

人工microRNAs对拟南芥At1g13770和At2g23470基因的特异沉默

李文超, 赵淑清

山西大学生物技术研究所,化学生物学与分子工程教育部重点实验室, 太原 030006

LI Wen-Chao, ZHAO Shu-Qing

Key Laboratory of Chemical Biology and Molecular Engineering of Ministry of Education, Institute of Biotechnology, Shanxi University, Taiyuan 030006, China

- 摘要
- 参考文献
- 相关文章

Download: PDF (465KB) [HTML](#) (1KB) Export: BibTeX or EndNote (RIS) [Supplementary data](#)

摘要 DUF647 (Domain of unknown function 647) 蛋白家族是在真核生物中广泛存在的、高度保守的蛋白家族。拟南芥中该基因家族共有6个成员, 迄今为止拟南芥DUF647家族中4个成员的功能尚不清楚。文章以拟南芥内源MIR319a前体为骨架, 构建了敲减DUF647家族中2个基因At1g13770和At2g23470表达的人工microRNAs(Artificial microRNAs, amiRNAs)。利用WMD(Web microRNA designer)平台设计分别靶向At1g13770和At2g23470基因的amiRNAs序列, 通过重叠PCR置换拟南芥MIR319a前体序列。构建融合amiRNAs前体的植物表达载体pCHF3-amiRNAs, 在农杆菌介导下转化拟南芥。RT-PCR分析表明, amiRNAs能够显著抑制At1g13770和At2g23470基因的表达, 获得了抑制效果明显的转基因株系。At2g23470-amiRNA转基因植株At2g23470转录水平的下调导致育性严重下降。文章为进一步研究这两个基因的功能奠定了良好的基础。

关键词: 拟南芥 DUF647基因家族 人工microRNA 基因沉默

Abstract: DUF647 (domain of unknown function 647) protein family is found in diverse eukaryotic organisms and highly conserved in eukaryotes. It has 6 members in *Arabidopsis* genome. So far, the function of 4 members of *Arabidopsis* DUF647 family is unknown. In this report, using an endogenous *Arabidopsis* MIR319a precursor as the backbone, we constructed two artificial microRNAs (amiRNAs) to knock down the expression of two DUF647 family genes At1g13770 and At2g23470. Using the WMD (Web microRNA Designer) platform, we designed two amiRNAs targeting At1g13770 and At2g23470 genes, respectively. Both amiRNAs sequences were engineered into the MIR319a precursor using overlapping PCR and the amiRNAs backbones were transferred into the binary vector pCHF3. The resulting plasmids that harbor amiRNAs stem loop fragments were transformed into *Arabidopsis* by *Agrobacterium*-mediated floral dipping. Upon constitutive expression of these two amiRNAs, the target genes were efficiently down-regulated in transgenic line. The decreased level of At2g23470 transcript in At2g23470-amiRNA transgenic plants resulted in severe sterility. This work will facilitate the functional analysis of At1g13770 and At2g23470 genes in *Arabidopsis* growth and development.

Keywords: [Arabidopsis](#), [DUF647 gene family](#), [artificial microRNAs](#), [gene silencing](#)

收稿日期: 2011-07-03; 出版日期: 2012-03-25

基金资助:

山西省国际科技合作计划(编号: 2009081005), 山西省留学人员科技活动项目择优资助项目, 山西省回国留学人员科研资助项目(编号: 201003)和太原市科技明星专项(编号: 11014902)资助

通讯作者 赵淑清 Email: shuqing@sxu.edu.cn

Service

- ▶ 把本文推荐给朋友
- ▶ 加入我的书架
- ▶ 加入引用管理器
- ▶ Email Alert
- ▶ RSS

作者相关文章

- ▶ 李文超
- ▶ 赵淑清

引用本文:

李文超, 赵淑清. 人工microRNAs对拟南芥At1g13770和At2g23470基因的特异沉默. 遗传, 2012, 34(3): 348-355.

LI Wen-Chao, ZHAO Shu-Qing. Specific gene silencing of At1g13770 and At2g23470 by artificial microRNAs in *Arabidopsis*. HEREDITAS, 2012, V34 (3): 348-355.

链接本文:

http://www.chinagene.cn/Jwk_yC/CN/10.3724/SP.J.1005.2012.00348 或 http://www.chinagene.cn/Jwk_yC/CN/Y2012/V34/I3/348

- [1] Tong HY, Leasure CD, Hou XW, Yuen GG, Briggs W, He ZH. Role of root UV-B sensing in *Arabidopsis* early seedling development. *Proc Natl Acad Sci USA*, 2008, 105(52): 21039-21044.
- [2] Leasure CD, Tong HY, Yuen GG, Hou XW, Sun XF, He ZH. ROOT UV-B SENSITIVE2 acts with ROOT UV-B SENSITIVE1 in a root ultraviolet B-sensing pathway. *Plant Physiol*, 2009, 150(4): 1902-1915.

