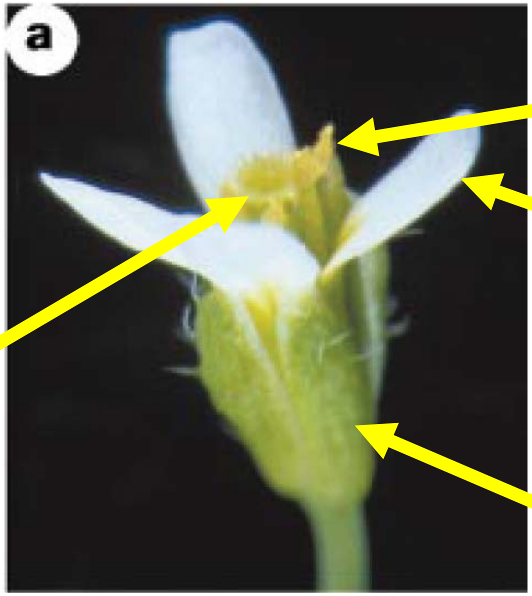
Genetic Specification of floral organ identity

Initiating floral development

Deciding when to initiate flowering - induced mutations
- in Nature

Flower structure of Arabidopsis

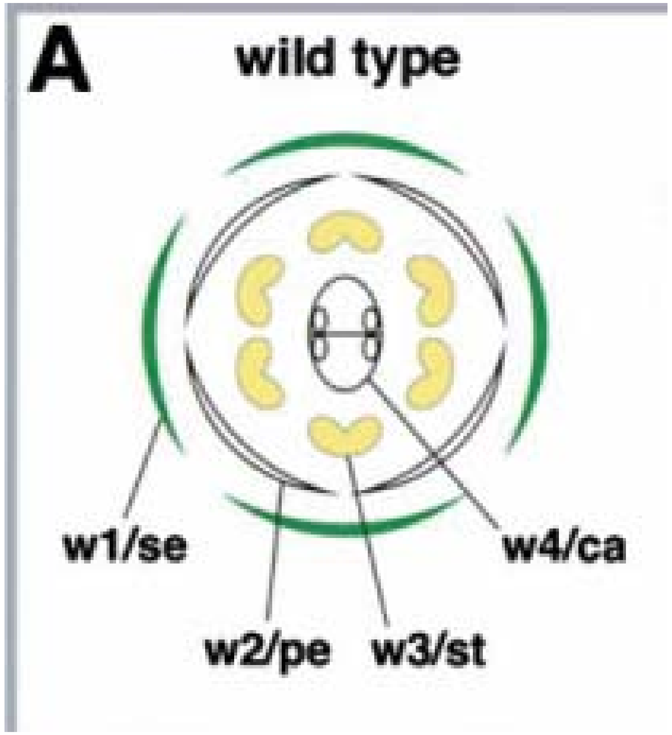


Stamens

Petals

Carpels

Sepals



In Arabidopsis:

Whorl 1	**4 sepals**
Whorl 2	**4 petals**
Whorl 3	**6 stamens**
Whorl 4	**2 carpels**

Why Arabidopsis ?

- short generation time, 8 weeks from seed to seed

- small, easily grown at high density in glasshouse or culture room

- diploid, small genome size, 125 Mb

- genome completely sequenced, 25,000 genes

- efficient transformation by Agrobacterium-mediated transformation

- many mutants described

Mutations that affect flower development placed in classes

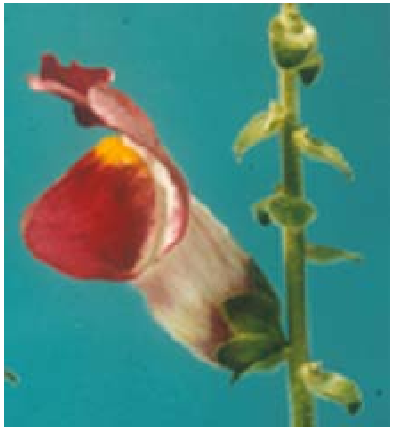
Alter the organs formed in two adjacent whorls

