

POC tutorial#3: Annotation

This tutorial will run automatically in Quicktime.
To run the tutorial at your own pace use the
internal controllers within the tutorial.

-  button goes to next slide
-  button goes to previous slide
-  button goes to last slide
-  button goes to previous slide

Annotation Methods and Standards

- A. What does functional annotation mean?**
- B. What are the data used for annotation?**
- C. What are the components of an annotation?**
- D. Example 1: Annotation of gene expression.**
- E. Example 2: Annotation of phenotypes.**

What does functional annotation mean?

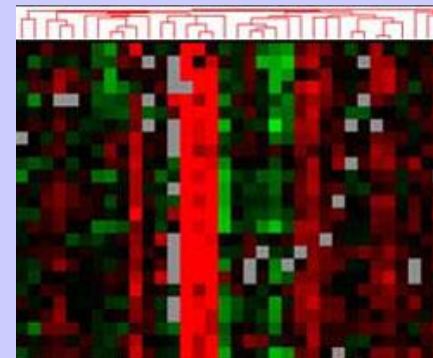
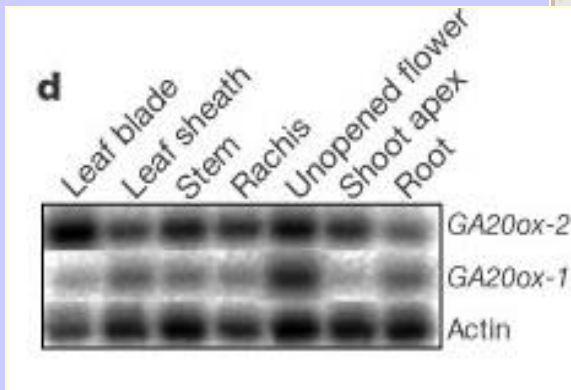
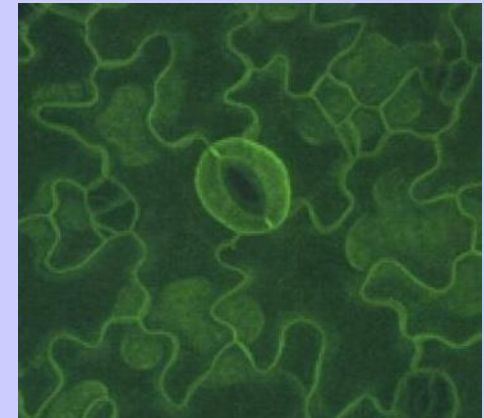
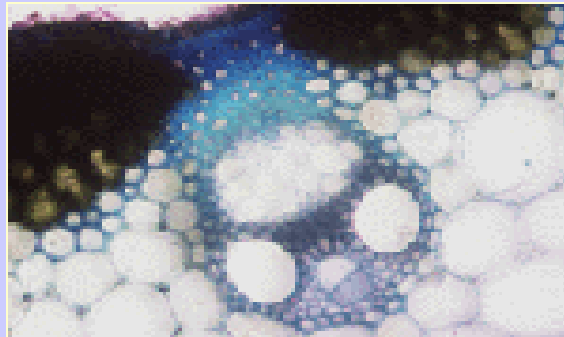
Functional annotation is defined as the process of collecting information about and describing a gene's biological identity—its various aliases, molecular function, biological role(s), subcellular localization, and its expression domains within the plant.

- Berardini et.al. (2004) Plant Phys135:745-755

We use the plant ontology for describing two additional aspects of gene products: gene expression and phenotypic expression within the organism.

What data are used for annotation?

Phenotype, gene expression
and protein localization



Components of an annotation

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TAIR Annotation Search [Help]

Your query for annotations based on the gene **ARF8** resulted in 20 records.

Displaying 1 - 20 of 20 records on page 1 of 1 pages.

