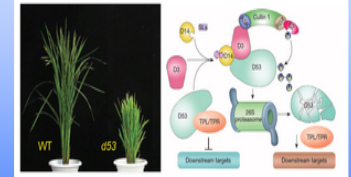




# 植物基因组学国家重点实验室

State Key Laboratory of Plant Genomics (SKLPG)  
Institute of Genetics and Developmental Biology, Institute of Microbiology  
Chinese Academy of Sciences



**DWARF 53 acts as a repressor of strigolactone signalling in rice (*Nature* 504: 401-405, 2013)**

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## 科研工作

- ❖ 在研课题
- ❖ 专利
- ❖ 出版物
- ❖ 发表论文

## 2017年

序号	作者	文章题目	杂志	年卷页	影响因子	类型
1	Song, X.#, Lu, Z.#, Yu, H.#, Shao, G., Xiong, J., Meng, X., Jing, Y., Liu, G., Xiong, G., Duan, J., Yao, X., Liu, C., Li, H., Wang, Y., and Li, J.*	IPA1 functions as a downstream transcription factor repressed by D53 in strigolactone signaling in rice	<i>Cell Res</i>	2017, 27: 1128-1141	15.606	A
2	Bi, G., and Zhou J.M.*	MAP kinase signaling pathways: a hub of plant-microbe interactions	<i>Cell Microbe</i>	<i>Host</i> 2017, 21: 270-273	14.946	A
3	Hu, J.#, Yang, H.#, Mu, J., Lu, T., Peng, J., Deng, X., Kong, Z., Bao, S., Cao, X., and Zuo, J.*	Nitric oxide regulates protein methylation during stress responses in plants	<i>Mol Cell</i>	2017, 67: 702-710	14.714	A
4	Du, H.#, Yu, Y.#, Ma, Y.#, Gao, Q.#, Cao, Y.#, Chen, Z., Ma, B., Qi, M., Li, Y., Zhao, X., Wang, J., Liu, K., Qin, P., Yang, X., Zhu, L., Li, S.*, and Liang, C.*	Sequencing and <i>de novo</i> assembly of a near complete <i>indica</i> rice genome	<i>Nat Commun</i>	2017, 8: 15324	12.124	A
5	Wang, H., Vieira, F., Crawford, J., Chu, C.*, and Nielsen, R.*	Asian wild rice is a hybrid swarm with extensive gene flow and feralization from domesticated rice	<i>Genome Res</i>	2017, 27: 1029-1038	11.922	A
6	Yang, Y.#, Zhang, X.#, Ma, X.#, Zhao, T.#, Sun, Q., Huan, Q., Wu, S., Du, Z.*, and Qian, W.*	<i>Trans</i> -splicing enhances translational efficiency in <i>C. elegans</i>	<i>Genome Res</i>	2017, 27: 1525-1535	11.922	A
7	Song, X., and Cao, X.*	Context and complexity: analyzing methylation in trinucleotide	<i>Trends Plant Sci</i>	2017, 22: 351-353	11.911	A