- [3] Ge L, Peer W, Robert S, Swarup R, Ye S, Prigge M, Cohen JD, Friml J, Murphy A, Tang D, Estelle M. *Arabidopsis ROOT UVB SENSITIVE2/WEAK AUXIN RESPONSE1* is required for polar auxin transport. *Plant Cell*, 2010, 22(6): 1749-1761. 
- [4] Bartel DP. MicroRNAs: genomics, biogenesis, mechanism, and function. *Cell*, 2004, 116(2): 281-297.
- [5] Voinnet O. Origin, biogenesis, and activity of plant microRNAs. *Cell*, 2009, 136(4): 669-687.
- [6] 毛颖波, 薛学义, 陈晓亚. 植物小RNA与RNA干扰: 生物学功能与应用前景. 中国科学(C辑: 生命科学), 2009, 39(1): 31-43.
- [7] Schwab R, Ossowski S, Riester M, Warthmann N, Weigel D. Highly specific gene silencing by artificial microRNAs in *Arabidopsis*. *Plant Cell*, 2006, 18(5): 1121-1133. 
- [8] Warthmann N, Chen H, Ossowski S, Weigel D, Hervé P. Highly specific gene silencing by artificial miRNAs in rice. *PLoS One*, 2008, 3(3): e1829.
- [9] Khraiwesh B, Ossowski S, Weigel D, Reski R, Frank W. Specific gene silencing by artificial microRNAs in *Physcomitrella patens*: An alternative to targeted gene knockouts. *Plant Physiol*, 2008, 148(2): 684-693. 
- [10] Molnar A, Bassett A, Thuenemann E, Schwach F, Karkare S, Ossowski S, Weigel D, Baulcombe D. Highly specific gene silencing by artificial microRNAs in the unicellular alga *Chlamydomonas reinhardtii*. *Plant J*, 2009, 58(1): 165-174. 
- [11] Zhao T, Wang W, Bai X, Qi YJ. Gene silencing by artificial microRNAs in *Chlamydomonas*. *Plant J*, 2009, 58(1): 157-164. 
- [12] Höfgen R, Willmitzer L. Storage of competent cells for *Agrobacterium* transformation. *Nucl Acids Res*, 1988, 16(20): 9877. 
- [13] Clough SJ, Bent AF. Floral dip: a simplified method for *Agrobacterium*-mediated transformation of *Arabidopsis thaliana*. *Plant J*, 1998, 16(6): 735-743. 
- [14] Zhao SQ, Li XF, Guo JB. Expression of the Pathogenesis-related gene promoter-GUS reporter fusion in *Arabidopsis*. *Acta Bot Sin*, 2003, 46(8): 982-987.
- [15] Wesley SV, Helliwell CA, Smith NA, Wang MB, Rouse DT, Liu Q, Gooding PS, Singh SP, Abbott D, Stoutjesdijk PA, Robinson SP, Gleave AP, Green AG, Waterhouse PM. Construct design for efficient, effective and high-throughput gene silencing in plants. *Plant J*, 2001, 27(6): 581-590. 
- [16] Lu R, Martin-Hernandez AM, Peart JR, Malcuit I, Baul-combe DC. Virus-induced gene silencing in plants. *Methods*, 2003, 30(4): 296-303.
- [17] Alvarez JP, Pekker I, Goldshmidt A, Blum E, Amsalem Z, Eshed Y. Endogenous and synthetic microRNAs stimulate simultaneous, efficient, and localized regulation of multiple targets in diverse species. *Plant Cell*, 2006, 18(5): 1134-1151. 
- [18] Niu QW, Lin SS, Reyes JL, Chen KC, Wu HW, Yeh SD, Chua NH. Expression of artificial microRNAs in transgenic *Arabidopsis thaliana* confers virus resistance. *Nat Biotechnol*, 2006, 24(11): 1420-1428. 
- [19] Qu J, Ye J, Fang RX. Artificial microRNA-mediated virus resistance in plants. *J Virol*, 2007, 81(12): 6690-6699.
- [20] Ossowski S, Schwab R, Weigel D. Gene silencing in plants using artificial microRNAs and other small RNAs. *Plant J*, 2008, 53(4): 674-690. 
- [21] Schmid M, Davison TS, Henz SR, Pape UJ, Demar M, Vingron M, Schölkopf B, Weigel D, Lohmann JU. A gene expression map of *Arabidopsis thaliana* development. *Nat Genet*, 2005, 37(5): 501-506
- [22] Goff SA, Ricke D, Lan TH, Presting G, Wang RL, Dunn M, Glazebrook J, Sessions A, Oeller P, Varma H, Hadley D, Hutchison D, Martin C, Katagiri F, Lange BM, Briggs S. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *japonica*). *Science*, 2002, 296(5565): 92-100.
- [23] Yu J, Hu SN, Wang J, Wong GKS, Li SG, Liu B, Deng YJ, Dai L, Zhou Y, Zhang XQ, Cao ML, Liu J, Sun JD, Tang JB, Chen YJ, Huang XB, Lin W, Ye C, Tong W, Cong LJ, Yang HM. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *indica*). *Science*, 2002, 296(5565): 79-92.
- [24] Rensing SA, Lang D, Zimmer AD, Terry A, Salamov A, Shapiro H, Nishiyama T, Perroud PF, Lindquist EA, Kamisugi Y, Tanahashi T, Sakakibara K, Fujita T, Oishi K, Boore JL. The *Physcomitrella* genome reveals evolutionary insights into the conquest of land by plants. *Science*, 2008, 319(5859): 64-69.
- [25] Swarbreck D, Wilks C, Lamesch P, Berardini TZ, Garcia-Hernandez M, Foerster H, Li DH, Meyer T, Muller R, Ploetz L, Radenbaugh A, Singh S, Swing V, Tissier C, Zhang PF, Huala E. The *Arabidopsis* Information Resource (TAIR): gene structure and function annotation. *Nucleic Acids Res*, 2008, 36(Database issue): D1009-D1014.
- [26] Ferro M, Salvi D, Brugière S, Miras S, Kowalski S, Lou-wagie M, Garin J, Joyard J, Rolland N. Proteomics of the chloroplast envelope membranes from *Arabidopsis thaliana*. *Mol Cell Proteomics*, 2003, 2(5): 325-345.
- [27] Dunkley TPJ, Hester S, Shadforth IP, Runions J, Weimar T, Hanton SL, Griffin JL, Bessant C, Brandizzi F, Hawes C, Watson RB, Dupree P, Lilley KS. Mapping the *Arabidopsis* organelle proteome. *Proc Natl Acad Sci USA*, 2006, 103(17): 6518-6523. 
- [1] 李捷 陈旭 罗莉琼 于晶 明凤. ANAC092参与调控花药发育的功能初探[J]. 遗传, 2013, 35(7): 913-922
- [2] 郭敏霞 傅永福. 拟南芥SUMO底物的研究进展[J]. 遗传, 2013, 35(6): 727-734
- [3] 王增光 柴国华 王芝瑶 唐贤丰 孙长江 周功克 马三梅. 拟南芥AtGA3OX1和AtGA3OX2基因影响茎秆次生细胞壁增厚的分子机理[J]. 遗传, 2013, 35(5): 655-665
- [4] 李延安, 祁林林, 孙加强, 刘宏宇, 李传友. 莱莉酸诱导侧根形成缺陷突变体asa1-1抑制子(soa)的鉴定与遗传分析[J]. 遗传, 2011, 33(9): 1003-1010
- [5] 付乾堂, 余迪求. 拟南芥AtWRKY25、AtWRKY26和AtWRKY33在非生物胁迫条件下的表达分析[J]. 遗传, 2010, 32(8): 848-856

