

实用生物信息技术

玉米BES1/BZR1转录因子家族初探

**Primary analyse of transcription factor family**

**BES1/BZR1 in maize**

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# What are phytohormones?



**Frits Went, 1903-1990**

“.....characterized by the property of serving as chemical messengers, by which the activity of certain organs is coordinated with that of others”.

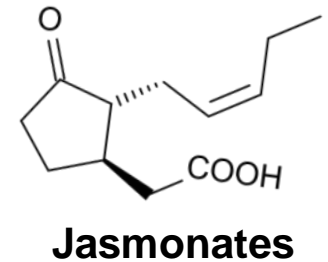
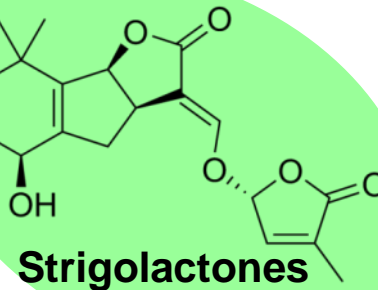
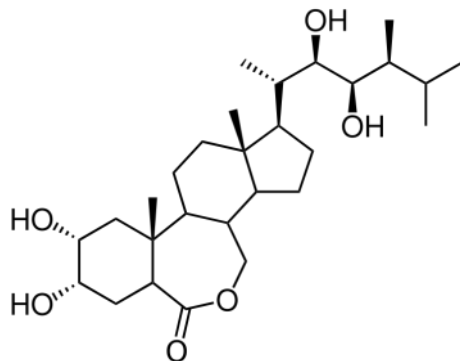
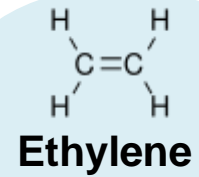
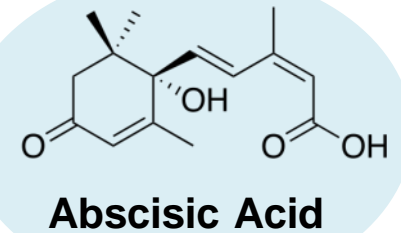
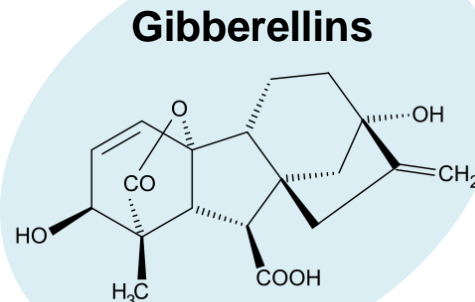
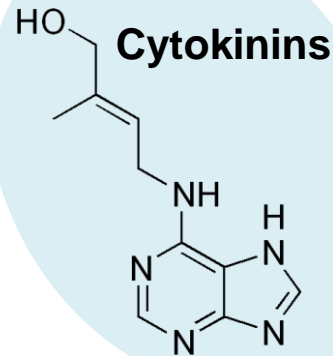
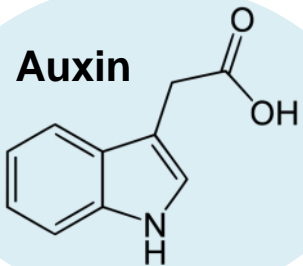
*-Frits Went and Kenneth Thimann, 1937*

Phytohormones regulate cellular activities (division, elongation and differentiation, pattern formation, organogenesis, reproduction, sex determination, and responses to abiotic and biotic stress.

