

The role of auxin signaling pathway in defending virus infection

生长素信号通路在抵抗病毒侵染中的作用

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汇报内容

模式作物-水稻的介绍

生长素信号通路和水稻矮缩病毒 (*Rice dwarf virus*, RDV) 侵染的关系

OsARF12 转录因子的生物信息学分析

模式作物-水稻的介绍

Oryza sativa subsp. *japonica*

粳稻



Oryza sativa subsp. *indica*

籼稻



水稻基因组

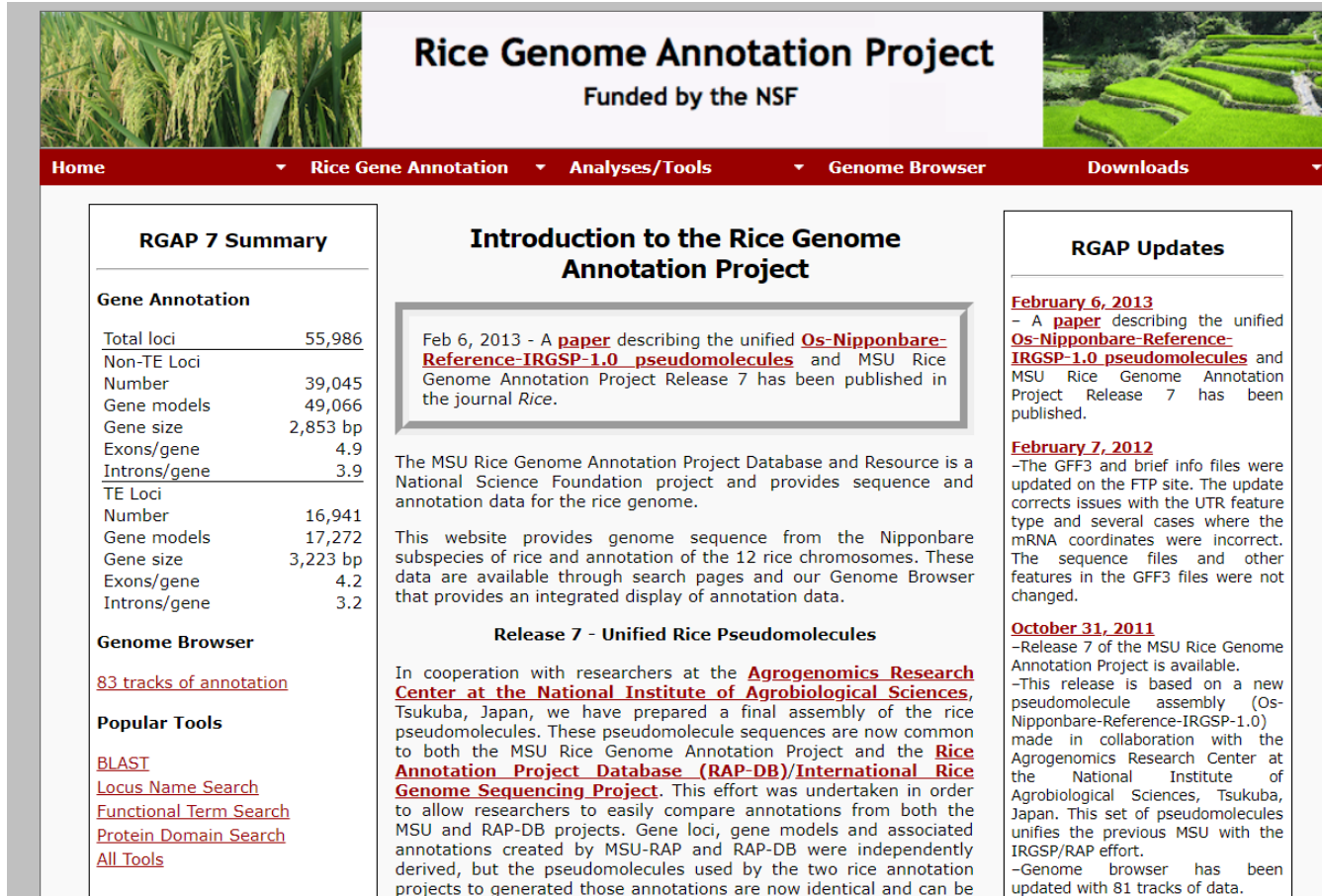
亚种	基因组大小	染色体数目	编码基因数目
粳稻	420Mb	24条	32000-50000
籼稻	466Mb	24条	46022-55615

Goff et al., 2002. A draft sequence of the rice genome (*Oryza sativa* L. ssp. japonica). *Science*, 296(5565), 92-100.