Keyword Category	Relationship Type	Keyword	Evidence Code Evidence Description Evidence With: Reference	Annotated By/ Date Last Modified
biological process	involved in	flower development	<i>inferred from genetic interaction:</i> double mutant analysis: ARF6: Nagpal P, et al. (2005)	The Arabidopsis Information Resource/ 2005-10-13
biological process	involved in	response to auxin stimulus	<i>inferred from mutant phenotype:</i> analysis of physiological response: none: Nagpal P, et al. (2005)	The Arabidopsis Information Resource/ 2005-10-13
biological process	represses	fruit development	<i>inferred from mutant phenotype:</i> analysis of visible trait: none: Goetz, et al. (2006)	Donghui Li/ 2006-08-24
molecular function	has	transcription factor activity	<i>traceable author statement:</i> original experiments are traceable through an article: none: Ulmasov, et al. (1999)	The Arabidopsis Information Resource/ 2004-02-10
plant structure	expressed in	flower	<i>inferred from expression pattern:</i> expression library screening: none: Nagpal P, et al. (2005)	The Arabidopsis Information Resource/ 2005-10-13
plant structure	expressed in	flower	<i>inferred from expression pattern:</i> Transcript levels (e.g. Northern): none: Goetz, et al. (2006)	Donghui Li/ 2006-08-24
plant structure	expressed in	ovule	<i>inferred from direct assay:</i> localization of GUS fusion protein: none: Goetz, et al. (2006)	Donghui Li/ 2006-08-24
plant structure	expressed in	female gametophyte	<i>inferred from direct assay:</i> localization of GUS fusion protein: none: Goetz, et al. (2006)	Donghui Li/ 2006-08-24