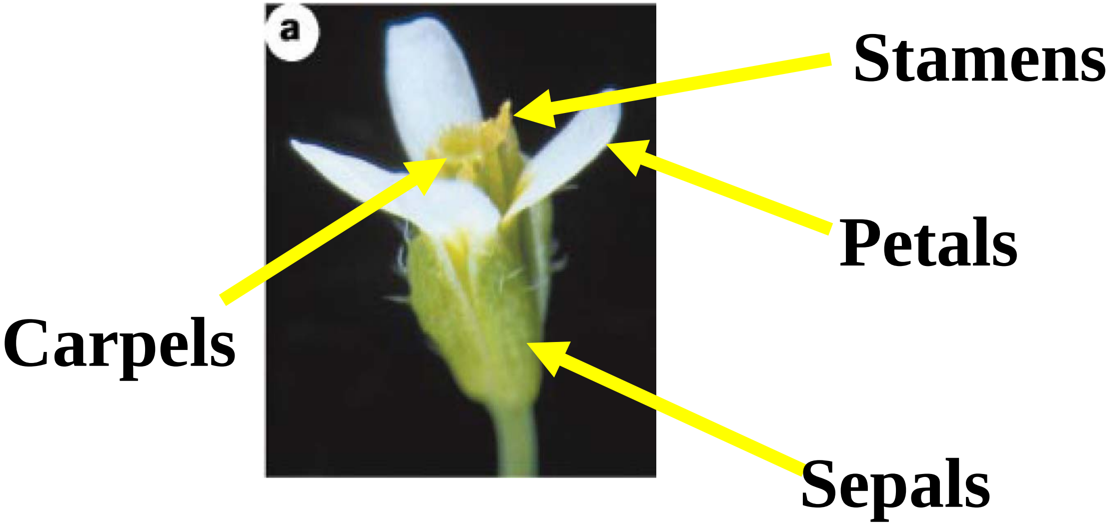
A mutants : affect sepals and petals

B mutants : affect petals and stamens

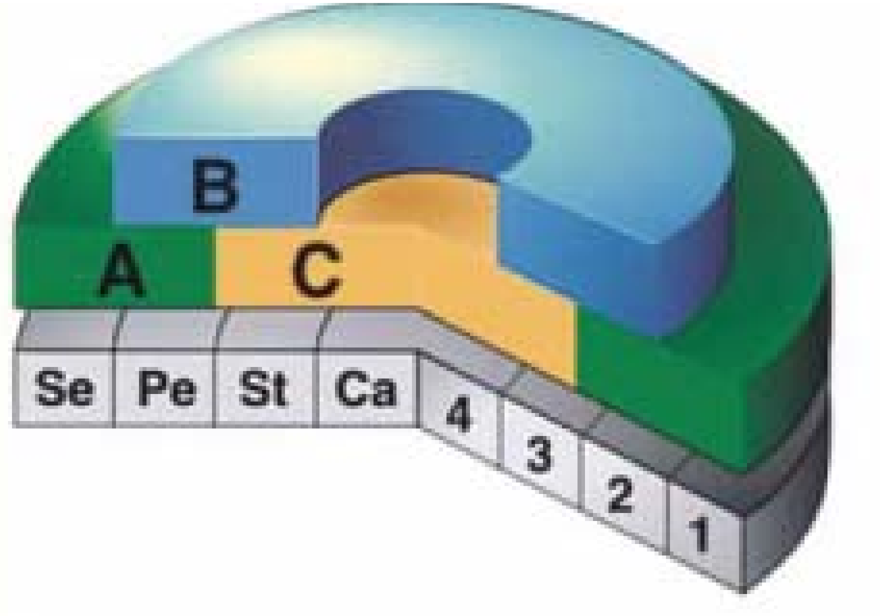
C mutants : affect stamens and carpels

Antirrhinum



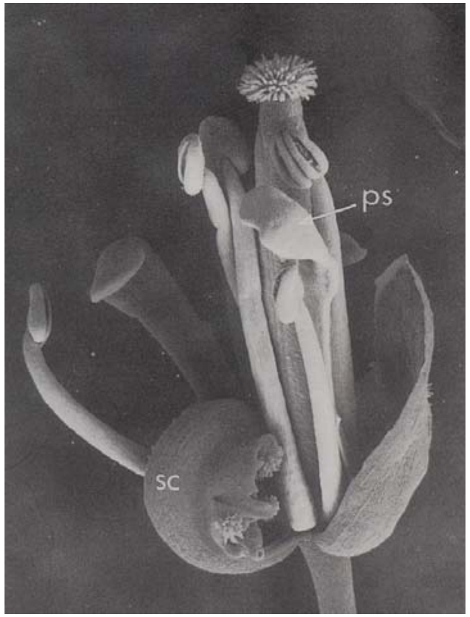