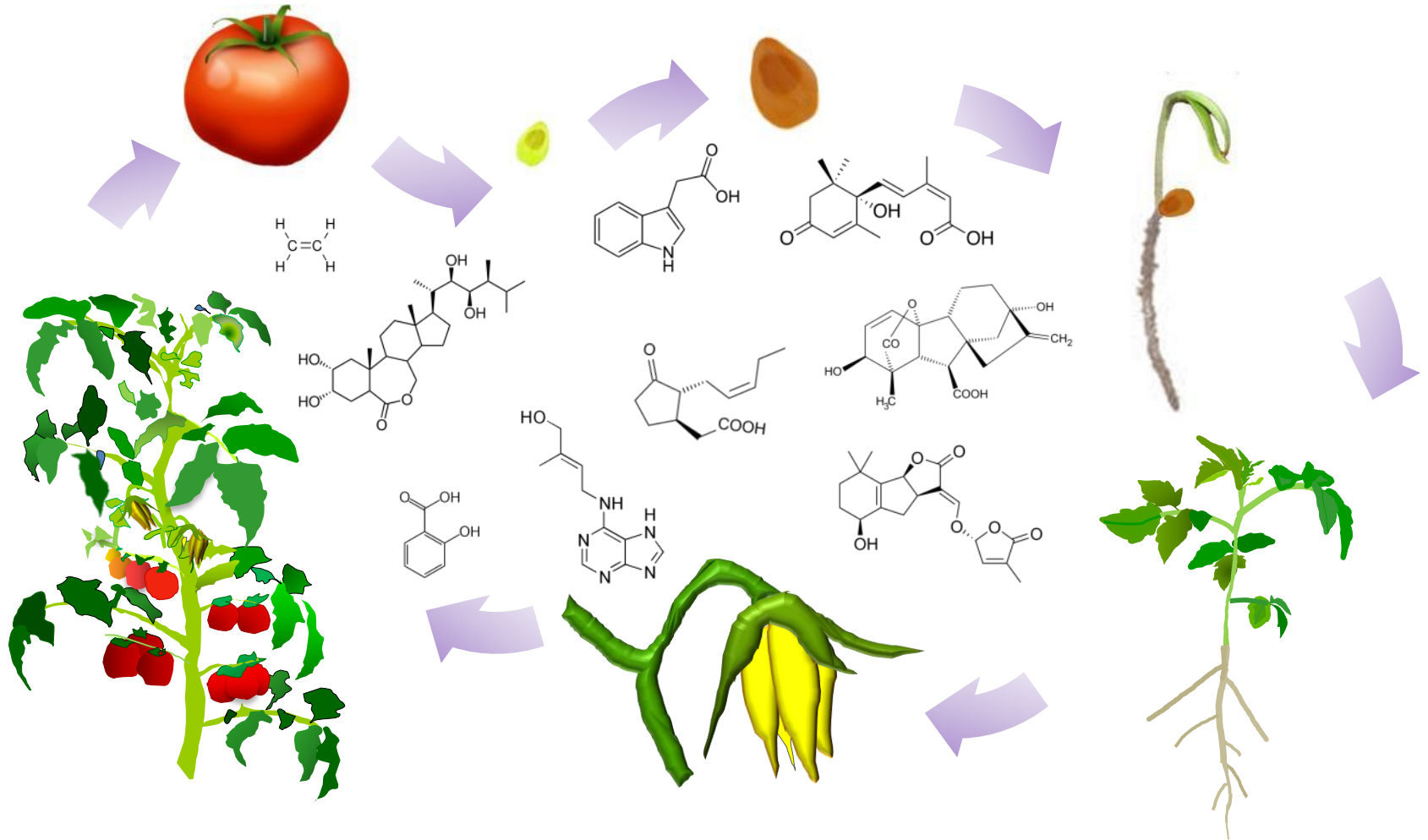


**Kenneth Thimann, 1904-1997**

# Phytohormones



# Phytohormones regulate all stages of the plant life cycle



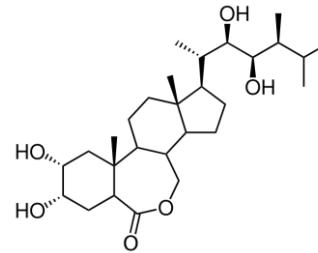
# Brassinosteroids

## Plant Steroid Hormones

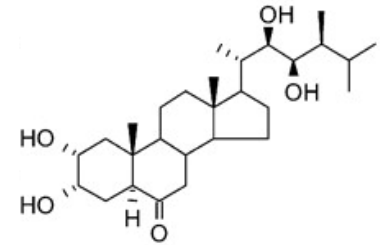
**Brassinosteroids (BRs) are a family of about 70 structurally related compounds that contribute to:**

- Growth
- Cell division, elongation, and differentiation
- Stress tolerance
- Reproductive development

**Brassinolide and castasterone are steroids like some animal hormones** (Oestariol, Ecdysone)



Brassinolide (BL)