Yu et al., 2002. draft sequence of the rice genome (*Oryza sativa* L. ssp. indica). *science*, 296(5565), 79-92.

Project, I. R. G. S., & Sasaki, T. (2005). The map-based sequence of the rice genome. *Nature*, 436(7052), 793

常用的水稻数据库



The screenshot shows the Rice Genome Annotation Project website. At the top, there are two images: a close-up of rice panicles on the left and a terraced rice field on the right. The main title is "Rice Genome Annotation Project" with the subtitle "Funded by the NSF". Below this is a navigation bar with links for Home, Rice Gene Annotation, Analyses/Tools, Genome Browser, and Downloads. The main content area is divided into three columns. The left column is titled "RGAP 7 Summary" and contains a table of statistics for Gene Annotation and TE Loci, followed by a link to "83 tracks of annotation" and a section for "Popular Tools" including BLAST, Locus Name Search, Functional Term Search, Protein Domain Search, and All Tools. The middle column is titled "Introduction to the Rice Genome Annotation Project" and features a highlighted box with a news item from Feb 6, 2013, about a paper in the journal Rice. Below this is a paragraph about the MSU Rice Genome Annotation Project Database and Resource, followed by a paragraph about the website's purpose and a section for "Release 7 - Unified Rice Pseudomolecules" which describes the collaboration between MSU and the National Institute of Agrobiological Sciences. The right column is titled "RGAP Updates" and lists three updates: February 6, 2013 (unified Os-Nipponbare-Reference-IRGSP-1.0 pseudomolecules), February 7, 2012 (GFF3 and brief info files updated), and October 31, 2011 (Release 7 of the MSU Rice Genome Annotation Project available).

Rice Genome Annotation Project

Funded by the NSF

Home Rice Gene Annotation Analyses/Tools Genome Browser Downloads

RGAP 7 Summary

Gene Annotation	
Total loci	55,986
Non-TE Loci	
Number	39,045
Gene models	49,066
Gene size	2,853 bp
Exons/gene	4.9
Introns/gene	3.9
TE Loci	
Number	16,941
Gene models	17,272
Gene size	3,223 bp
Exons/gene	4.2
Introns/gene	3.2

Gene Annotation

Total loci 55,986

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Genome Browser

[83 tracks of annotation](#)

Popular Tools

[BLAST](#)

[Locus Name Search](#)

[Functional Term Search](#)

[Protein Domain Search](#)

[All Tools](#)

Introduction to the Rice Genome Annotation Project

Feb 6, 2013 - A [paper](#) describing the unified [Os-Nipponbare-Reference-IRGSP-1.0 pseudomolecules](#) and MSU Rice Genome Annotation Project Release 7 has been published in the journal *Rice*.

The MSU Rice Genome Annotation Project Database and Resource is a National Science Foundation project and provides sequence and annotation data for the rice genome.

This website provides genome sequence from the Nipponbare subspecies of rice and annotation of the 12 rice chromosomes. These data are available through search pages and our Genome Browser that provides an integrated display of annotation data.

Release 7 - Unified Rice Pseudomolecules

In cooperation with researchers at the [Agrogenomics Research Center at the National Institute of Agrobiological Sciences](#), Tsukuba, Japan, we have prepared a final assembly of the rice pseudomolecules. These pseudomolecule sequences are now common to both the MSU Rice Genome Annotation Project and the [Rice Annotation Project Database \(RAP-DB\)/International Rice Genome Sequencing Project](#). This effort was undertaken in order to allow researchers to easily compare annotations from both the MSU and RAP-DB projects. Gene loci, gene models and associated annotations created by MSU-RAP and RAP-DB were independently derived, but the pseudomolecules used by the two rice annotation projects to generated those annotations are now identical and can be

RGAP Updates

February 6, 2013
- A [paper](#) describing the unified [Os-Nipponbare-Reference-IRGSP-1.0 pseudomolecules](#) and MSU Rice Genome Annotation Project Release 7 has been published.

