

Supplementary Material

Expression of key auxin biosynthesis genes correlates with auxin and starch content of developing wheat (*Triticum aestivum*) grains

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Table S1. Primers used for expression analysis of *TaTAR2* and *TaYUC* genes

Gene group	Primer sequence	Product size (bp)
<i>TaTAR2-A1</i>	F: 5'-CTACTACTCGTCGTACCCTGCC-3'	251
<i>TaTAR2-B1</i>	R: 5'-CGGTGAAGAGCATGATGTTCG-3'	
<i>TaTAR2-D1</i>		
<i>TaTAR2-A2</i>	F: 5'-CGACCATGTTTGAGGCCTTC-3'	114
<i>TaTAR2-B2</i>	R: 5'-CCATGAACCAGCACACGTTA-3'	
<i>TaTAR2-D2</i>		
<i>TaTAR2-A3</i>	F: 5'-TCATGCTCTTCACCGTGTCA-3'	113
<i>TaTAR2-B3</i>	R: 5'-GCTTTGCTCCATGAACTTGC-3'	
<i>TaTAR2-D3</i>		
<i>TaTAR2-A4</i>	F: 5'-ATCAACCTCGAGCTCGGC-3'	117
<i>TaTAR2-B4</i>	R: 5'-CTGGGCATTGGAGAAGTAGC-3'	
<i>TaTAR2-A5</i>	F: 5'-CACATGCATCGTCTCATCCC-3'	122
	R: 5'-ACCACTGCCTTATTGCTCCT-3'	
<i>TaTAR2-B5</i>	F: 5'-TTAGAAGAAGGGTGACGCGT-3'	186
<i>TaTAR2-B6</i>	R: 5'-GTCGCCGGTTTATGTGGTAC-3'	
<i>TaTAR2-U</i>		
<i>TaYUC9-A1</i>	F: 5'-ACCAAGGAGATCTGGAACGT-3'	164
<i>TaYUC9-B</i>	R: 5'-GGGGTGTGGATCTTCATGGA-3'	
<i>TaYUC9-D1</i>		
<i>TaYUC9-A2</i>	F: 5'-ACGAGGGAGATCATGAACGC-3'	204
<i>TaYUC9-D2</i>	R: 5'-GATCTTGTCGTAGGTGCCGA-3'	
<i>TaYUC10-A</i>	F: 5'-GTCCGATTCATGTAATGACAAAG-3'	209
<i>TaYUC10-B1</i>	R: 5'-GGTGCCAACATCAATCACTG-3'	
<i>TaYUC10-B2</i>		
<i>TaYUC10-D</i>		
<i>TaYUC11-A1</i>	F: 5'-CCAGAGATCGTTGGCCTACA-3'	108
<i>TaYUC11-A2</i>	R: 5'-CCCACATCCAACAACAAGCA-3'	
<i>TaYUC11-D</i>		