		sequences				
8	Yu, F., and Xie, Q.*	Non-26S proteasome endomembrane trafficking pathways in ABA signaling	<i>Trends Sci</i>	<i>Plant</i> 2017, 22: 976-985	11.911	A
9	Hu, B.*, and Chu, C.*	Node-based transporter: switching phosphorus distribution	<i>Nat Plants</i>	2017, 3: 17002	10.300	A
10	Zhang, B.#, Zhang, L.#, Li, F.#, Zhang, D., Liu, X., Wang, H., Xu, Z., Chu, C.*, and Zhou, Y.*	Control of secondary cell wall patterning involves xylan deacetylation by a GDSE esterase	<i>Nat Plants</i>	2017, 3: 17017	10.300	A
11	Tang, J.*, and Chu, C.*	MicroRNAs in crop improvement: fine-tuners for complex traits	<i>Nat Plants</i>	2017, 3: 17077	10.300	A
12	Yin, K., Gao, C.*, and Qiu, J.*	Progress and prospects in plant genome editing	<i>Nat Plants</i>	2017, 3: 17107	10.300	A
13	Qi, J.#, Wu, B.#, Feng, S.#, Lü, S., Guan, C., Zhang, X., Qiu, D., Hu, Y., Zhou, Y., Li, C., Long, M.*, and Jiao, Y.*	Mechanical regulation of organ asymmetry in leaves	<i>Nat Plants</i>	2017, 3: 724-733	10.300	A
14	Wang, C.#, Liu, W.#, Wang, G.#, Li, J., Dong, L., Han, L., Wang, Q., Tian, J., Yu, Y., Gao, C., and Kong, Z.*	KTN80 confers precision to microtubule severing by specific targeting of katanin complexes in plant cells	<i>EMBO J</i>	2017, 36: 3435-3447	9.792	A
15	Guan, C., Wu, B., Yu, T., Wang, Q., Krogan, T., Liu, X., and Jiao, Y.*	Spatial auxin signaling controls leaf flattening in <i>Arabidopsis</i>	<i>Curr Biol</i>	2017, 27: 2940-2950	8.851	A
16	Lin, T.#, Xu, X.#, Ruan, J.#, Liu, S., Wu, S., Shao, X., Wang, X., Gan, L., Qin, B., Yang, Y., Cheng, Z., Yang, S., Zhang, Z., Xiong, G., Huang, S., Yu, H.*, and Li, J.*	Genome analysis of <i>Taraxacum kok-saghyz</i> Rodin provides new insights into rubber biosynthesis	<i>Natl Sci Rev</i>	2017, 0: 1-12	8.843	A
17	Meng, X.#, Yu, H.#, Zhang, Y., Zhuang, F., Song, X., Gao, S., Gao, C.*, and Li, J.*	Construction of a genome-wide mutant library in rice using CRISPR/Cas9	<i>Mol Plant</i>	2017, 10: 1238-1241	8.827	A
18	Lu, X., Xiong, Q., Cheng, T., Li, Q., Liu, X., Bi, Y., Li, W., Zhang, W., Ma, B., Lai, Y., Du, W., Man, W., Chen, S.*, and Zhang, J.*	A <i>PP2C-1</i> allele underlying a quantitative trait locus enhances soybean 100-seed weight	<i>Mol Plant</i>	2017, 10: 670-684	8.827	A
19	Chen, Q., Liu, R., Wang, Q., and Xie, Q.*	ERAD tuning of the HRD1 complex component AtOS9 is modulated by an ER-bound E2, UBC32	<i>Mol Plant</i>	2017, 39: 692-706	8.827	A
20	Xiong, Q.#, Ma, B.#*, Lu, X.#, Huang, Y., He, S., Yang, C., Yin, C., Zhao, H., Zhou, Y., Zhang, W., Wang, W., Li, Z., Chen, S.*, and Zhang, J.*	Ethylene-inhibited jasmonic acid biosynthesis promotes mesocotyl/coleoptile elongation of etiolated rice seedlings	<i>Plant Cell</i>	2017, 29: 1053-1072	8.726	A
21	Wang, J., Tian, C., Zhang, C., Shi, B., Cao, X., Zhang, T., Zhao, Z., Wang, J., and Jiao, Y.*	Cytokinin signaling activates <i>WUSCHEL</i> expression during axillary meristem initiation	<i>Plant Cell</i>	2017, 29: 1374-7387	8.726	A
22	Hu, Q.#, Li, Y.#, Wang, H., Shen, Y., Zhang,	Meiotic chromosome association	<i>Plant Cell</i>	2017, 29: 1	8.726	A