February 7, 2012
-The GFF3 and brief info files were updated on the FTP site. The update corrects issues with the UTR feature type and several cases where the mRNA coordinates were incorrect. The sequence files and other features in the GFF3 files were not changed.

October 31, 2011
-Release 7 of the MSU Rice Genome Annotation Project is available.
-This release is based on a new pseudomolecule assembly (Os-Nipponbare-Reference-IRGSP-1.0) made in collaboration with the Agrogenomics Research Center at the National Institute of Agrobiological Sciences, Tsukuba, Japan. This set of pseudomolecules unifies the previous MSU with the IRGSP/RAP effort.
-Genome browser has been updated with 81 tracks of data.

水稻基因组注释计划

<http://rice.plantbiology.msu.edu/>

其他水稻数据库



RiceGE: Rice Functional Genomic Express Database (Jan. 16, 2018)

[[For the older RiceGE release v 6.1, please click to visit.](#)]

<http://signal-genet.salk.edu/cgi-bin/RiceGE>



<http://www.ricedata.cn/gene/>



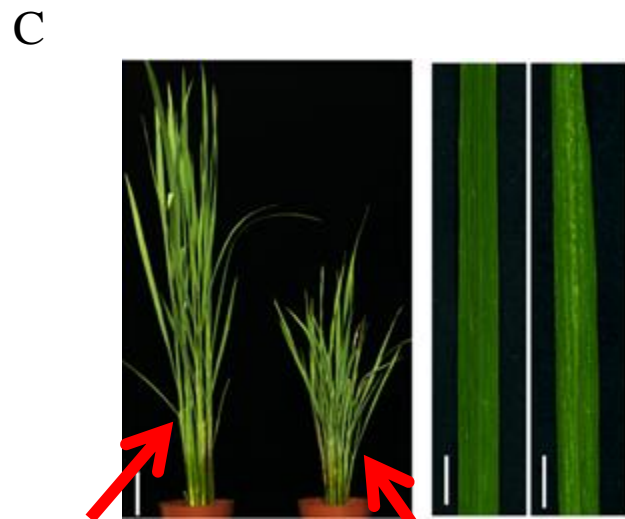
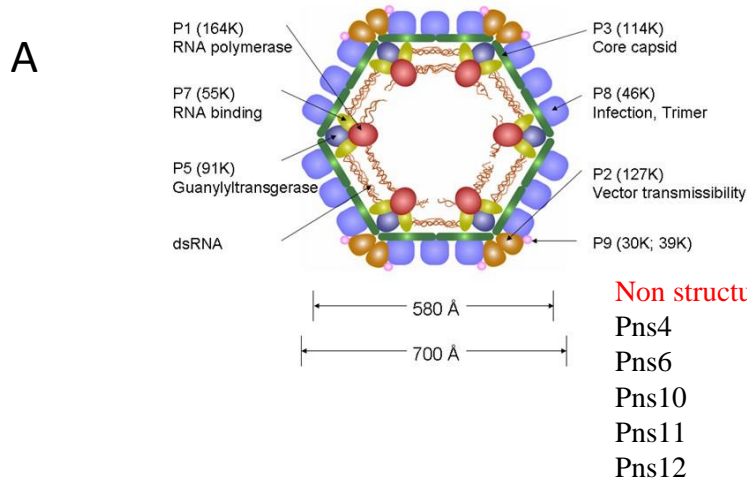
3000份水稻SNP数据库 http://snp-seek.irri.org/_snp.zul