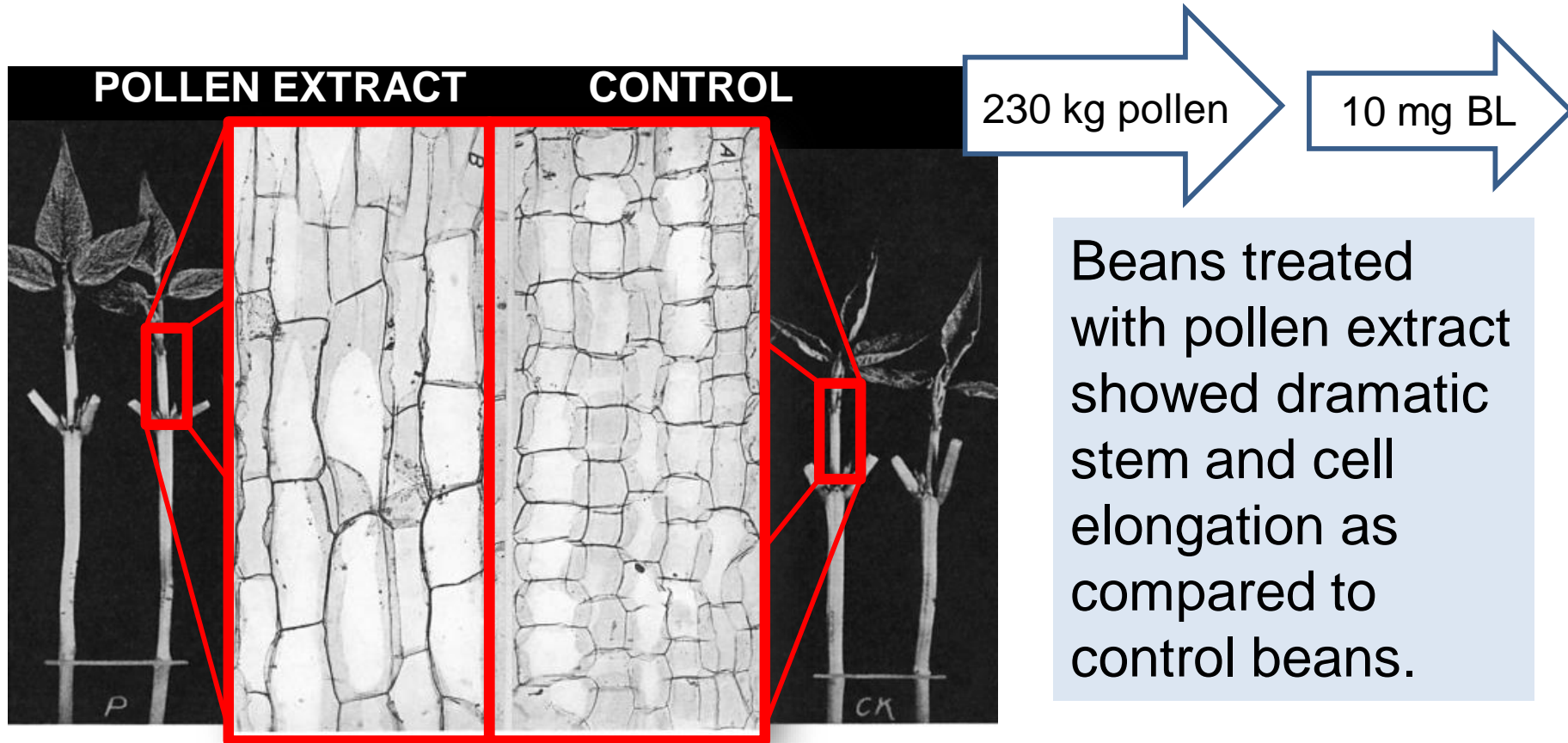


Castasterone (CS)



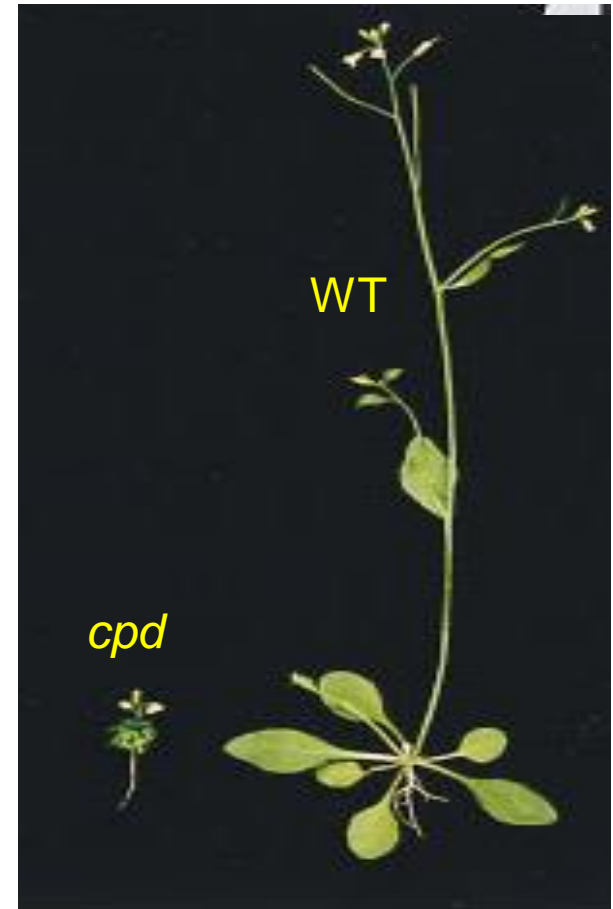
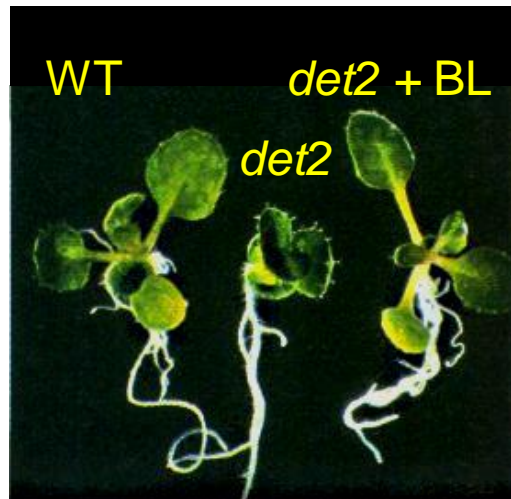
BR-deficient plants are severely dwfed (矮化)