	C., Du, G., Tang, D., and Cheng, Z.*	interacts with TOP3 $\alpha$ and regulates meiotic recombination in rice		1697-1708		
23	Zhang, F.#, Tang, D.#, Shen, Y., Xue, Z., Shi, W., Ren, L., Du, G., Li, Y., and Cheng, Z.*	The F-Box protein ZYGO1 mediates bouquet formation to promote homologous pairing, synapsis, and recombination in rice meiosis	<i>Plant Cell</i>	2017, 29: 2597-2609	8.726	A
24	Wang, J.#, Yu, H.#, Xiong, G., Lu, Z., Jiao, Y., Meng, X., Liu, G., Chen, X., Wang, Y.*, and Li, J.*	Tissue-specific ubiquitination by IPA1 INTERACTING PROTEIN1 modulates IPA1 protein levels to regulate plant architecture in rice	<i>Plant Cell</i>	2017, 29: 697-707	8.726	A
25	Wang, F., Cheng, S., Wu, Y., Ren, B., and Qian, W.*	A bacterial receptor PcrK senses the plant hormone cytokinin to promote adaptation to oxidative stress	<i>Cell Rep</i>	2017, 21: 2940-2951	8.282	A
26	Ni, M.#, Ma, W.#, Wang, X.#, Gao, M.#, Dai, Y., Wei, X., Zhang, L., Peng, Y., Chen, S., Ding, L., Tian, Y., Li, J., Wang, H., Wang, X., Xu, G., Guo, W., Yang, Y., Wu, Y., Heuberger, S., Tabashnik, B.*, Zhang, T.*, and Zhu, Z.*	Next-generation transgenic cotton: pyramiding RNAi and Bt counters insect resistance	<i>Plant Biotechnol J</i>	2017, 15: 1204-1213	7.443	A
27	Deng, X., and Cao, X.*	Roles of pre-mRNA splicing and polyadenylation in plant development	<i>Curr Opin Plant Biol</i>	2017, 35: 45-53	7.357	A
28	Song, X., and Cao, X.*	Transposon-mediated epigenetic regulation contributes to phenotypic diversity and environmental adaptation in rice	<i>Curr Opin Plant Biol</i>	2017, 36: 111-118	7.357	A
29	Zhang, L.#, Ni, H.#, Du, X., Wang, S., Ma, X., Numberger, T., Guo, H.*, and Hua, C.*	The <i>Verticillium</i> -specific protein VdSCP7 localizes to the plant nucleus and modulates immunity to fungal infections	<i>New Phytol</i>	2017, 215: 368-381	7.330	A
30	Zhou, L.#, Zhao, P.#, Chi, Y., Wang, D., Wang, P., Liu, N., Cai, D.*, Wu, Z.*, and Zhong, N.*	Controlling the hydrolysis and loss of nitrogen fertilizer (urea) by using a nanocomposite favors plant growth	<i>ChemSusChem</i>	2017, 10: 2068-2079	7.226	A
31	Cai, Z.#, Yuan, Z.#, Zhang, H., Pan, Y., Wu, Y., Tian, X., Wang, F., and Qian, W.*	Fatty acid DSF binds and allosterically activates histidine kinase RpfC of phytopathogenic bacterium <i>Xanthomonas campestris</i> pv. <i>campestris</i> to regulate quorum-sensing and virulence	<i>PLoS Pathog</i>	2017, 13: e1006304	6.608	A
32	Zhou, T., Zhao, Y., and Guo, H.*	Secretory proteins are delivered to the septin-organized penetration interface during root infection by <i>Verticillium dahliae</i>	<i>PLoS Pathog</i>	2017, 13: e1006275	6.608	A
33	Li, Q., Lu, X., Song, Q., Chen, H., Wei, W., Tao, J., Bian, X., Shen, M., Ma, B., Zhang,	Selection for a zinc-finger protein contributes to seed oil increase during soybean domestication	<i>Plant Physiol</i>	2017, 173: 2208-2224	6.456	A