GO

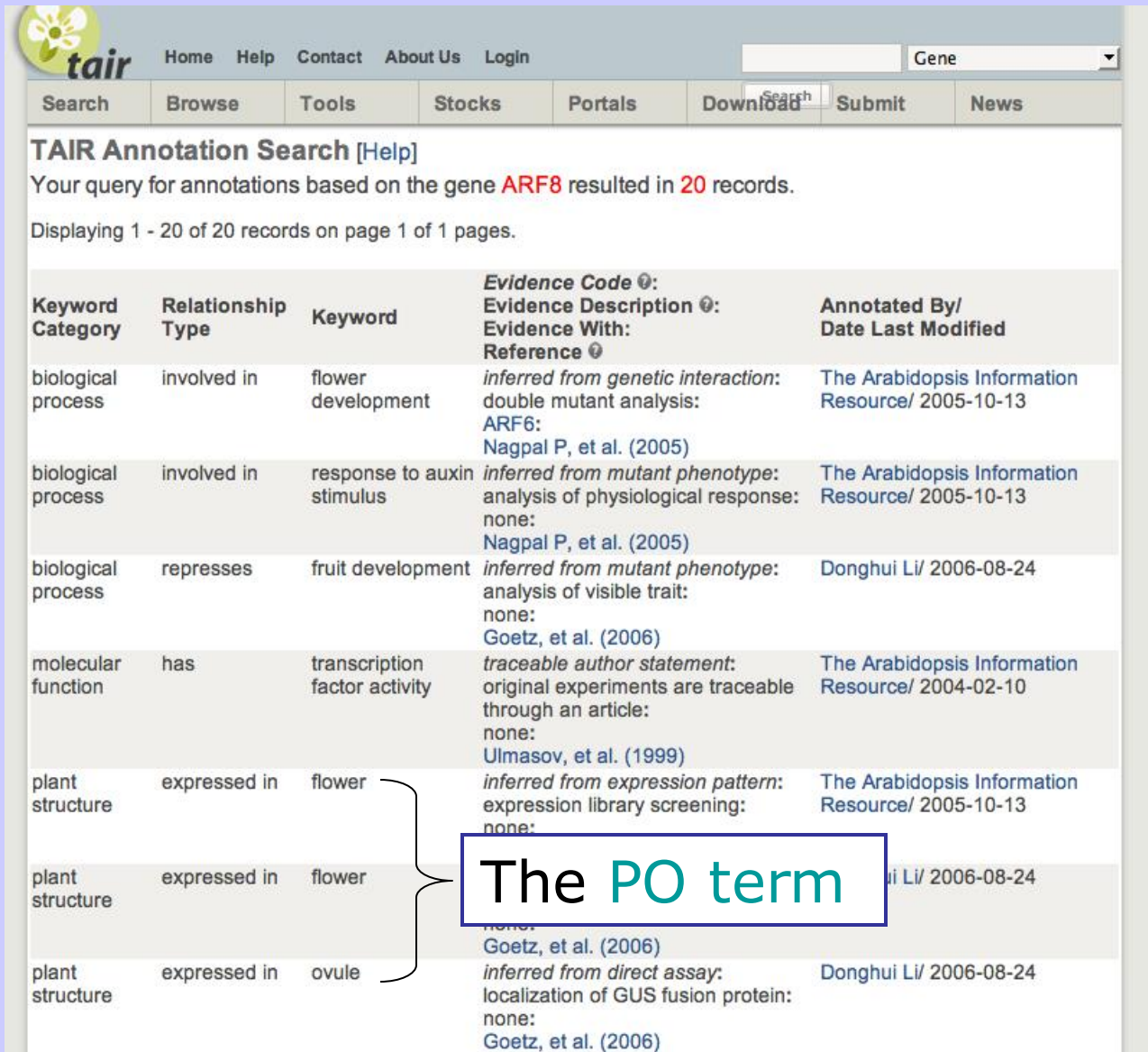
PO

Components of an annotation “data object”

The screenshot shows the TAIR (The Arabidopsis Information Resource) website. The search results for the gene **ARF8** are displayed. A callout box points to the gene name **ARF8** in the search results, with the text: "The name of the gene or germplasm being annotated." The search results table includes columns for Keyword Category, Relationship Type, Key, Evidence Code, Evidence Description, Evidence With, Reference, and Annotated By/Date Last Modified.

Keyword Category	Relationship Type	Key	Evidence Code	Evidence Description	Evidence With	Reference	Annotated By/Date Last Modified
biological process			none:				Information 10-13
biological process			none:				Information 10-13
biological process	represses	fruit development	inferred from mutant phenotype:	analysis of visible trait:			Donghui Li/ 2006-08-24
molecular function	has	transcription factor activity	traceable author statement:	original experiments are traceable through an article:			The Arabidopsis Information Resource/ 2004-02-10
plant structure	expressed in	flower	inferred from expression pattern:	expression library screening:			The Arabidopsis Information Resource/ 2005-10-13
plant structure	expressed in	flower	inferred from expression pattern:	Transcript levels (e.g. Northern):			Donghui Li/ 2006-08-24
plant structure	expressed in	ovule	inferred from direct assay:	localization of GUS fusion protein:			Donghui Li/ 2006-08-24

Components of an annotation “PO term”



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TAIR Annotation Search [Help]

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biological process	involved in	response to auxin stimulus	<i>inferred from mutant phenotype:</i> analysis of physiological response: none: Nagpal P, et al. (2005)	The Arabidopsis Information Resource/ 2005-10-13
biological process	represses	fruit development	<i>inferred from mutant phenotype:</i> analysis of visible trait: none: Goetz, et al. (2006)	Donghui Li/ 2006-08-24
molecular function	has	transcription factor activity	<i>traceable author statement:</i> original experiments are traceable through an article: none: Ulmasov, et al. (1999)	The Arabidopsis Information Resource/ 2004-02-10
plant structure	expressed in	flower	<i>inferred from expression pattern:</i> expression library screening: none:	The Arabidopsis Information Resource/ 2005-10-13
plant structure	expressed in	flower	none: Goetz, et al. (2006)	Li/ 2006-08-24
plant structure	expressed in	ovule	<i>inferred from direct assay:</i> localization of GUS fusion protein: none: Goetz, et al. (2006)	Donghui Li/ 2006-08-24

The PO term

Components of an annotation “ontology aspect”

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TAIR Annotation Search [Help]

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biological process	represses	fruit development	<i>inferred from mutant phenotype:</i> analysis of visible trait: none: Goetz, et al. (2006)	Donghui Li/ 2006-08-24
molecular function	has	transcription factor activity	<i>traceable author statement:</i> original experiments are traceable through an article: none: Ulmasov, et al. (1999)	The Arabidopsis Information Resource/ 2004-02-10
plant structure	expressed in	flower	<i>inferred from expression pattern:</i> expression library screening: none: Nagpal P, et al. (2005)	The Arabidopsis Information Resource/ 2005-10-13
plant structure	e			Donghui Li/ 2006-08-24
plant structure	expressed in	ovule	Goetz, et al. (2006) <i>inferred from direct assay:</i> localization of GUS fusion protein: none: Goetz, et al. (2006)	Donghui Li/ 2006-08-24

Components of an annotation "relationship type"

TAIR Annotation Search [Help]

Your query for annotations based on the gene **ARF8** resulted in **20** records.

Displaying 1 - 20 of 20 records on page 1 of 1 pages.