# Pollen extract was found to promote cell and stem elongation (1941)

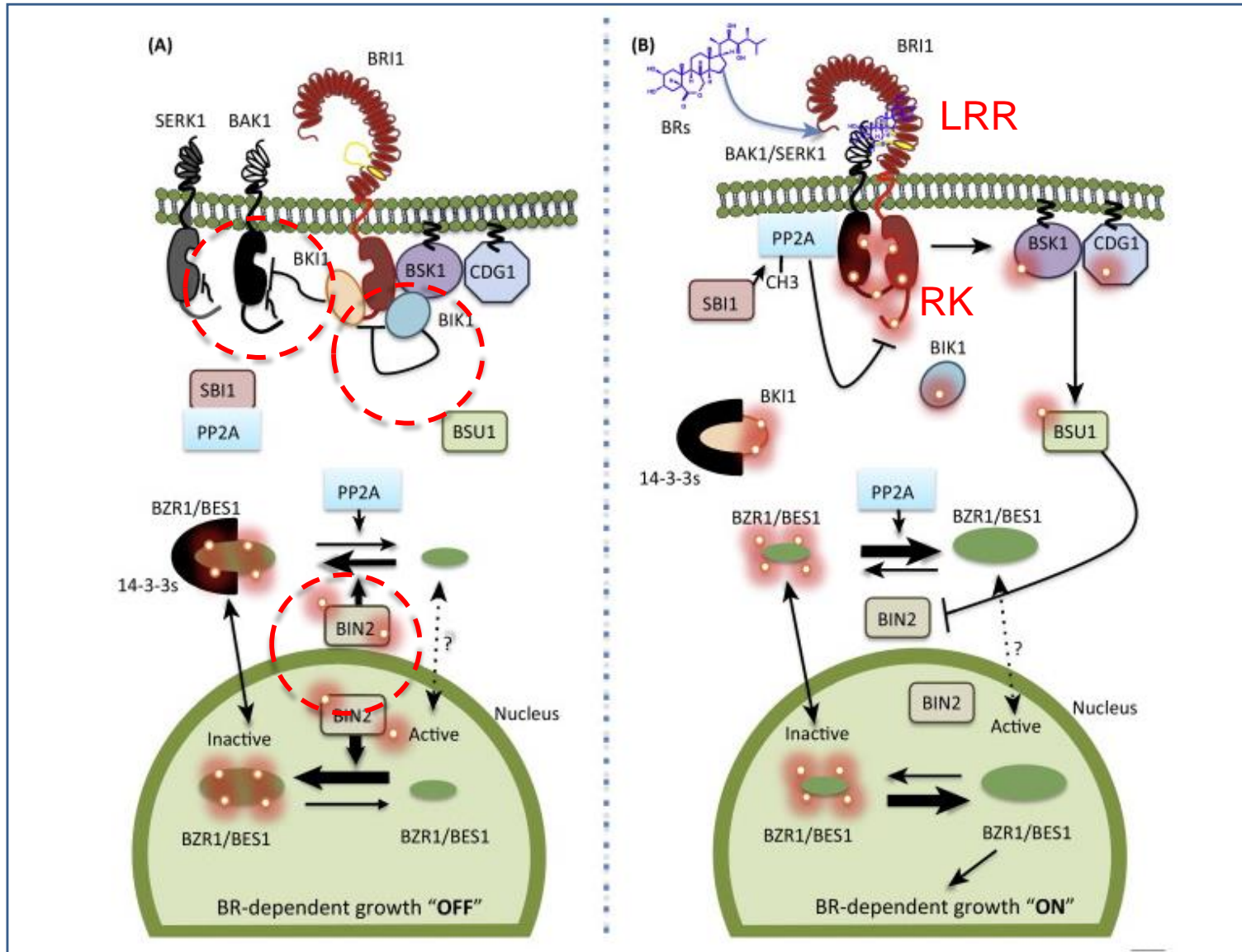


# Characterization of *det2* and *cpd* showed that BRs are essential

In 1996, two *Arabidopsis* mutants, *de-etiolated2* (*det2*) and *constitutive photomorphogenic dwarf* (*cpd*) were shown to be BR-deficient.