- [6] 张红宇, 徐培洲, 杨华, 吴先军.拟南芥的印记基因和印记表达调控[J]. 遗传, 2010,32(7): 670-676
- [7] 谢崇波, 金谷雷, 徐海明, 朱军.拟南芥在盐胁迫环境下SOS转录调控网络的构建及分析[J]. 遗传, 2010,32(6): 639-646
- [8] 江志强, 郭红卫.植物激素信号网络的进化[J]. 遗传, 2010,37(4): 219-230
- [9] 张云飞, 曹光宇, 瞿礼嘉, 顾红雅.拟南芥MYB转录因子基因*AtMYB17*的鉴定及其可能的调控分析[J]. 遗传, 2009,36(2): 99-107
- [10] 张亮生, 马成荣, 戴茜, 王翼飞.拟南芥和水稻SET结构域基因家族全基因组鉴定、分类和表达[J]. 遗传, 2009,31(2): 186-198
- [11] 喻达时, 赵琼, 邓克勤, 郭新红.拟南芥CK1A基因功能初步研究[J]. 遗传, 2009,31(10): 1037-1042
- [12] 刘鹏, 韦伟, 欧阳寿强, 张劲松, 陈受宜, 张万科.大豆受体类激酶分析[J]. 遗传, 2009,36(10): 611-619
- [13] 王保, 桑亚林, 宋建, 高新起, 张宪省.水稻*OsARGOS*基因的异源表达促进细胞分裂和生长并导致器官增大[J]. 遗传, 2009,36(1): 31-40
- [14] 陶苏丹, 陈喜文, 刘佳, 明铭, 郑男秀, 陈德富.拟南芥谷胱甘肽S-转移酶Zeta类Ser73位点特性分析[J]. 遗传, 2008,35(8): 507-512
- [15] 郭景康, 吴 坚, 戴 茜, 王 超, 罗 磊, 袁 一, 王永华, 王 健*.热激转录因子家族在水稻和拟南芥中的比较分析[J]. 遗传, 2008,35(2): 105-118

Copyright 2010 by 遗传