Keyword Category	Relationship Type	Keyword	Annotated By/ Date Last Modified
biological process	involved in		The Arabidopsis Information Resource/ 2005-10-13
biological process	involved in		The Arabidopsis Information Resource/ 2005-10-13
biological process	represses		Donghui Li/ 2006-08-24
molecular function	has	traceable	The Arabidopsis Information Resource/ 2004-02-10
plant structure	expressed in	flower	none: Ulmasov, et al. (1999) inferred from expression pattern: expression library screening: none: Nagpal P, et al. (2005) inferred from expression pattern: Transcript levels (e.g. Northern): none: Goetz, et al. (2006)
plant structure	expressed in	flower	Donghui Li/ 2006-08-24
plant structure	expressed in	ovule	inferred from direct assay: localization of GUS fusion protein: none: Goetz, et al. (2006)

The **relationship** between the gene and the PO term. This is currently used only in TAIR database annotations

Components of an annotation “evidence code”

The screenshot shows the TAIR (The Arabidopsis Information Resource) website. The top navigation bar includes links for Home, Help, Contact, About Us, and Login. Below this is a search bar with a dropdown menu set to 'Gene'. The main content area is titled 'TAIR Annotation Search [Help]' and displays the results for a query based on the gene ARF8, resulting in 20 records. A table lists these annotations, with columns for Keyword Category, Relationship Type, Keyword, Evidence Code, Evidence Description, Evidence With, Reference, and Annotated By/Date Last Modified. A callout box points to the 'Evidence Code' column, which contains codes like 'inferred from genetic interaction: double mutant analysis: ARF6: Nagpal, et al. (2005)'. The table also shows various biological processes and plant structures associated with ARF8, such as 'flower development', 'response to auxin stimulus', and 'fruit development'.

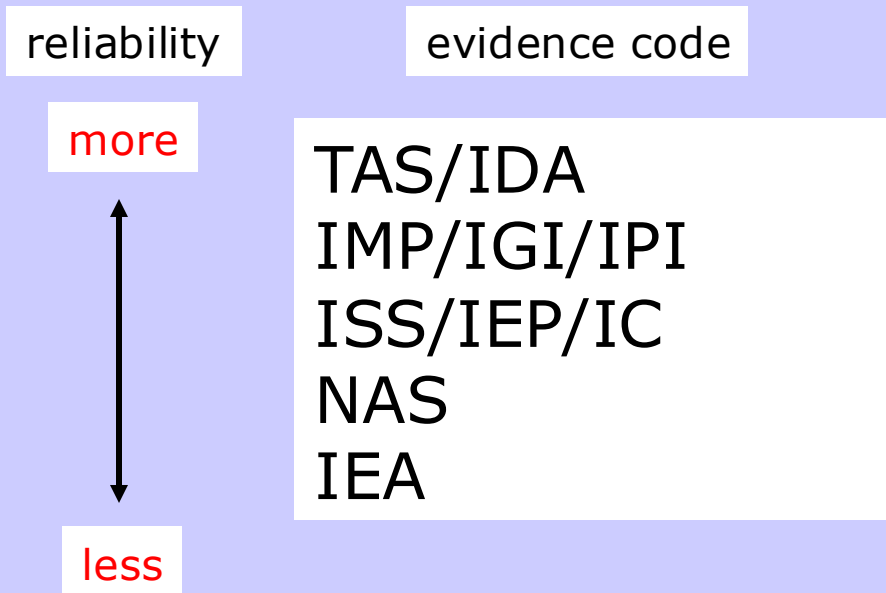
Keyword Category	Relationship Type	Keyword	Evidence Code	Evidence Description	Evidence With	Reference	Annotated By/Date Last Modified
biological process	involved in	flower development	inferred from genetic interaction: double mutant analysis: ARF6: Nagpal, et al. (2005)				The Arabidopsis Information Resource/ 2005-10-13
biological process	involved in	response to auxin stimulus	inferred from mutant phenotype: an biological response: (2005)				The Arabidopsis Information Resource/ 2005-10-13
biological process	represses	fruit development	inferred from mutant phenotype: (2005)				Donghui Li/ 2006-08-24
plant structure	expressed in	flower	inferred from expression pattern: expression library screening: none: Nagpal P, et al. (2005)				The Arabidopsis Information Resource/ 2004-02-10
plant structure	expressed in	flower	inferred from expression pattern: Transcript levels (e.g. Northern): none: Goetz, et al. (2006)				Donghui Li/ 2006-08-24
plant structure	expressed in	ovule	inferred from direct assay: localization of GUS fusion protein: none: Goetz, et al. (2006)				Donghui Li/ 2006-08-24

The evidence code gives information about the experimental evidence supporting the annotation.

