## Responsive changes of DNA methylation in wheat (*Triticum aestivum*) under water deficit

Hongying Duan, Jingyun Li, Yanqiu Zhu, Wenjing Jia, Huihui Wang, Lina Jiang, Yanqing Zhou\*

## **Supplementary information**

Table S1 The sequence of adapters and primers in MSAP

Table S2 The cycling conditions in pre-amplification of MSAP

Table S3 The pattern of DNA methylation in wheat seedlings under water deficit

## **Supplementary information**

Table S1 The sequence of adapters and primers in MSAP

No.	Adapter and primer	Sequence		
1	EcoRI adapter	5'-CTCGTAGACTGCGTACC		
		CTGACGCATGGTTAA-5'		
2	MspI and HpaII adapter	5'-GACGATGAGTCTAGAA		
		CTACTCAGATCTTGC-5'		
3	MspI and HpaII adapter	5'- GATCATGAGTCCTGCT		
		GCTCGTCCTAGTACT-5'		
4	EcoRI pre-amplification primer	5'-GACTGCCTACCAATTCA-3'		
5	Mspl/HpaII pre-amplification primer	5'-GATGAGTCTAGAACGGT-3'		
6	Selective amplification primer	Eo: 5'-GACTGCCTACCAATTC		
		MHo: 5'-GATGAGTCTAGAACGGT		
7	EcoRI selective amplification primer	E1:Eo-AAC E2:Eo-AAG E3:Eo-ACA		
		E4:Eo-ACT E5:Eo-AGG E6:Eo-ACC		
		E7:Eo-ACG E8:Eo-AGC		
8	Mspl/HpaII selective amplification primer	MH4: MHo-ACA MH5: MHo-ACC		
		MH6: MHo-CCG MH7: MHo-ACT		
		МН8: МНо-ТАА		

Table S2 The cycling conditions in pre-amplification of MSAP

Cycle name	Temperature (°C)	Time	Number of cycles
Pre-PCR_1	72.0	1m	1
Pre-PCR_2	94.0	45s	
	65.0	30s	1
	72.0	1m	
Touch-down PCR	94.0	30s	
	64.3	30s	12
	72.0	1m	
PCR	94.0	30s	
	55.9	30s	20
	72.0	1m	
Elongation	72.0	30s	1
Store	4.0	-	-

The annealing temperature of Touch-down PCR was respectively  $64.3^{\circ}$ C,  $63.6^{\circ}$ C,  $62.9^{\circ}$ C,  $62.2^{\circ}$ C,  $61.5^{\circ}$ C,  $60.8^{\circ}$ C,  $60.1^{\circ}$ C,  $59.4^{\circ}$ C,  $58.7^{\circ}$ C,  $58.0^{\circ}$ C,  $57.3^{\circ}$ C and  $56.6^{\circ}$ C, respectively.

Table S3 The pattern of DNA methylation in wheat seedlings under water deficit

No.	Band				Change of methylation pattern		Type of methylation pattern
	H1	M1	Hx	Mx	СК	Treatment	
1	1	1	1	1	CCGG GGCC	CCGG GGCC	A1
2	1	0	1	0	CCGG CCGG GGCC GGCC	CCGG CCGG GGCC GGCC	A2 A
3	0	1	0	1	CCGG GGCC	CCGG GGCC	A3
4	1	1	1	0	CCGG GGCC	CCGG CCGG GGCC GGCC	B1
5	1	1	0	1	CCGG GGCC	CCGG GGCC	B2
6	0	1	0	0	CCGG GGCC	CCGG GGCC	B3 B
7	1	0	0	0	CCGG CCGG GGCC GGCC	CCGG GGCC	B4
8	1	1	0	0	CCGG GGCC	CCGG GGCC	B5
9	0	1	1	1	CCGG GGCC	CCGG GGCC	C1
10	1	0	1	1	CCGG CCGG GGCC GGCC	CCGG GGCC	C2
11	0	0	0	1	CCGG GGCC	CCGG GGCC	C C3
12	0	0	1	1	CCGG GGCC	CCGG GGCC	C4

H and M represented *EcoRI/HpaII* (H) and *EcoRI/MspI* (M), H1 and M1: bands amplified from genome of wheat seedlings under the normal condition, Hx and Mx: bands amplified from genome of wheat seedling treated with PEG<sub>6000</sub> solution. Scores of 1 and 0 indicated the presence or absence of bands in MSAP, "1 1", "1 0" and "0 1" was considered to be the pattern of non-methylation, hemi-methylation or full-methylation, respectively.