日本水稻表达谱数据库 <http://ricexpro.dna.affrc.go.jp/index.html>

生长素信号通路和水稻矮缩病毒 (*Rice dwarf virus*, RDV) 侵染的关系

水稻矮缩病毒 (*Rice dwarf virus*, RDV) 简介



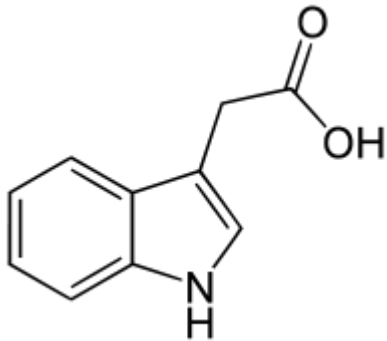
健康

感病

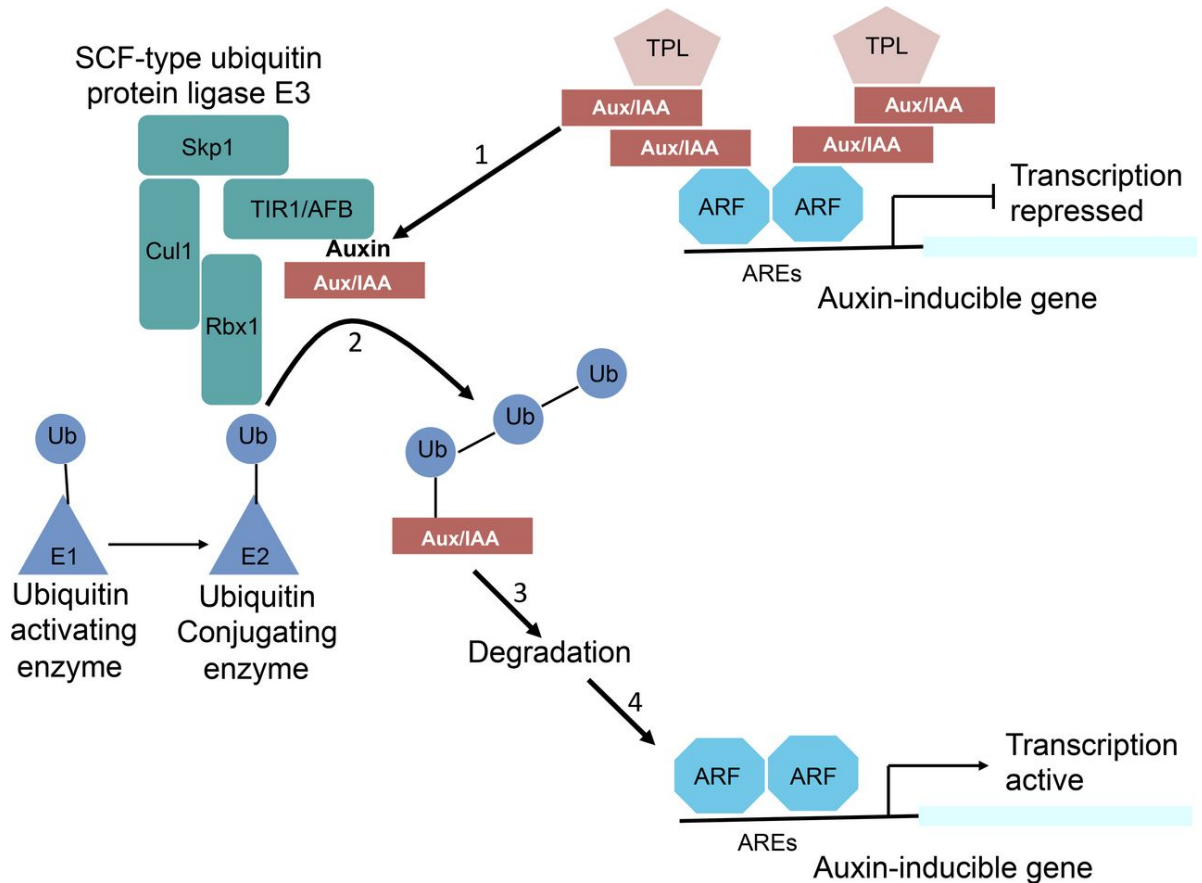
感病

健康

经典的生长素信号通路

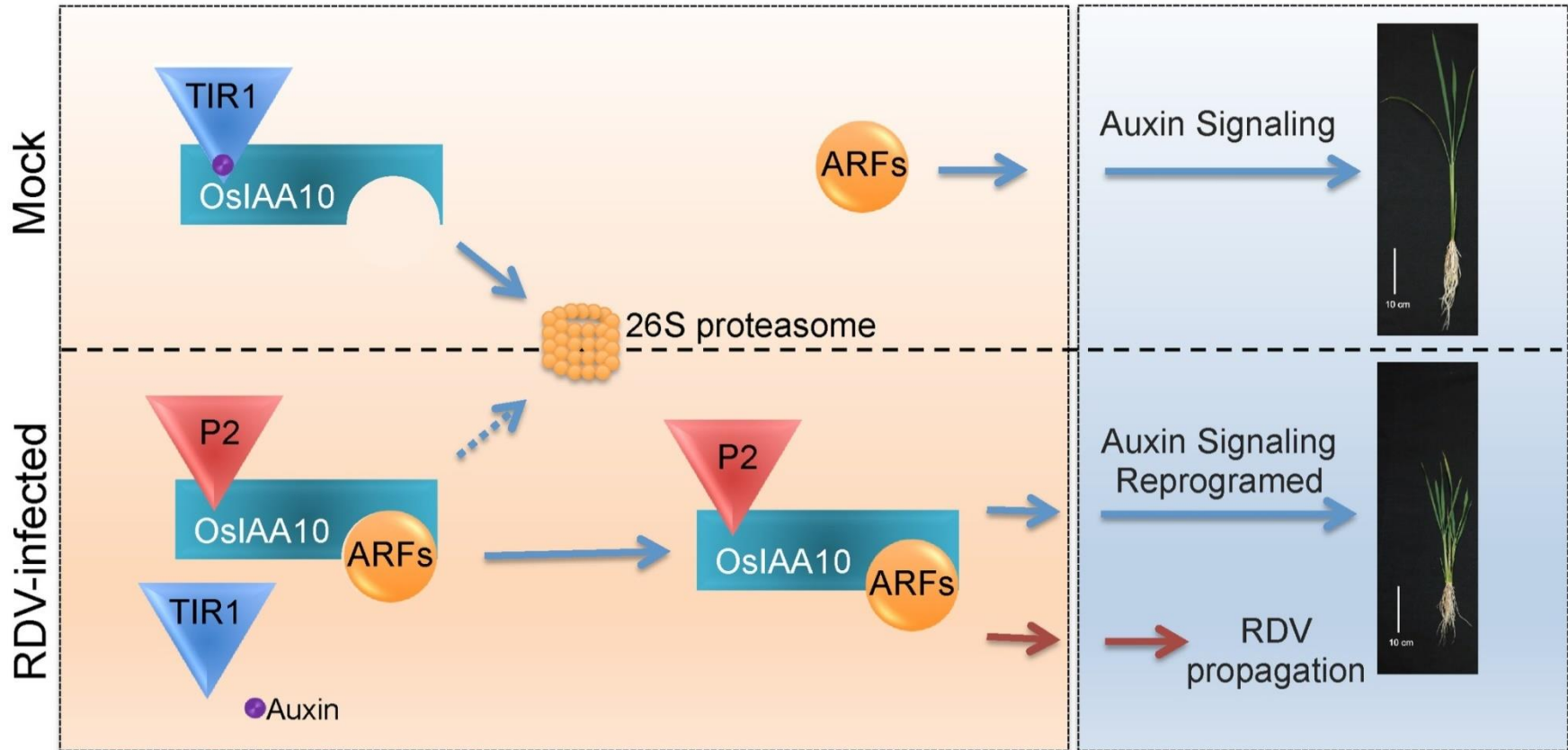


IAA :indole-3-acetic acid



Leyser O. Auxin signaling[J]. Plant physiology, 2017: pp. 00765.2017.

水稻矮缩病毒P2蛋白通过和水稻OsIAA10蛋白相互作用，抑制OsIAA10降解，抑制生长素信号通路，增强病毒侵染和症状发展



Jin et al., PLoS pathogens, 2016

转录因子的定义及功能

定义：本质是与DNA特异性结合的一系列蛋白质。一般有不同的功能区域，如DNA结合结构域与效应结构域。

功能：转录因子不单与基因上游的启动子区域结合，也可以和其它转录因子形成转录因子复合体来调控基因的转录

植物转录因子数据库



Plant Transcription Factor Database

v4.0

Previous version: v1.0, v2.0, v3.0

[Home](#) [BLAST](#) [Prediction](#) [RegMap](#) [ATRM](#) [Download](#) [Help](#) [About](#) [Links](#)

(e.g., LFY)