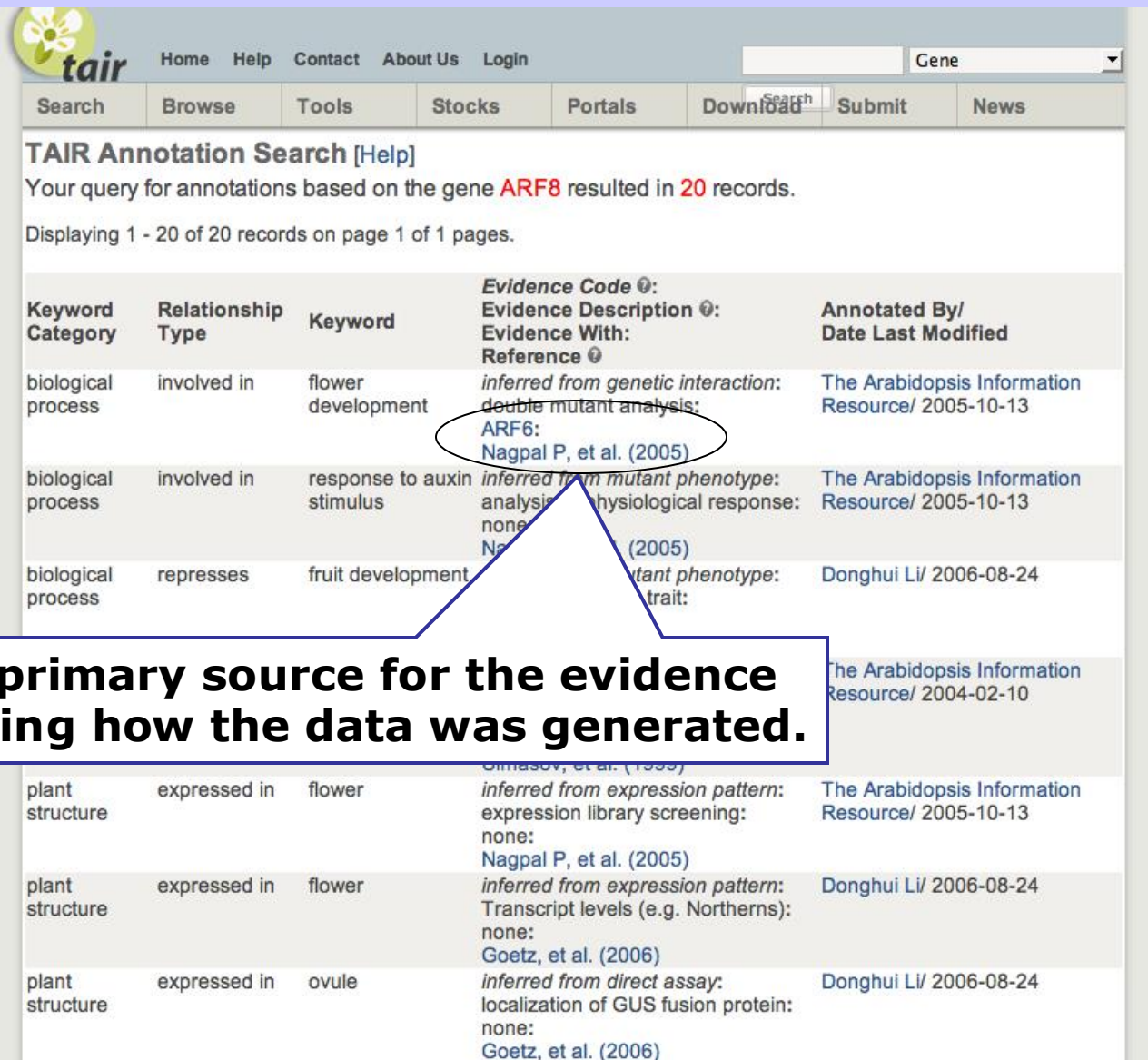
Using the evidence codes

The evidence codes can be used to evaluate the strength of the evidence supporting the annotation.

More direct or reliable evidence means the association is more reliable.