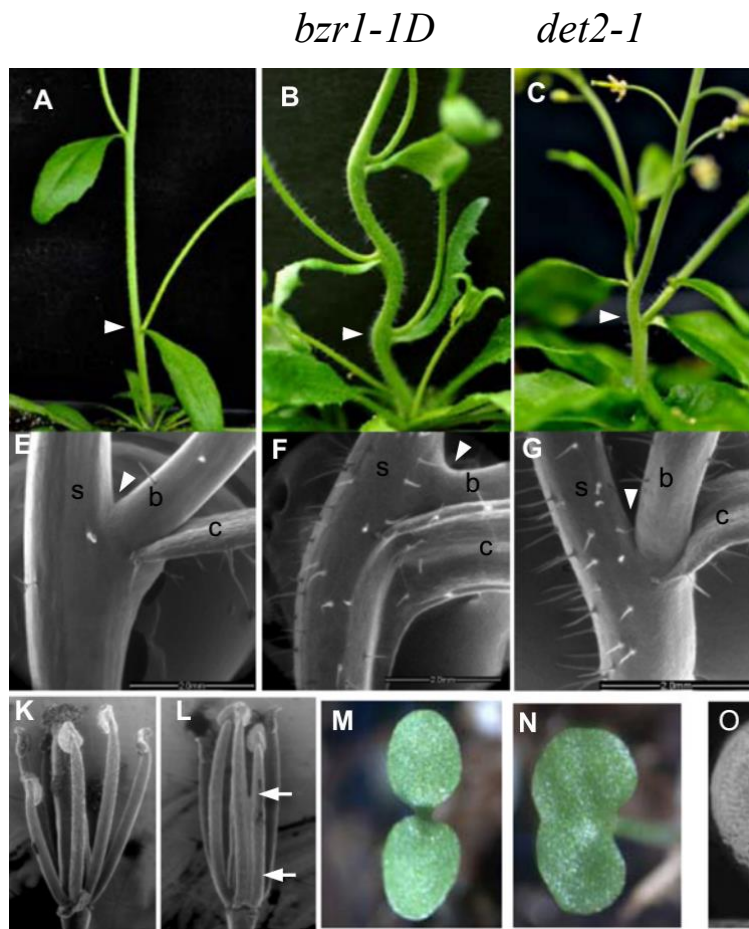


# Brassinosteroid signaling



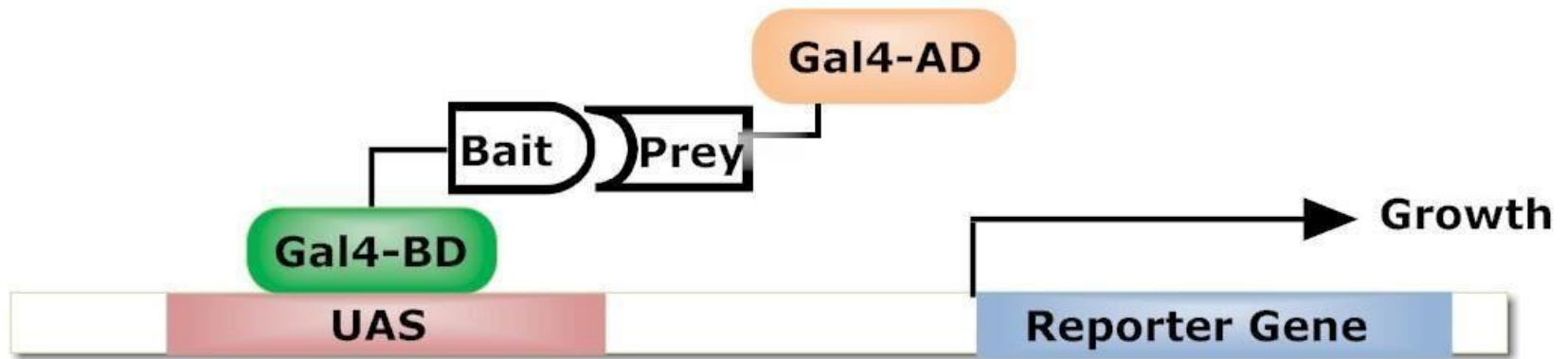


# Activation of BR signaling represses CUC gene expression and causes organ fusion phenotypes.



- BR-hypersensitive mutants *bzr1-1D* display organ-fusion phenotypes, whereas BR-insensitive mutants *det2-1* show enhanced organ boundaries.
- The BR-activated transcription factor BZR1 directly represses the CUP-SHAPED COTYLEDON (CUC) family of organ boundary identity genes.
- In WT plants, BZR1 accumulates at high levels in the nuclei of central meristem and organ primordia but at a low level in organ boundary cells to allow CUC gene expression.

# The same signal pathway exist in maize? For density tolerance of maize?



**Yeast Two Hybrid System**

bait : BZR1    prey : CUC promoter



# UniProtKB - Q8S307(BZR1\_ARATH) family&domain

Protein

**Protein BRASSINAZOLE-RESISTANT 1**

Gene

**BZR1**

Organism

*Arabidopsis thaliana* (Mouse-ear cress)

Status



Reviewed - Annotation score: ●●●●● - Experimental evidence at protein level<sup>i</sup>

## Family & Domains



Reviewed (11)

Swiss-Prot



Unreviewed (1,459)

TrEMBL

### Popular organisms

A. thaliana (17)

Rice (12)

Rice (4)

ARAAL (4)

Brassica oleracea var. oleracea (12)