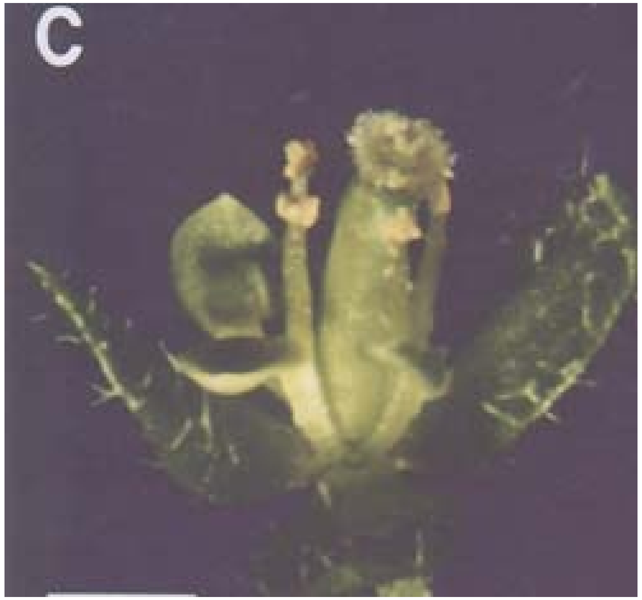
Specification of floral organ identity occurs in four circular domains called whorls and is controlled by three genetic functions called A,B and C



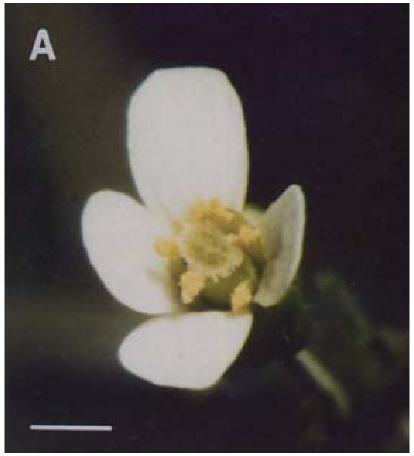
A function mutations affect flower development in Whorl 1 and 2