Components of an annotation “data source”



TAIR Annotation Search [Help]

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biological process	involved in	response to auxin stimulus	<i>inferred from mutant phenotype:</i> <i>analysis:</i> <i>physiological response:</i> <i>none:</i> Nagpal P, et al. (2005)	The Arabidopsis Information Resource/ 2005-10-13
biological process	represses	fruit development	<i>inferred from mutant phenotype:</i> <i>trait:</i> Nagpal P, et al. (2005)	Donghui Li/ 2006-08-24
plant structure	expressed in	flower	<i>inferred from expression pattern:</i> <i>expression library screening:</i> <i>none:</i> Nagpal P, et al. (2005)	The Arabidopsis Information Resource/ 2005-10-13
plant structure	expressed in	flower	<i>inferred from expression pattern:</i> <i>Transcript levels (e.g. Northern):</i> <i>none:</i> Goetz, et al. (2006)	Donghui Li/ 2006-08-24
plant structure	expressed in	ovule	<i>inferred from direct assay:</i> <i>localization of GUS fusion protein:</i> <i>none:</i> Goetz, et al. (2006)	Donghui Li/ 2006-08-24

The primary source for the evidence detailing how the data was generated.

Components of an annotation “date annotated”

TAIR Annotation Search [Help]

Your query for annotations based on the gene **ARF8** resulted in **20** records.

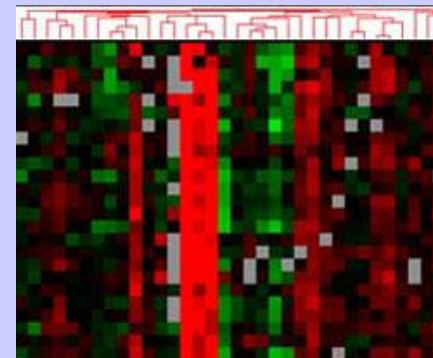
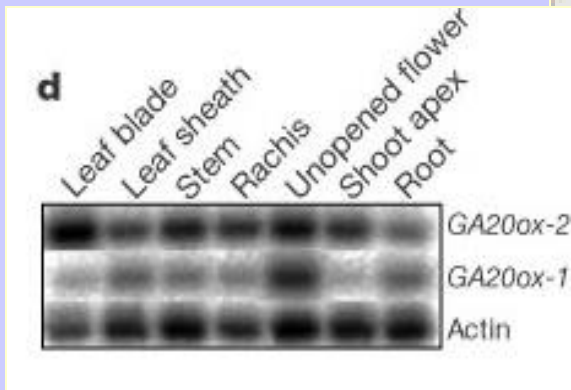
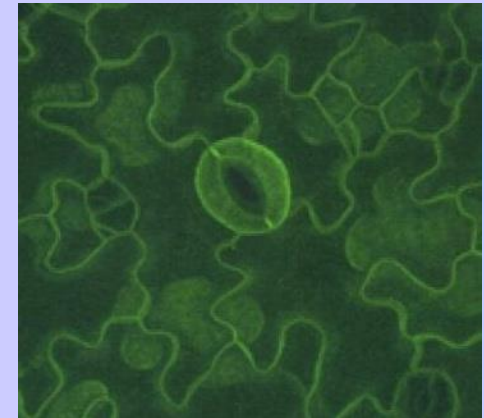
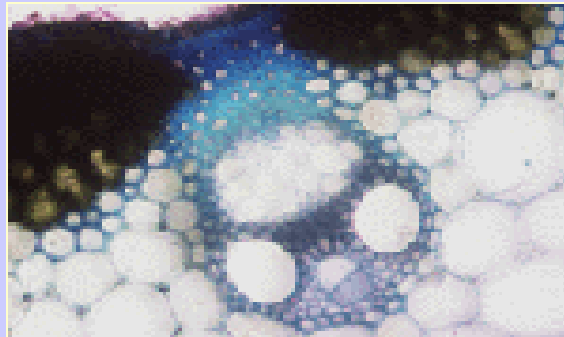
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molecular function	has	transcription factor activity	<i>traceable author:</i> original ex	The Arabidopsis Information Resource/ 2004-02-10
plant structure	expressed in	flower	<i>inferred from expression pattern:</i> Transcript levels (e.g. Northern): none: Goetz, et al. (2006)	The Arabidopsis Information Resource/ 2005-10-13
plant structure	expressed in	ovule	<i>inferred from direct assay:</i> localization of GUS fusion protein: none: Goetz, et al. (2006)	Donghui Li/ 2006-08-24

Information about when the annotation was made can be used to determine how up to date the annotation is.