### Sequence similarities<sup>i</sup>

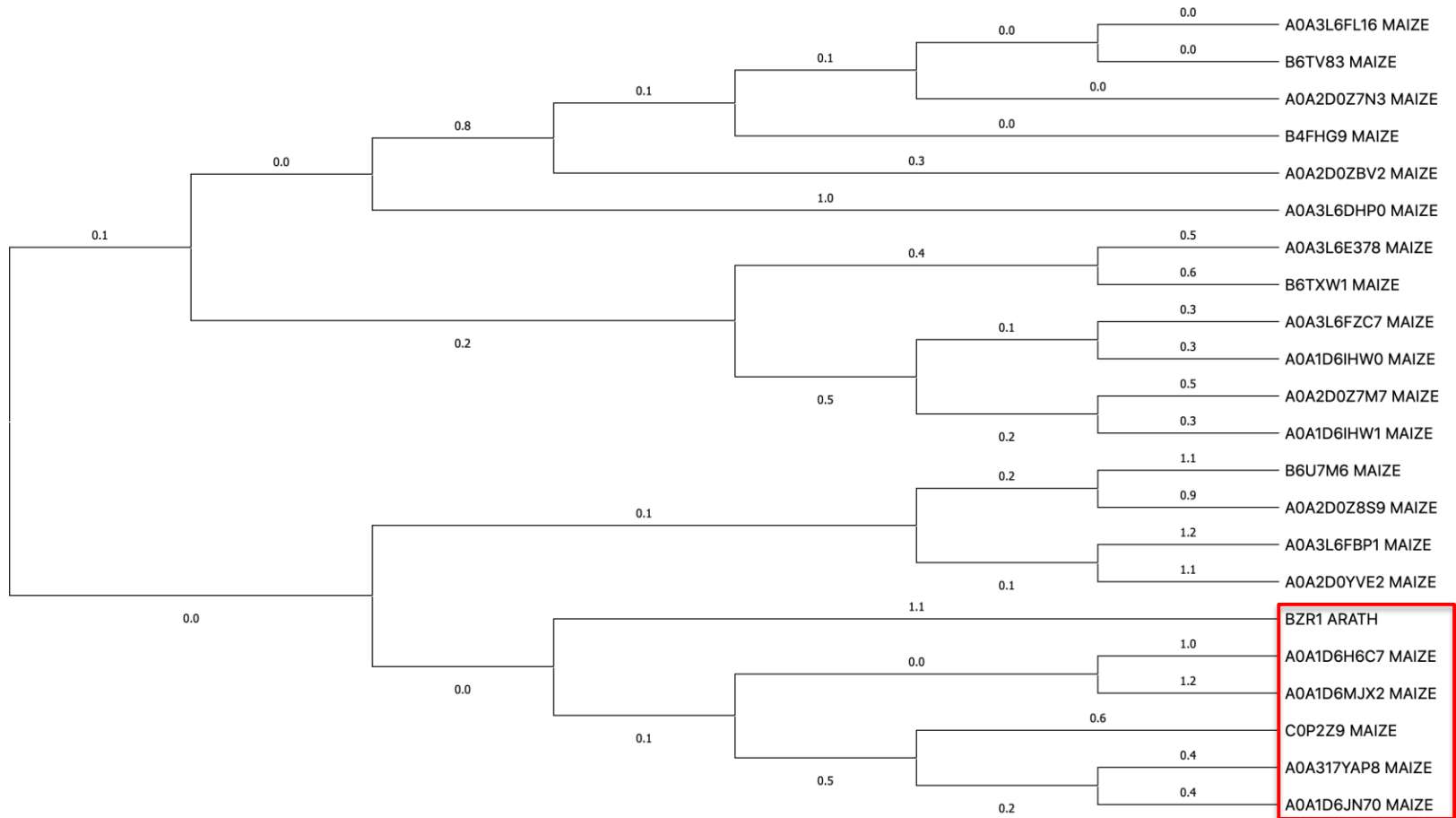
Belongs to the BZR/LAT61 family. (

The screenshot shows a search result table for UniProtKB entries. The table has columns for Entry, Entry name, Organism, and Remove. There are four entries listed, all from Zea mays (Maize). Below the table, there are buttons for 'Align', 'BLAST', 'Map Ids', 'Download', 'Full View', 'Remove', and 'Clear'. A 'Download' dialog box is open, showing options to 'Download selected (0)' or 'Download all (21)'. The 'Format' is set to 'FASTA (canonical)', and 'Compressed' is selected. There are 'Go' and 'Close' buttons in the dialog.

Entry	Entry name	Organism	Remove
<input type="checkbox"/> A0A3L6DHP0	A0A3L6DHP0_MAIZE	Zea mays (Maize)	
<input type="checkbox"/> A0A317YAP8	A0A317YAP8_MAIZE	Zea mays (Maize)	
<input type="checkbox"/> A0A2D0ZBV2	A0A2D0ZBV2_MAIZE	Zea mays (Maize)	
<input type="checkbox"/> A0A3L6E378	A0A3L6E378_MAIZE	Zea mays (Maize)	



# phylogenetic tree construction



Phylogenetic tree of BZR/LAT61 family of maize and Arabidopsis

# The introduction of AHD

Number of hormone related genes in the database

Hormone	# of Genes (support evidence)				All
	Genetic study			Gene Ontology annotation	
	Mutant	Transgenic	Other		
auxin	59	2	0	323	335
gibberellin	25	10	0	146	149
cytokinin	18	8	0	72	80
abscisic acid	78	1	0	252	290
ethylene	31	6	0	156	169
jasmonic acid	33	7	0	152	171
salicylic acid	22	2	0	116	135
brassinosteroid	35	2	0	43	73
ALL hormone	283	37	0	923	1046