Browse by Family

AP2 (4461)	ARF (4578)	ARR-B (2354)	B3 (10609)	BBR-BPC (1256)
BES1 (1549)	C2H2 (17740)	C3H (9693)	CAMTA (1343)	CO-like (2125)
CPP (1612)	DBB (1651)	Dof (5655)	E2F/DP (1781)	EIL (1234)
ERF (21129)	FAR1 (7527)	G2-like (9874)	GATA (5335)	GRAS (9304)
GRF (1876)	GeBP (1564)	HB-PHD (477)	HB-other (2277)	HD-ZIP (8602)
HRT-like (249)	HSF (4574)	LBD (7216)	LFY (253)	LSD (957)
M-type_MADS (7541)	MIKC_MADS (6918)	MYB (22032)	MYB_related (15369)	NAC (19997)
NF-X1 (403)	NF-YA (2461)	NF-YB (3099)	NF-YC (2446)	NZZ/SPL (109)
Nin-like (2766)	RAV (690)	S1Fa-like (359)	SAP (164)	SBP (4168)
SRS (1327)	STAT (214)	TALE (4433)	TCP (4187)	Trihelix (6256)
VOZ (635)	WOX (2358)	WRKY (14549)	Whirly (530)	YABBY (1719)
ZF-HD (2589)	bHLH (28698)	bZIP (15498)		

Jin JP, Tian F, Yang DC, Meng YQ, Kong L, Luo JC and Gao G. (2017). PlantTFDB 4.0: toward a central hub for transcription factors and regulatory interactions in plants. *Nucleic Acids Research*, 45(D1):D1040-D1045.

OsARF12 转录因子的生物信息学分析

OsARF12 蛋白保守结构域分析 (Pfam)



B3 domain :135-237aa DNA 结合结构域



Auxin response domain:261-344aa 生长素响应结构域



AUX_IAA domain :690-809aa IAA蛋白互作结构域

OsARF12的启动子顺式调控元件分析



MYB:转录因子结合位点

MYC:转录因子结合位点

ABRE: 脱落酸 (ABA)响应元件

TATC-box:赤霉素(GA)响应元件

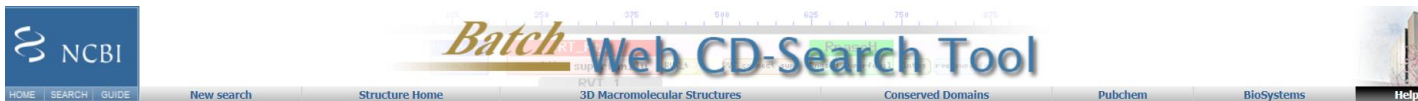
TCA-element: 水杨酸 (SA)的响应元件

TGACG-motif:茉莉酸 (JA)响应元件

<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>
PlantCARE, a database of plant cis-acting regulatory elements and a portal to tools for in silico analysis of promoter sequences
Magali Lescot et al., Nucleic Acids Res. 2002 Jan 1;30(1):325-327.

+	Blue	
+	Yellow	ABRE
+	Dark Red	ABRE3a
+	Red	ABRE4
+	Green	AT~TATA-box
+	Blue	Box 4
+	Light Pink	CAAT-box
+	Magenta	CARE
+	Green	CGTCA-motif
+	Light Blue	CTAG-motif
+	Dark Blue	G-box
+	Brown	GA-motif
+	Olive	HD-Zip 1
+	Orange	MSA-like
+	Pink	MYB
+	Light Green	MYC
+	Purple	STRE
+	Red	TATA-box
+	Cyan	TATC-box
+	Light Purple	TCA-element
+	White	TGACG-motif
+	Blue	Unnamed__4
+	Yellow	as-1

OsARF12和拟南芥ATARF6, ATARF8保守结构域比较

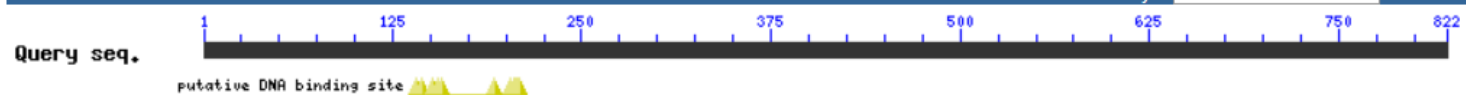


Domain families on selected sequences

H-zoom: 1x View Concise Results Show functional sites

Q#1 -> ((Local ID))