What datatypes are used for annotation?

Phenotype, gene expression
and protein localization



Example 1: Sources of phenotype data

□ 1: DNA Res. 2002 Feb 28;9(1):11-7.

[Related Articles](#), [Links](#)

Positional cloning of rice semidwarfing gene, sd-1: rice "green revolution gene" encodes a mutant enzyme involved in gibberellin synthesis.

Monna L, Kitazawa N, Yoshino R, Suzuki J, Masuda H, Maehara Y, Tanji M, Sato M, Nasu S, Minobe Y.

Plant Genome Center, Tsukuba, Ibaraki, Japan. monna@pgcdna.co.jp

A rice semidwarfing gene, sd-1, known as the "green revolution gene," was isolated by positional cloning and revealed to encode gibberellin 20-oxidase, the key enzyme in the gibberellin biosynthesis pathway. Analysis of 3477 segregants using several PCR-based marker technologies, including cleaved amplified polymorphic sequence, derived-CAPS, and single nucleotide polymorphisms revealed 1 ORF in a 6-kb candidate interval. Normal-type rice cultivars have an identical sequence in this region, consisting of 3 exons (558, 318, and 291 bp) and 2 introns (105 and 1471 bp). Dee-Geo-Woo-Gen-type sd-1 mutants have a 383-bp deletion from the genome (278-bp deletion from the expressed sequence), from the middle of exon 1 to upstream of exon 2, including a 105-bp intron, resulting in a frame-shift that produces a termination codon after the deletion site. The radiation-induced sd-1 mutant Calrose 76 has a 1-bp substitution in exon 2, causing an amino acid substitution (Leu [CTC] to Phe [TTC]). Expression analysis suggests the existence of at least one more locus of gibberellin 20-oxidase which may prevent severe dwarfism from developing in sd-1 mutants.

PMID: 11939564 [PubMed - indexed for MEDLINE]

Information about the mutant phenotype is obtained from reading papers.

Example 1: sd-1 mutant phenotype in Gramineae

1: DNA Res. 2002 Feb 28;9(1):11-7.

Positional cloning of rice semidwarfing gene, sd-1: rice "green revolution gene" encodes enzyme involved in gibberellin synthesis.

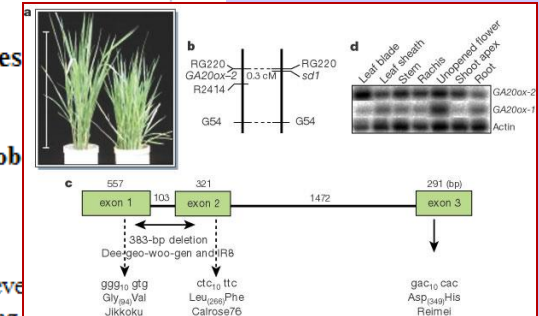
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PMID: 11939564 [PubMed - indexed for MEDLINE]

Related Articles, Links



Mutants in sd-1 have shorter stems due to a defect in expression of a gene involved in GA biosynthesis.

Example 1: sd-1 annotation

1: DNA Res. 2002 Feb 28;9(1):11-7.

Positional cloning of rice semidwarfing gene, sd-1: rice "green revolution gene" encodes enzyme involved in gibberellin synthesis.

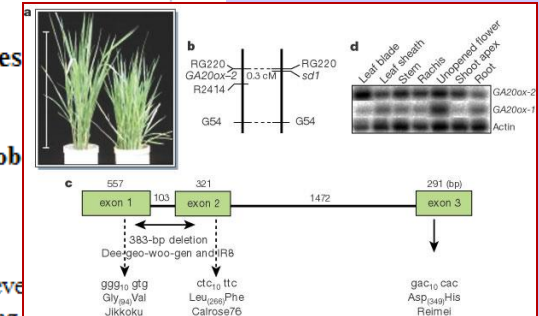
Monna L, Kitazawa N, Yoshino R, Suzuki J, Masuda H, Maehara Y, Tanji M, Sato M, Nasu S, Minobe Y, et al.

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PMID: 11939564 [PubMed - indexed for MEDLINE]

Related Articles, Links



Therefore: sd-1 would be annotated to the plant structure term stem (PO:0009047) with the evidence code IMP (inferred from mutant phenotype).