- ☐ **Root** (258 mutants 150 genes)
  - ☐ **Primary root** (215 mutants 123 genes)
    - long (120 mutants, 63 genes)
    - short (93 mutants, 82 genes)
    - abnormal (3 mutants, 5 genes)
    - rescued by hormone (1 mutant, 1 gene)
    - reduced ethylene phenotype (1 mutant, 1 gene)
    - slightly longer than *abi2-1* (1 mutant, 1 gene)
    - display auxin resistance (1 mutant, 1 gene)
    - short and reduced sensitivity to MeJA (1 mutant, 1 gene)
  - ☐ **Lateral root** (114 mutants 67 genes)
  - ☐ **Root hairs** (59 mutants 36 genes)
  - ☐ **Agravitropic root** (34 mutants 27 genes)
  - ☐ **Swollen primary roots or lateral roots** (15 mutants 15 genes)
  - ☐ **Other** (43 mutants 43 genes)
- ☐ **Cotyledon/Leaf** (222 mutants 164 genes)
- ☐ **Hypocotyl/Stem** (261 mutants 150 genes)
- ☐ **Flower** (126 mutants 98 genes)
- ☐ **Silique/Seed** (161 mutants 130 genes)
- ☐ **Embryo** (19 mutants 22 genes)
- ☐ **Stress** (120 mutants 88 genes)

# the information of bzs1-1D mutant

## General information

<b>Mutant name</b>	bzs1-1D
<b>Mutant/Transgenic plant</b>	mutant
<b>Ecotype</b>	Col-0
<b>Mutagenesis type</b>	other
<b>Dominant/Recessive/Semi-dominant</b>	dominant
<b>PMID</b>	<a href="#">11970900</a>
<b>Comment</b>	No comment

## Mutated genes

Locus name	Alias	Hormone	Mutated site	Paper description
<a href="#">AT1G75080</a>	BZR1	brassinosteroid	Pro234 to Leu	BRZ resistant, bri1 suppressor

## Phenotype information

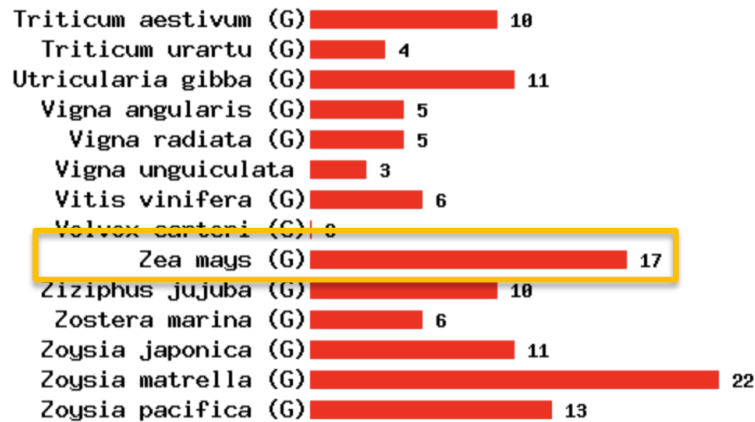
Organ	Attribute	No hormone
Cotyledon/Leaf	Hyponastic or epinastic leaves	hyponastic leaves
	Leaf color	dark green leaf
	Leaf size	small leaves
	Petiole	shortened petiole
	Rounded or narrow leaves	rounded leaves
	Rumpled or serrated leaves	rumpled leaves
	Vasculature pattern	abnormal
Silique/Seed	Silique shape	bent siliques
Flower	Flowering time under long day	late flowering

# Plant Transcription Factor Database

Browse by Family

AP2 (4461)	ARF (4578)	ARR-B (2354)	B3 (10609)	BBR-BPC (1256)
<b>BES1 (1549)</b>	C2H2 (17740)	C3H (9693)	CAMTA (1343)	CO-like (2125)
CPP (1612)	DI		L781)	EIL (1234)
ERF (21129)	FA		35)	GRAS (9304)
GRF (1876)	Gi		(2277)	HD-ZIP (8602)
HRT-like (249)	HR			LSD (957)
M-type_MADS (7541)	M		ted (15369)	NAC (19997)
NF-X1 (403)	NI		446)	NZZ/SPL (109)
Nin-like (2766)	R		)	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)		

**BES1 Family Introduction**  
**Download Sequences**  
**Multiple Sequences Alignment**  
**Phylogenetic Tree**



Distribution of BES1 family in different species

Species	TF ID	Description
<i>Zea mays</i> (17)	AC194970.5_FGP002	BES1 family protein
	GRMZM2G069486_P01	BES1 family protein
	GRMZM2G069486_P02	BES1 family protein
	GRMZM2G069486_P03	BES1 family protein
	GRMZM2G102514_P01	BES1 family protein
	GRMZM2G152172_P01	BES1 family protein
	GRMZM2G307241_P01	BES1 family protein
	GRMZM2G307241_P02	BES1 family protein
	GRMZM2G369018_P01	BES1 family protein
	GRMZM2G446515_P03	BES1 family protein
	GRMZM2G446515_P04	BES1 family protein
	GRMZM2G446515_P05	BES1 family protein
	GRMZM2G446515_P06	BES1 family protein
	GRMZM5G812774_P01	BES1 family protein
	GRMZM5G852801_P01	BES1 family protein
	GRMZM5G868061_P01	BES1 family protein
	GRMZM6G287292_P01	BES1 family protein