Redundancy: Concise Results Show functional sites



Specific hits

B3

Auxin_resp

Superfamilies

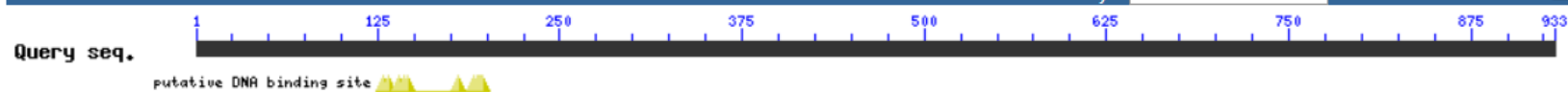
BfiI_C_EcoRII_M_

Auxin_resp s

AUX_IAA

Q#2 -> ATARF6 ((Local ID))

Redundancy: Concise Results Show functional sites



Specific hits

B3

Auxin_resp

Superfamilies

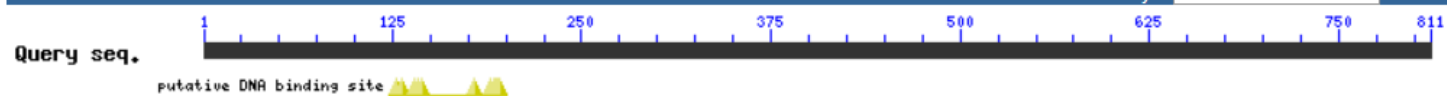
BfiI_C_EcoRII_M_B

Auxin_resp s

AUX_IAA

Q#3 -> ATARF8 ((Local ID))

