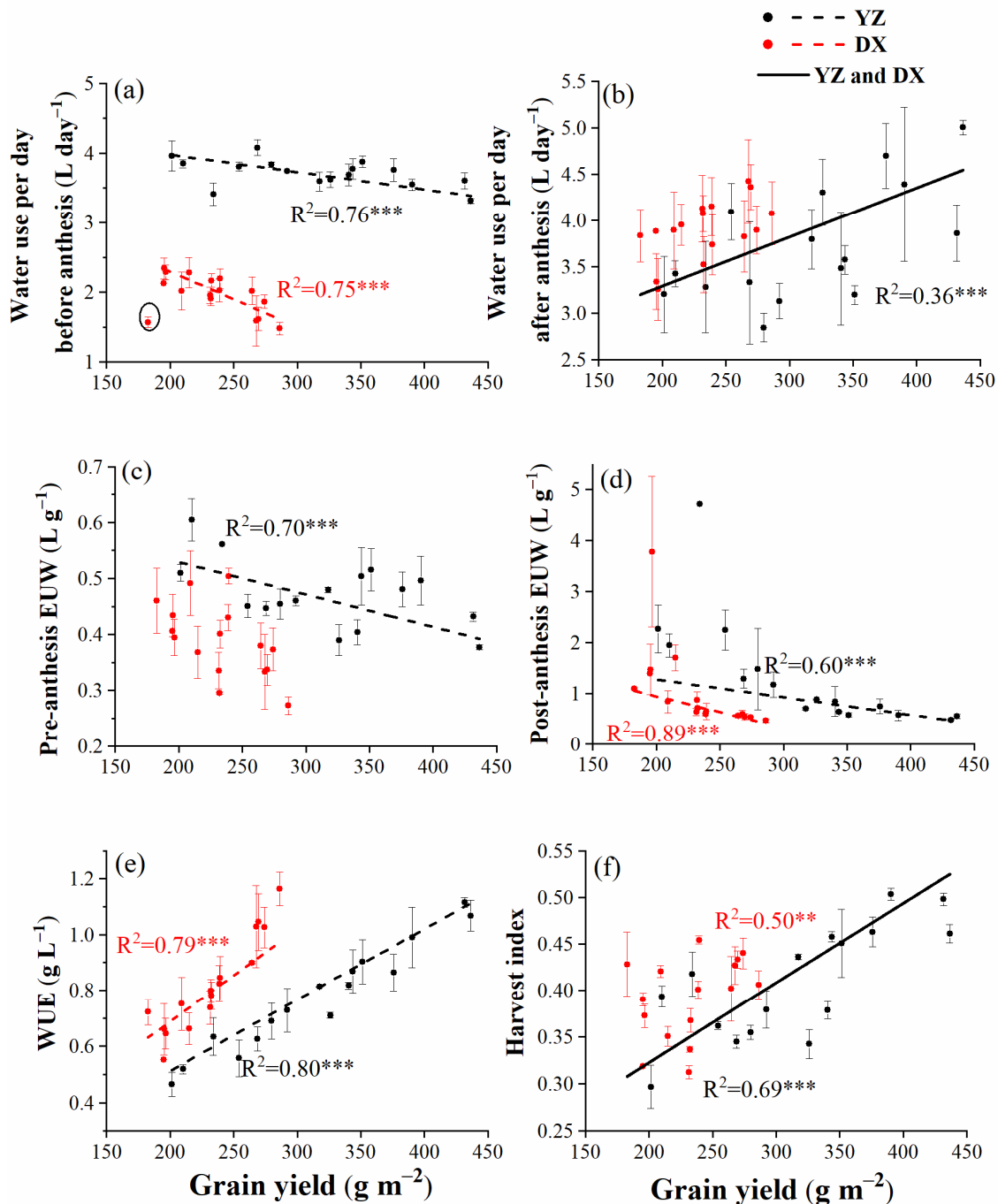


Figure S2. The relationship between grain yield and (a) water use per day before anthesis, (b) water use per day after anthesis, (c) Pre-anthesis effective use of water (EUW), (d) post-anthesis EUW, (e) water use efficiency (WUE), and (f) harvest index. Fitted data are the mean $\pm$ one standard error of the mean of three replications for 16 genotypes; a single regression is fitted where the two sites did not differ significantly and only the statistically significant linear regressions are shown.