Example 1-1: Germplasm phenotype

NASC
The European Arabidopsis Stock Centre

Home |
Links |

Search Results

Search result for 'form photo '. Viewing records 1 to 10 of 160 hits. 10 results per page

| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | next

NW30

Name: brevipedicellus

Price: £ 2.25

Donor
Maarten Koornneef

Locus
bp

Photo


Stock type: individual line

Add to Basket

Description
Form

Phenotype
short pedicels, siliques bent downwards, reduced plant height.

NW32

Name: eceriferum

Price: £ 2.25

Donor
Maarten Koornneef

Locus
cer2

Photo


Stock type: individual line

Add to Basket

Description
Form

Phenotype
very bright green stems and siliques, complete absence of lobed plates and tube-shaped structures on the epicuticular wax layer, same as vc2 of G. Redei, group II of Koornneef.

Example 2: Expression of AGL21 “the data”

Title					
MADS-box gene expression in lateral primordia, meristems and differentiated tissues of Arabidopsis thaliana roots.					
Possibly related to:					
• MADS-box gene evolution beyond flowers: Expression in pollen, endosperm, guard cells, roots and trichomes.					
Article ID	Volume	Year	Page Start	Issue	Type
22654	214	2002	365	3	research_article
PubSource			Publication ID		
# 2996 PLANTA			500322694		
This paper describes the expression pattern of the AGL21 locus assayed by <i>in situ</i> hybridization.					
http://tesuque.stanford.ec (link)					
Authors					
Burgeff, C., Liljegren, S. J., Tapia-Lopez, R., Yanofsky, C., Alvarez-Buylla, E. R.					
Abstract					
Although MADS-box genes involved in flower and fruit development have been well characterized, the function of MADS-box genes expressed in vegetative structures has yet to be explored. At least seven members of this family are grouped in clades of genes that are preferentially expressed in roots of Arabidopsis thaliana (L.) Heynh.. We report here the cloning of the AGL21 MADS-box gene, which belongs to the ANR1 clade, and the mRNA <i>in situ</i> expression patterns of this and two other root MADS-box genes. AGL17 appears to be a lateral root cap marker in the root tip, and towards the elongation zone this gene is expressed in the epidermal cells. AGL21 is highly expressed in lateral root primordia and it has a punctate expression pattern in the primary root meristem. AGL12 also has a punctate expression pattern in the primary root meristem. AGL12 and AGL21 are also expressed in the central cylinder of differentiated roots and both are expressed in developing embryos. This study, combined with previous phylogenetic analyses, indicates that these MADS-box genes may play distinct regulatory roles during root development.					

Example 2: Expression of AGL21 “annotation”

Title

MADS-box gene expression in lateral primordia, meristems and differentiated tissues of *Arabidopsis thaliana* roots.

Possibly related to:

- [MADS-box gene evolution beyond flowers: Expression in pollen, endosperm, guard cells, roots and trichomes.](#)

Article ID	Volume	Year	Page Start	Issue	Type
22654	214	2002	365	3	research_article

PubSource **Publication ID**

2996

Sc

2002-

<http://tesque.stanford.edu>
(link)

Authors

Burgeff, C., Liljegren, S. J., Tapia-Lopez, R., Yanovsky, C., Alvarez-Buylla, E. R.

Abstract

Although MADS-box genes involved in **flower** and fruit **development** have been well characterized, the function of MADS-box genes expressed in **vegetative** structures has yet to be explored. At least seven members of this family are grouped in clades of genes that are preferentially expressed in roots of *Arabidopsis thaliana* (L.) Heynh.. We report here the cloning of the **AGL21** MADS-box gene, which belongs to the **ANR1** clade, and the mRNA in situ expression patterns of this and two other **root** MADS-box genes. **AGL17** appears to be a **lateral root** cap marker in the **root tip**, and towards the **elongation zone** this gene is expressed in the epidermal cells. **AGL21** is highly expressed in **lateral root** primordia and it has a punctate expression pattern in the **primary root meristem**. **AGL12** also has a punctate expression pattern in the **primary root meristem**. **AGL12** and **AGL21** are also expressed in the central cylinder of differentiated roots and both are expressed in developing embryos. This study, combined with previous phylogenetic analyses, indicates that these MADS-box genes may play distinct regulatory roles during **root development**.

End of tutorial