10.1071/FP21111

Functional Plant Biology

Supplementary Material

Site-specific, genotypic and temporal variation in photosynthesis and its related biochemistry in wheat (*Triticum aestivum*)

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Supplementary Table S1. Considered growth traits, their categories and growth stage/s of data collection of considered wheat genotypes.

Category	Trait	Growth stage/s of data collection		
	Total spike weight			
	Total above ground biomass (AGB)	Heading, 14-dpa, 30-dpa and Complete		
Growth-related traits	Total biomass (TB)	maturity (CM)		
	Plant height			
	Total biomass without spikes (BWS)			
	Photosynthesis area: total spikes (PAS)			
	Photosynthesis area: spike, main tiller			
	(PASM)			
	Photosynthesis area: total flag leaves (PAFL)			
	Photosynthesis area: flag leaf, main tiller			
Photosynthesis-related traits	(PAFLM)	Heading, 14-dpa and 30-dpa		
	Photosynthesis area: total leaves (PAL)			
	Photosynthesis area: total (PAT)			
	Spike area index (SAI)			
	Ratio between total spike area and total leaf			
	area (PAS/ PAL)			
	Harvest index (HI)	·		
Harvest-related traits	Total harvest (TH)	CM		
naivest-telated traits	Spike number	CIVI		
	Tiller number			

Supplementary Table S2. Summary of the multivariate analysis (after data transformation) showing the effect of genotype, organ type (spikes and flag leaves), growth stage and their interactions on Vc_{max} , J_{max} and TPU for wheat spikes and flag leaves. Abbreviations: ***, P < 0.001.

	Individual effect			Interaction effect			
Traits	Genotype effect	Organ type effect	Growth stage effect	Genotype X Organ type	Genotype X Growth stage	Organ type X Growth stage	Genotype X Organ type X Growth stage
Vc_{max}	***	***	***	***	***	***	**
(μ mol CO ₂ m ⁻² s ⁻¹) J_{max} (μ molem ⁻² s ⁻¹)	***	***	***	***	***	***	***
<i>TPU</i> (μmol m ⁻² s ⁻¹)	***	***	***	***	***	***	**

Supplementary Table S3. Summary of multivariate analysis showing multiple comparisons of Vc_{max} , J_{max} and TPU between growth stages. Abbreviation: 3 dpa, three days post anthesis; 14 dpa, fourteen days post anthesis; 30 dpa, thirty days post anthesis; ns, not significant; *, P < 0.05; **, P < 0.01; ***, P < 0.001.

		Spikes					
Growth stage	e comparison			Trait	iits		
stage a	stage b	Vc_{max}	J_{max}	TPU	Vc_{max}	J_{max}	TPU
Heading	3-dpa	**	**	ns	ns	ns	ns
Heading	14-dpa	**	*	*	***	***	**
Heading	30-dpa	*	**	**	***	***	***
3-dpa	14-dpa	***	***	***	**	***	**
3-dpa	30-dpa	ns	ns	ns	***	***	***
14-dpa	30-dpa	***	***	***	***	***	***

Supplementary Table S4. Multiple comparisons of Vc_{max} , J_{max} and TPU between wheat genotypes. Summary of multivariate analysis is shown (transformed data: square root). Abbreviations: 3 dpa, three days post anthesis; 14 dpa, fourteen days post anthesis; 30 dpa, thirty days post anthesis; ns, not significant; *, P < 0.05; **, P < 0.01; ***, P < 0.001.

			Spikes			Flag leaves	
Genotype	comparison	Traits					
Genotype a	Genotype b	Vc_{max}	J_{max}	TPU	Vc_{max}	J_{max}	TPU
Huandoy	Amurskaja 75	ns	ns	ns	ns	*	*
Huandoy	Greece 25	***	***	***	ns	ns	*
Amurskaja 75	Greece 25	***	***	***	ns	ns	ns

Supplementary Table S5. List of primer sequences of genes selected for qRT-PCR

Primer abbreviation	Sequence (5'3')	Metabolism	Reference	
rbcL	F: GGCTGCAGTAGCTGCCGAATCT			
rocL	R: TCCCCAGCAACAGGCTCGATGT			
rbcS	F: AGCCTCAGCAGCGTCAGCAAT			
1003	R: CGTGGATAGGGGTGGCAGGTAAGA			
SPP1	F: GCGCACGGGAAGGAGTTTTTCTTCT	Rubisco biosynthesis and	Vicente et al, 2015	
SFF1	R: GACCTCCGTAGACATCATCCAGCCC	sucrose metabolism	vicente et ai, 2013	
SPS1	F: AGAAGGCTCTGCCTCCCATTTGGTC			
SFS1	R: AGGATCATCGGCTTGTGCGGGTT			
SUS1	F: GTATGTTCACCAGGGCAAGGGCA			
3031	R: GGCGTCAAACTCAGCAAGCAGC			
4DD : 1 : C :	F: GCTCTCCAACAACATTGCCAAC		Vicente et al, 2015	
ADP riosylation factor	R: GCTTCTGCCTGTCACATACGC			
TaActin-F TaSand-F	F: TTGCTGACCGTATGAGCAAG	Housekeeping genes		
	R: ACCCTCCAATCCAGACACTG		Bachir et al. 2017	
	F: TGCCTTGCCCATAAGAAATC		Dacini et al. 2017	
1uSunu-1	R: GTGCGGACCAGTTGCTTTAT			