apetala2





apetala2



Wild-type

Sepals → carpelloid organs

petals → Absent or stamenoid

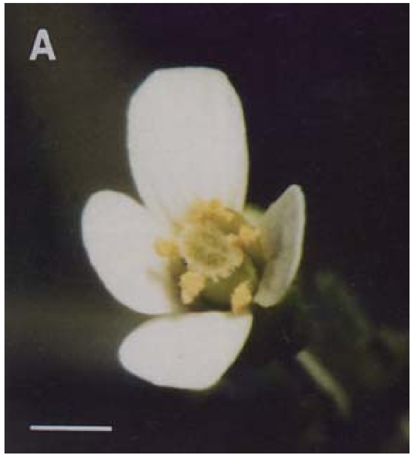
stamens → normal

carpels → normal

B function mutations affect flower development in Whorl 2 and 3

apetala3

pistillata



Wild-type

Sepals →	normal
petals →	Sepals or absent
stamens →	carpelloid
carpels →	normal

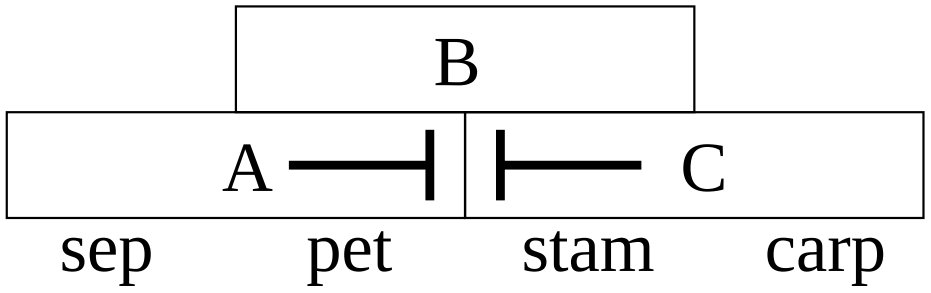
C function mutations affect flower development in Whorls 3 and 4

agamous

Sepals →	normal
petals →	normal
stamens →	petals
carpels →	Sepals and flower inside a flower

Wild-type

Analysis of mutant phenotypes suggested ABC model

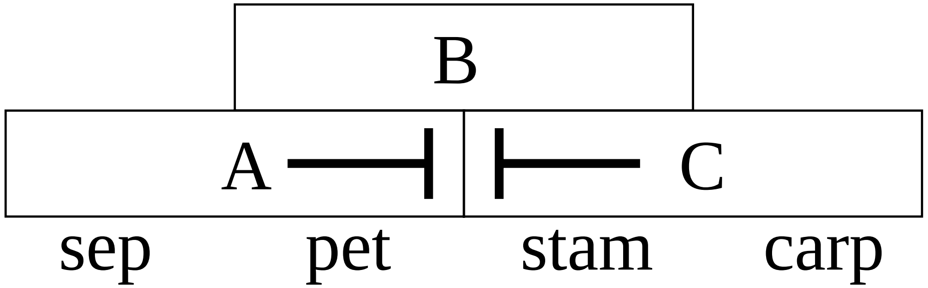


A function - APETALA1, APETALA2
B function - APETALA3 PISTILLATA
C function - AGAMOUS