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48	Peng, B.#, Pan, Y.#, Li, R.#, Wei, J., Liang, F., Wang, L., Wang, F., and Qian, W.*	An essential regulatory system originating from polygenic transcriptional rewiring of PhoP-PhoQ of <i>Xanthomonas campestris</i>	<i>Genetics</i>		2017, 206: 2207-2223	4.556	A	
49	Wu, S.#*, Li, K.#, Li, Y., Zhao, T., Li, T., Yang, Y., and Qian, W.*	Independent regulation of gene expression level and noise by histone modifications	<i>PLoS Biol</i>	<i>Comput</i>	2017, 13: e1005585	4.542	A	
50	Xu, N., Luo, X., Li, W., Wang, Z., and Liu, J.*	The bacterial effector AvrB-induced RIN4 hyperphosphorylation is mediated by receptor-like cytoplasmic kinase complex in <i>Arabidopsis</i>	<i>Mol Microbe Interact</i>	<i>Plant</i>	2017, 30: 502-512	4.332	A	
51	Xiao, Y., Liu, D., Zhang, G., Tong, H.*, and Chu, C.*	Brassinosteroids regulate OFP1, a DLT interacting protein, to modulate plant architecture and grain morphology in rice	<i>Front Plant Sci</i>		2017, 1: 5125	4.291	A	
52	Bai, C.#, Wang, P.#, Fan, Q., Fu, W., Wang, L., Zhang, Z., Song, Z., Zhang, G.*, and Wu, J.*	Analysis of the role of the drought-induced gene <i>DR15</i> and salinity-induced gene <i>SI1</i> in <i>Alternanthera philoxeroides</i> plasticity using a virus-based gene silencing tool	<i>Front Plant Sci</i>		2017, 8: 1579	4.291	A	
53	Yin, C., Zhao, H., Ma, B., Chen, S.*, and Zhang, J.*	Diverse roles of ethylene in regulating agronomic traits in rice	<i>Front Plant Sci</i>		2017, 8: 1676	4.291	A	
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56	Wang, M.*, Wu, H., Fang, J., Chu, C., and Wang, X.*	A long noncoding RNA involved in rice reproductive development by negatively regulating osa-miR160	<i>Sci Bull</i>		2017, 62: 470-475	4.092	A	
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58	Xie, C.#, Zhang, G.#, Zhang, Y#, Song, X., Guo, H., Chen, X.*, and Fang, R.*	<i>SRWD1</i> , a novel target gene of DELLA and WRKY proteins,	<i>Sci Bull</i>		2017, 62:1639-	4.092	A	