The circled genotype in (a) is genotype 021-128, which is not included in the linear regression. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

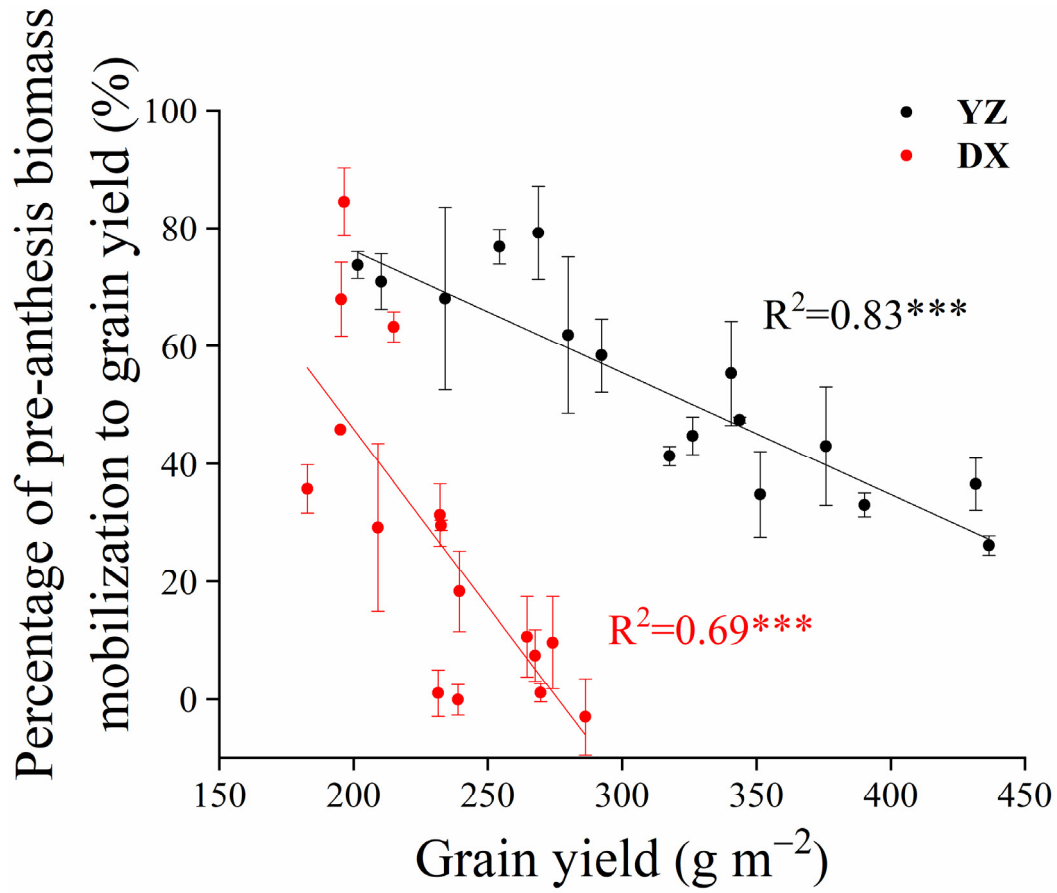


Figure S3. The relationship between grain yield and the percentage of pre-anthesis mobilization to grain yield. Fitted data are the mean $\pm$ one standard error of the mean of three replications for 16 genotypes. The significant linear regression equations are given. ***, $P < 0.001$.