# Download of genome sequence

## Transcripts (18)

<input type="checkbox"/>		Species	ID	Transcript Name	Define
<input type="checkbox"/>	<input checked="" type="checkbox"/>	A. thaliana	19658080	AT1G75080.1	Brassinosteroid signalling positive regulator (BZR1) family protein
<input type="checkbox"/>	<input checked="" type="checkbox"/>	Z. mays	30967094	AC194970.5_FGP002	(1 of 2) PTHR31506:SF3 - BES1/BZR1 HOMOLOG PROTEIN 1-RELATED
<input type="checkbox"/>	<input checked="" type="checkbox"/>	Z. mays	30992807	GRMZM2G369018_P01	(1 of 11) PF05687 - BES1/BZR1 plant transcription factor, N-terminal (BES1_N)
<input type="checkbox"/>	<input checked="" type="checkbox"/>	Z. mays	30993844	GRMZM2G102514_P01	(1 of 1) K14503 - brassinosteroid resistant 1/2 (BZR1_2)
<input type="checkbox"/>	<input checked="" type="checkbox"/>	Z. mays	30994259	GRMZM2G446515_P05	(1 of 1) PTHR31352:SF2 - BETA-AMYLASE 7
<input type="checkbox"/>	<input checked="" type="checkbox"/>	Z. mays	30994261	GRMZM2G446515_P04	(1 of 1) PTHR31352:SF2 - BETA-AMYLASE 7
<input type="checkbox"/>	<input checked="" type="checkbox"/>	Z. mays	30994262	GRMZM2G446515_P03	(1 of 1) PTHR31352:SF2 - BETA-AMYLASE 7

The Phytozome website and database provide you with access to gene families, individual genes, diversity and expression data for 52 released plant genomes.



*Arabidopsis thaliana* TAIR10

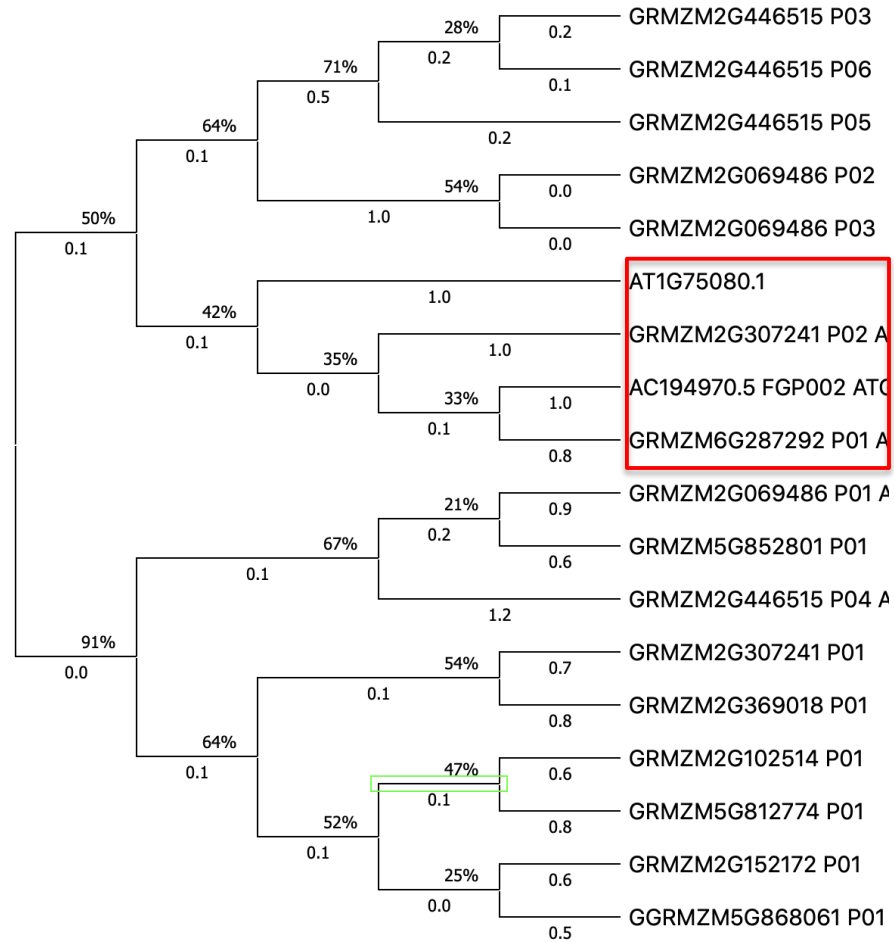


*Zea mays* Ensembl-18





# phylogenetic tree construction



Phylogenetic tree of CDS sequence of transcription factor genes of maize and Arabidopsis

## Database :

- UniProt
- Plant Transcription Factor Database
- Arabidopsis Hormone Database

## Tools:

- MEGA.(molecular evolutionary genetic analysis)

# 小组成员

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- Mitchell, J.W., and Whitehead, M.R. (1941) Responses of vegetative parts of plants following application of extract of pollen from *Zea mays*. *Bot. Gaz.* 102: 770-791.
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