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59	Deng, L.#, Wang, H.#, Sun, C., Li, Q., Jiang, H., Du, M., Li, C.* , and Li, C.*	Efficient generation of pink-fruited tomatoes using CRISPR/Cas9 system	<i>J Genet Genomics</i>	2017, 1-4	4.051	A
60	Wu, Q.#, Liu, X.#, Yin, D., Yuan, H., Xie, Q., Zhao, X., Li, X., Zhu, L., Li, S.* , and Li, D.*	Constitutive expression of <i>OsDof4</i> , encoding a C <sub>2</sub> -C <sub>2</sub> zinc finger transcription factor, confers its distinct flowering effects under long- and short-day photoperiods in rice ( <i>Oryza sativa</i> L.)	<i>BMC Plant Biol</i>	2017, 17: 166	3.964	A
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62	Zhang, M., Han, L., Wang, W., Wu, S., Jiao, G., Su, L., Xia, G.* , and Wang, H.*	Overexpression of <i>GhFIM2</i> propels cotton fiber development by enhancing actin bundle formation	<i>J Integr Biol</i>	2017, 59: 531-534	3.962	A
63	Zhang, M.#, Cheng, S.#, Wang, H., Wu, J., Luo, Y., Wang, Q., Wang, F.* , and Xia, G.*	iTRAQ-based proteomic analysis of defence responses triggered by the necrotrophic pathogen <i>Rhizoctonia solani</i> in cotton	<i>J Proteomics</i>	2017, 152: 226-235	3.914	A
64	Feng, X., Wang, C., Nan, J., Zhang, X., Wang, R., Jiang, G., Yuan, Q., and Lin, S.*	Updating the elite rice variety Kongyu 131 by improving the <i>Gn1a</i> locus	<i>Rice</i>	2017, 10: 35-46	3.739	A
65	Kan, J., Fang, R.* , and Jia, Y.*	Interkingdom signaling in plant-microbe interactions	<i>Sci China Life Sci</i>	2017, 60: 1-12	2.781	A
66	Qian, W., Chen, X., Fang, R., and Kang, L.*	Manipulation of biotic signaling: a new theory for smarter pest control	<i>Sci China Life Sci</i>	2017, 60: 781-784	2.781	A
67	Sun, L., Qin, J., Wang, K., and Zhang, J.*	Expansion of pathogen recognition specificity in plants using pattern recognition receptors and artificially designed decoys	<i>Sci China Life Sci</i>	2017, 60: 797-805	2.781	A
68	Du, X., Wang, S., Gao, F., Zhang, L., Zhao, J., Guo, H.* , and Hua, C.*	Expression of pathogenesis-related genes in cotton roots in response to <i>Verticillium dahliae</i> PAMP molecules	<i>Sci China Life Sci</i>	2017, 60: 852-860	2.781	A
69	Wang, W.#, Sun, Y., Han, L., Su, L., Xia, G.* , and Wang, H.*	Overexpression of <i>GhPFN2</i> enhances protection against <i>Verticillium dahliae</i> invasion in cotton	<i>Sci China Life Sci</i>	2017, 60: 861-867	2.781	A
70	Cao, J.#, Yu, Y.#, Huang, J., Liu, R., Chen, Y., Li, S.* , and Liu, J.*	Genome re-sequencing analysis uncovers pathogenecity-related genes undergoing positive selection in <i>Magnaporthe oryzae</i>	<i>Sci China Life Sci</i>	2017, 60: 880-890	2.781	A
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72	Yu, F., and Xie, Q.*	Ubiquitination modification precisely modulates the ABA signaling pathway in plants	<i>Hereditas</i>	2017, 39: 692-706	1.345 A
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74	钱韦*, 马旅雁, 谷立川, 张炼辉	Biofilm与c-di-GMP专刊序言——微生物的社会性、c-di-GMP调控及研究新技术	<i>生物工程学报</i>	2017, 33: 1351-1356	A
75	程寿廷, 王芳芳, 钱韦*	鉴定cyclic di-GMP效应蛋白: 高通量筛选策略与实验验证方法	<i>生物工程学报</i>	2017, 33: 1376-1389	A
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77	宋丽阳, 方荣祥*, 贾燕涛*	生物被膜在病原细菌与植物识别中的作用	<i>农业生物技术</i>	2017, 33: 1640-1653	A
78	汪鸿儒, 储成才*	野生稻并不“野”	<i>遗传</i>	2017, 39: 438-439	A
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80	Zhao, Y.*, Zhang, T., and Guo, H.	Penetration assays, fungal recovery and pathogenicity assays for <i>Verticillium dahliae</i>	<i>Bio-protocol</i>	2017, 7: 1-7	A
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82	Fang, C.#, Ma, Y.#, Wu, S.#, Liu, Z., Wang, Z., Yang, R., Hu, G., Zhou, Z., Yu, H., Zhang, M., Pan, Y., Zhou, G., Ren, H., Du, W., Yan, H., Wang, Y., Han, D., Shen, Y., Liu, S., Liu, T., Zhang, J., Qin, H., Yuan, J., Yuan, X., Kong, F., Liu, B., Li, J., Zhang, Z.*, Wang, G.*, Zhu, B.*, and Tian, Z.*	Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean	<i>Genome Biol</i>	2017, 18: 161	11.908 B
83	Wu, J.#, Yang, R.#, Yang, Z.#, Yao, S., Zhao, S., Wang, Y., Li, P., Song, X., Jin, L., Zhou, T., Lan, Y., Xie, L., Zhou, X., Chu, C., Qi, Y., Cao, X.*, and Li, Y.*	ROS accumulation and antiviral defence control by microRNA528 in rice	<i>Nat Plants</i>	2017, 3: 16203	10.300 B
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