

DWARF TILLER₁, a WUSCHEL-Related Homeobox Transcription Factor, Controls Tillering and Growth in Rice

PLoS Genetics

10, e1004154

DOI: [10.1371/journal.pgen.1004154](https://doi.org/10.1371/journal.pgen.1004154)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Heterologous over-expression of ACC SYNTHASE8 (ACS8) in <i>Populus tremula</i> x <i>P. alba</i> clone 717-1B4 results in elevated levels of ethylene and induces stem dwarfism and reduced leaf size through separate genetic pathways. <i>Frontiers in Plant Science</i> , 2014, 5, 514.	3.6	12
2	The rice <i>WUSCHEL</i> -related homeobox genes are involved in reproductive organ development, hormone signaling and abiotic stress response. <i>Gene</i> , 2014, 549, 266-274.	2.2	74
3	Improving rice tolerance to potassium deficiency by enhancing <i>OsHAK16p:WOX11</i> -controlled root development. <i>Plant Biotechnology Journal</i> , 2015, 13, 833-848.	8.3	79
4	Transcriptional regulation of the paper mulberry under cold stress as revealed by a comprehensive analysis of transcription factors. <i>BMC Plant Biology</i> , 2015, 15, 108.	3.6	81
5	MONOCULM 3, an Ortholog of <i>WUSCHEL</i> in Rice, Is Required for Tiller Bud Formation. <i>Journal of Genetics and Genomics</i> , 2015, 42, 71-78.	3.9	121
6	The <i>qTSN</i> Positive Effect on Panicle and Flag Leaf Size of Rice is Associated with an Early Down-Regulation of Tillering. <i>Frontiers in Plant Science</i> , 2015, 6, 1197.	3.6	14
7	MicroRNAs in Control of Plant Development. <i>Journal of Cellular Physiology</i> , 2016, 231, 303-313.	4.1	276
8	Sub-Functionalization in Rice Gene Families with Regulatory Roles in Abiotic Stress Responses. <i>Critical Reviews in Plant Sciences</i> , 2016, 35, 231-285.	5.7	3
9	The evolution of inflorescence diversity in the nightshades and heterochrony during meristem maturation. <i>Genome Research</i> , 2016, 26, 1676-1686.	5.5	51
10	<i>OsWOX3A</i> is involved in negative feedback regulation of the gibberellic acid biosynthetic pathway in rice (<i>Oryza sativa</i>). <i>Journal of Experimental Botany</i> , 2016, 67, 1677-1687.	4.8	58
11	Identification and Functional Divergence Analysis of <i>WOX</i> Gene Family in Paper Mulberry. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1782.	4.1	24
12	Recruitment of <i>IC-WOX</i> Genes in Root Evolution. <i>Trends in Plant Science</i> , 2018, 23, 490-496.	8.8	37
13	Lack of the β 1,3-Fucosyltransferase Gene (<i>Osfuct</i>) Affects Anther Development and Pollen Viability in Rice. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1225.	4.1	13
14	Quantitative Changes in the Transcription of Phytohormone-Related Genes: Some Transcription Factors Are Major Causes of the Wheat Mutant <i>dmc</i> Not Tillering. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1324.	4.1	22
15	Plant Stature Related receptor-like Kinase2 (<i>PSRK2</i>) acts as a factor that determines stem elongation toward gibberellins response in rice. <i>Bioscience, Biotechnology and Biochemistry</i> , 2018, 82, 1931-1941.	1.3	5
16	A web-based tool for the prediction of rice transcription factor function. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	7
17	Mutations in the microRNA172 binding site of SUPERNUMERARY BRACT (<i>SNB</i>) suppress internode elongation in rice. <i>Rice</i> , 2019, 12, 62.	4.0	19
18	How plants grow up. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 257-277.	8.5	31