Overlapping functions provide new identities
A opposes C and C opposes A

Interpretation of mutant phenotypes according to ABC model

Wild type

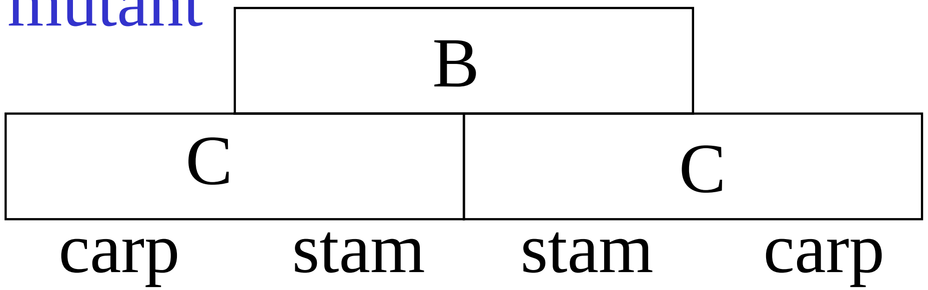


B

A ⊣ ⊢ C

sep pet stam carp

A mutant

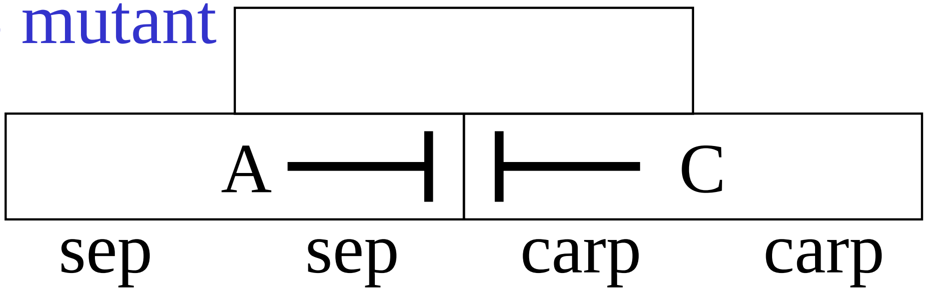


B

C C

carp stam stam carp

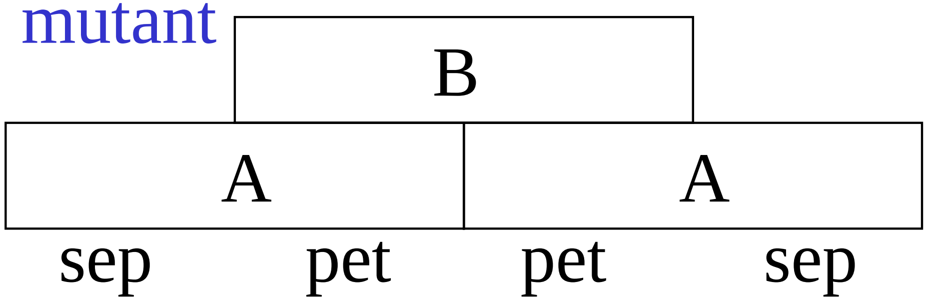
B mutant



A ⊣ ⊢ C

sep sep carp carp

C mutant



B

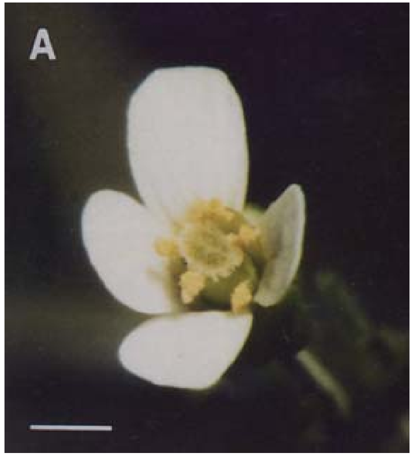
A A

sep pet pet sep

Double mutants

pi ag double mutant / loss of B and C function
All whorls are sepals
More whorls

Wild-type



ap2 pi double mutant /
loss of A and B function

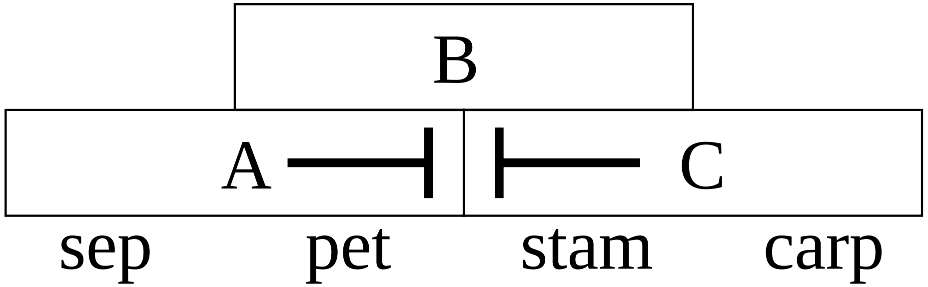
All whorls are carpels

ap2 ag double mutant / loss of A and C

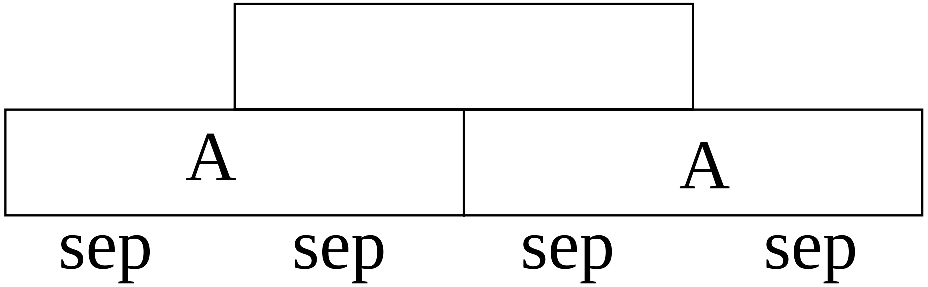
Leaves in 1st and 4th whorl
Modified petals/stamens in second and third
More whorls