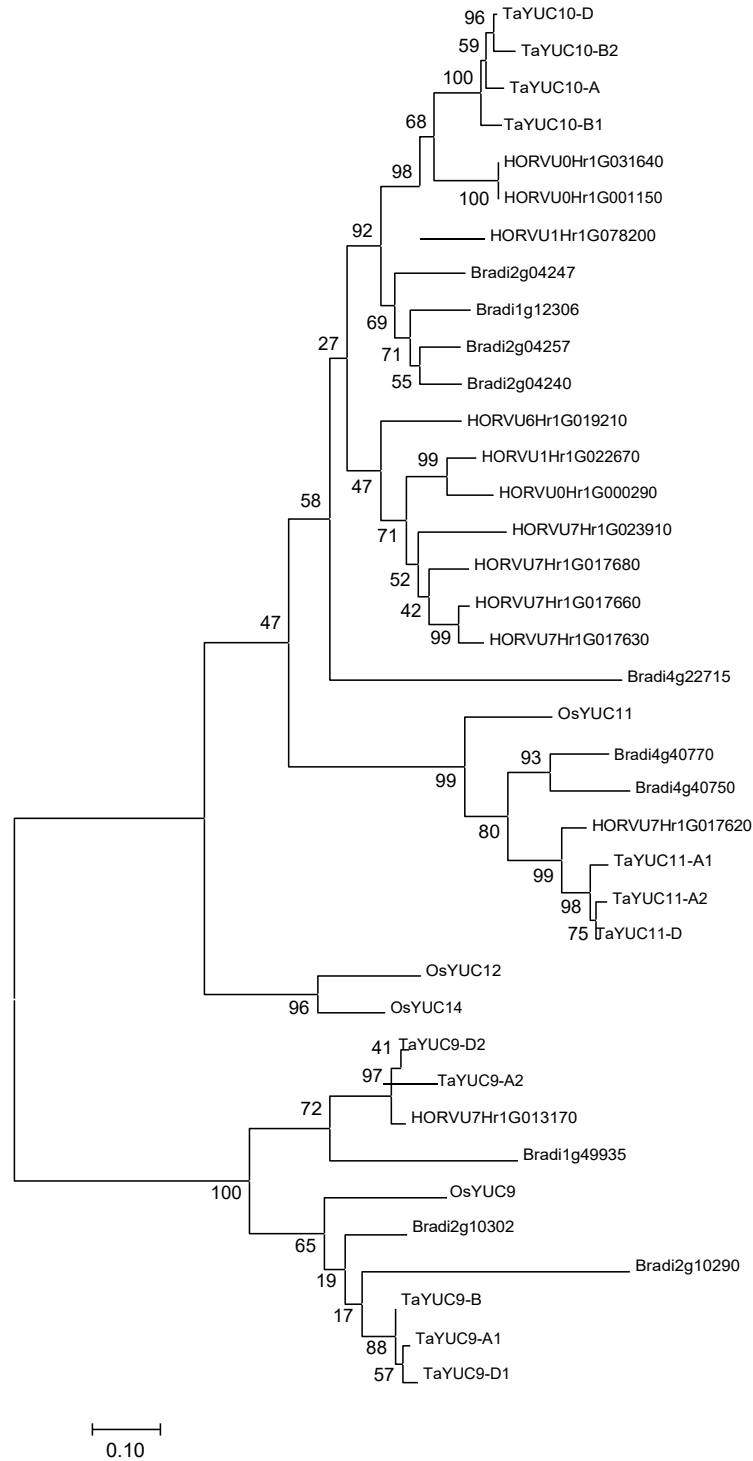


Fig. S1. Phylogenetic tree showing relationships between Clade II YUCCA proteins from *Triticum aestivum* (TaTAR), *Oryza sativa* (OsTAR), *Brachypodium distachyon* (Brad) and *Hordeum vulgare* (HORVU). The tree was constructed in MEGA7.0.26 (Kumar *et al.*, 2016) using the Maximum Likelihood method (Jones *et al.* 1992). Multiple sequence alignment was performed by MUSCLE (Edgar 2004). Bootstrap confidence levels were obtained using 500 replicates (Felsenstein 1985). Evolutionary distances were computed using Poisson correction method (Zuckerandl and Pauling 1965). Scale bar = 0.10, amino acid substitutions per site.

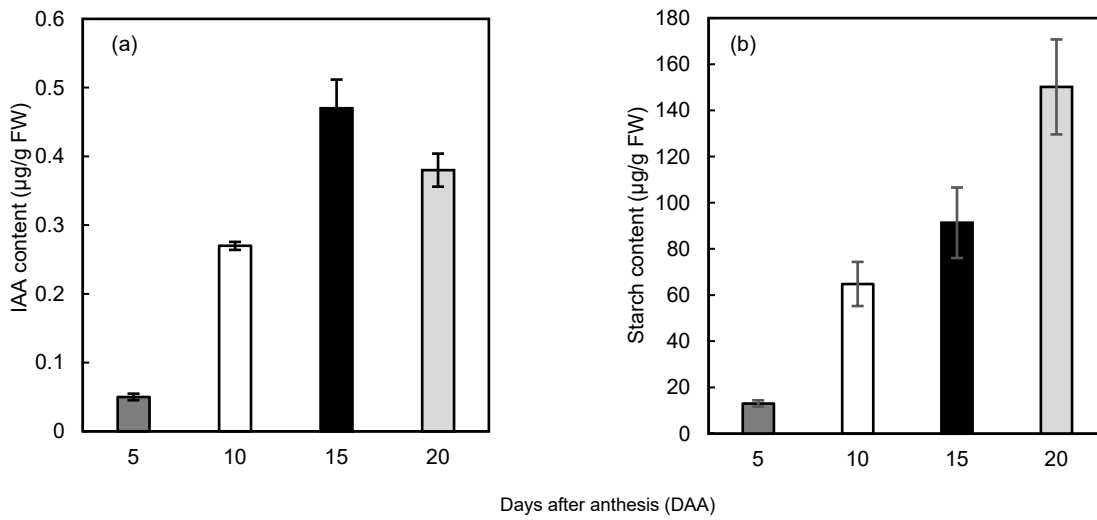


Fig. S2. Measurements of (a) IAA and (b) starch content in μg per g FW from 5, 10, 15 and 20 DAA wheat grain samples. All data points represent the mean of three biological replicates \pm the standard error of the means.