Redundancy: Concise Results Show functional sites



Specific hits

B3

Auxin_resp

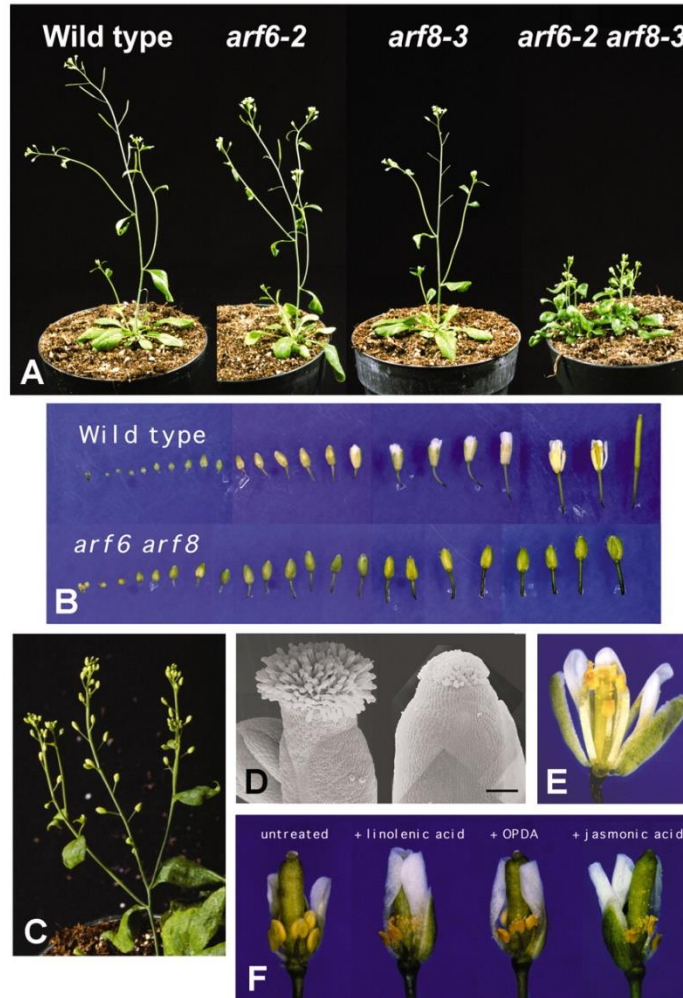
Superfamilies

BfiI_C_EcoRII_M_

Auxin_resp s

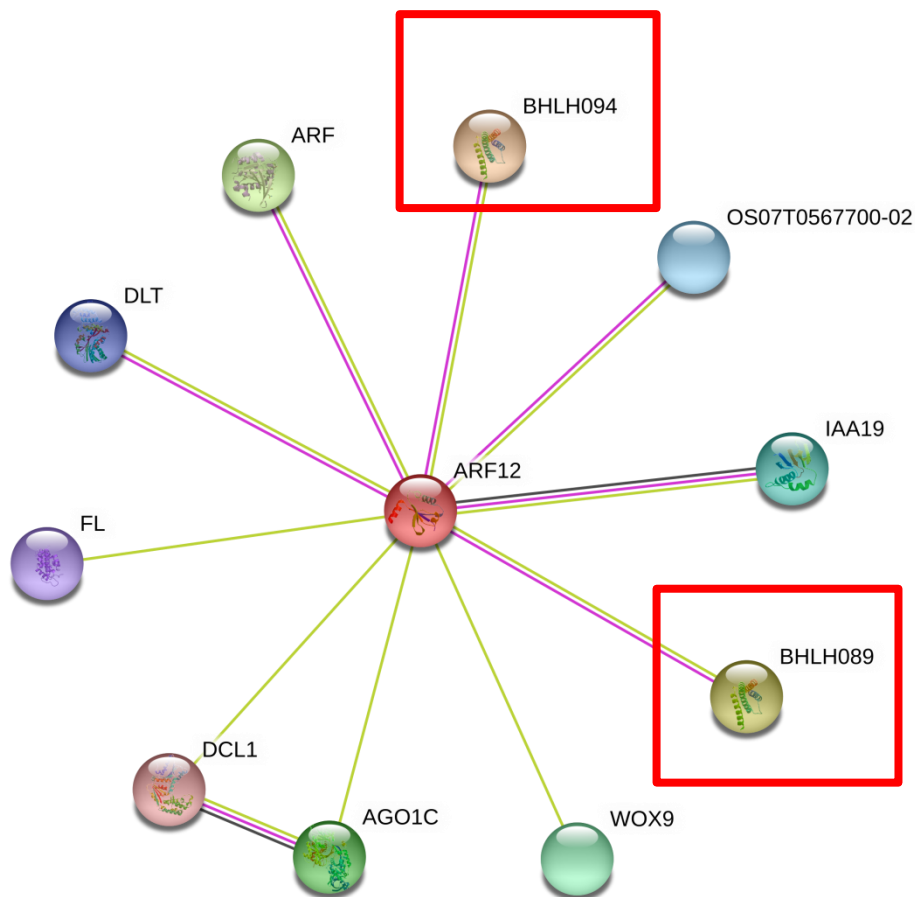
AUX_IAA

生长素响应因子ARF6和ARF8促进拟南芥中茉莉酸的产生和花的成熟



Nagpal et al., Development, 2005

OsARF12蛋白相互作用蛋白预测



Node Color	Node Content
colored nodes: query proteins and first shell of interactors	empty nodes: proteins of unknown 3D structure
white nodes: second shell of interactors	filled nodes: some 3D structure is known or predicted

Known Interactions	Predicted Interactions	Others
from curated databases	gene neighborhood	textmining
experimentally determined	gene fusions	co-expression
	gene co-occurrence	protein homology

BHLH094

BHLH089

茉莉酸通路响应基因的转录因子¹⁹

参考文献

1. Yu, J., Hu, S., Wang, J., Wong, G. K. S., Li, S., Liu, B., ... & Cao, M. (2002). draft sequence of the rice genome (*Oryza sativa* L. ssp. indica). *science*, 296(5565), 79-92.
2. Goff, S. A., Ricke, D., Lan, T. H., Presting, G., Wang, R., Dunn, M., ... & Hadley, D. (2002). A draft sequence of the rice genome (*Oryza sativa* L. ssp. japonica). *Science*, 296(5565), 92-100.
3. Project, I. R. G. S., & Sasaki, T. (2005). The map-based sequence of the rice genome. *Nature*, 436(7052), 793.
4. Jin, L., Qin, Q., Wang, Y., Pu, Y., Liu, L., Wen, X., ... & Li, Y. (2016). Rice dwarf virus P2 protein hijacks auxin signaling by directly targeting the rice OsIAA10 protein, enhancing viral infection and disease development. *PLoS pathogens*, 12(9), e1005847.
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6. Nagpal, P., Ellis, C. M., Weber, H., Ploense, S. E., Barkawi, L. S., Guilfoyle, T. J.,& Ecker, J. R. (2005). Auxin response factors ARF6 and ARF8 promote jasmonic acid production and flower maturation. *Development*, 132(18), 4107-4118.

致谢

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