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20	A mutation in the intron splice acceptor site of a GA3ox gene confers dwarf architecture in watermelon (<i>Citrullus lanatus</i> L.). <i>Scientific Reports</i> , 2020, 10, 14915.	3.3	16
21	Rice dwarf and low tillering 10 (OsDLT10) regulates tiller number by monitoring auxin homeostasis. <i>Plant Science</i> , 2020, 297, 110502.	3.6	16
22	The Rice Basic Helix-Loop-Helix 79 (OsbHLH079) Determines Leaf Angle and Grain Shape. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2090.	4.1	16
23	Genome-wide analysis of CsWOX transcription factor gene family in cucumber (<i>Cucumis sativus</i> L.). <i>Scientific Reports</i> , 2020, 10, 6216.	3.3	16
24	Identification and fine mapping of a multi-tillering semi-dwarf gene in rice. <i>Euphytica</i> , 2021, 217, 1.	1.2	0
25	Integration of high-density genetic mapping with transcriptome analysis uncovers numerous agronomic QTL and reveals candidate genes for the control of tillering in sorghum. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	4
26	What Does the WOX Say? Review of Regulators, Targets, Partners. <i>Molecular Biology</i> , 2021, 55, 311-337.	1.3	20
27	Conserved pleiotropy of an ancient plant homeobox gene uncovered by cis-regulatory dissection. <i>Cell</i> , 2021, 184, 1724-1739.e16.	28.9	103
28	A cluster of Ankyrin and Ankyrin-TPR repeat genes is associated with panicle branching diversity in rice. <i>PLoS Genetics</i> , 2021, 17, e1009594.	3.5	3
29	Genome-Wide Association Study of the Genetic Basis of Effective Tiller Number in Rice. <i>Rice</i> , 2021, 14, 56.	4.0	14
30	OsCKX5 Modulates Root System Morphology and Increases Nutrient Uptake in Rice. <i>Journal of Plant Growth Regulation</i> , 2022, 41, 2157-2170.	5.1	2
31	Dissection of the Genetic Basis of Rice Panicle Architecture Using a Genome-wide Association Study. <i>Rice</i> , 2021, 14, 77.	4.0	10
35	A Sheathed Spike Gene, TaWUS-like Inhibits Stem Elongation in Common Wheat by Regulating Hormone Levels. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11210.	4.1	8
36	The rice phosphoinositide-specific phospholipase C3 is involved in responses to osmotic stresses via modulating ROS homeostasis. <i>Plant Science</i> , 2021, 313, 111087.	3.6	4
37	A Genome-Wide Association Study Pinpoints Quantitative Trait Genes for Plant Height, Heading Date, Grain Quality, and Yield in Rye (<i>Secale cereale</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 718081.	3.6	12
39	SMALL REPRODUCTIVE ORGANS, a SUPERMAN-like transcription factor, regulates stamen and pistil growth in rice. <i>New Phytologist</i> , 2022, 233, 1701-1718.	7.3	11
40	miRNAomic Approach to Plant Nitrogen Starvation. <i>International Journal of Genomics</i> , 2021, 2021, 1-14.	1.6	3

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41	<i>WUSCHEL</i> -related homeobox family genes in rice control lateral root primordium size. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	26
42	Identification and Validation of Quantitative Trait Loci Mapping for Spike-Layer Uniformity in Wheat. International Journal of Molecular Sciences, 2022, 23, 1052.	4.1	3
43	A rice single cell transcriptomic atlas defines the developmental trajectories of rice floret and inflorescence meristems. New Phytologist, 2022, 234, 494-512.	7.3	41
45	The auxin-responsive transcription factor SIDOF9 regulates inflorescence and flower development in tomato. Nature Plants, 2022, 8, 419-433.	9.3	12
46	<i>WUSCHEL</i> -related homeobox genes cooperate with cytokinin to promote bulbil formation in <i>Lilium lancifolium</i> . Plant Physiology, 2022, 190, 387-402.	4.8	15
47	Genome-wide identification, expression analyses of Wuschel-related homeobox (WOX) genes in <i>Brachypodium distachyon</i> and functional characterization of BdWOX12. Gene, 2022, 836, 146691.	2.2	1
48	PtrWOX13A Promotes Wood Formation and Bioactive Gibberellins Biosynthesis in <i>Populus trichocarpa</i> . Frontiers in Plant Science, 0, 13, .	3.6	1
49	Genetic and molecular pathways controlling rice inflorescence architecture. Frontiers in Plant Science, 0, 13, .	3.6	4
50	Dynamic Transcriptome Changes Driven by the Mutation of OsCOP1 Underlie Flavonoid Biosynthesis and Embryogenesis in the Developing Rice Seed. Journal of Plant Growth Regulation, 2023, 42, 4436-4452.	5.1	4
51	High-resolution genetic linkage map and height-related QTLs in an oil palm (<i>Elaeis guineensis</i>) family planted across multiple sites. Physiology and Molecular Biology of Plants, 0, , .	3.1	0
52	Pan-genome Analysis of WOX Gene Family and Function Exploration of CsWOX9 in Cucumber. International Journal of Molecular Sciences, 2023, 24, 17568.	4.1	0
53	The roles of non-coding RNAs in male reproductive development and abiotic stress responses during this unique process in flowering plants. Plant Science, 2024, 341, 111995.	3.6	1
54	Identification and Expression Patterns of WOX Transcription Factors under Abiotic Stresses in <i>Pinus massoniana</i> . International Journal of Molecular Sciences, 2024, 25, 1627.	4.1	0