Interpretation of double mutant phenotypes according to ABC model

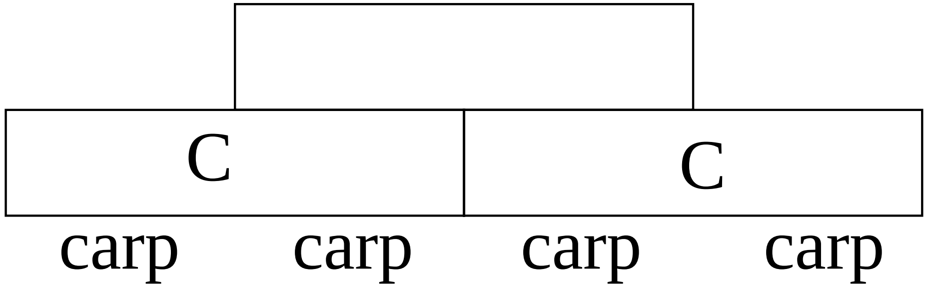
Wild type


B
A
C
sep pet stam carp

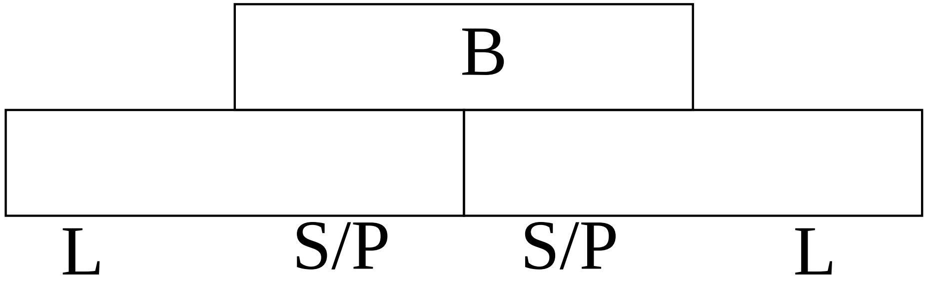
BC mutant


A
A
sep sep sep sep

AB mutant


C
C
carp carp carp carp

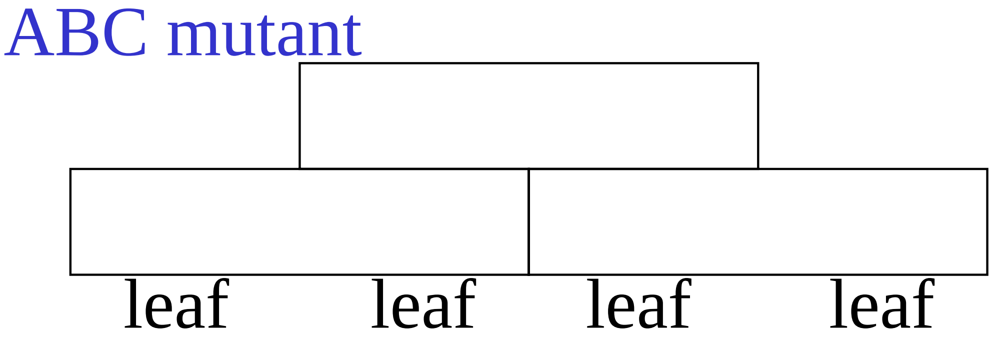
AC mutant


B
L S/P S/P L

ABC triple mutant phenotpe

ap2 pi ag triple mutant / loss of ABC function

All whorls leaf like



ABC mutant

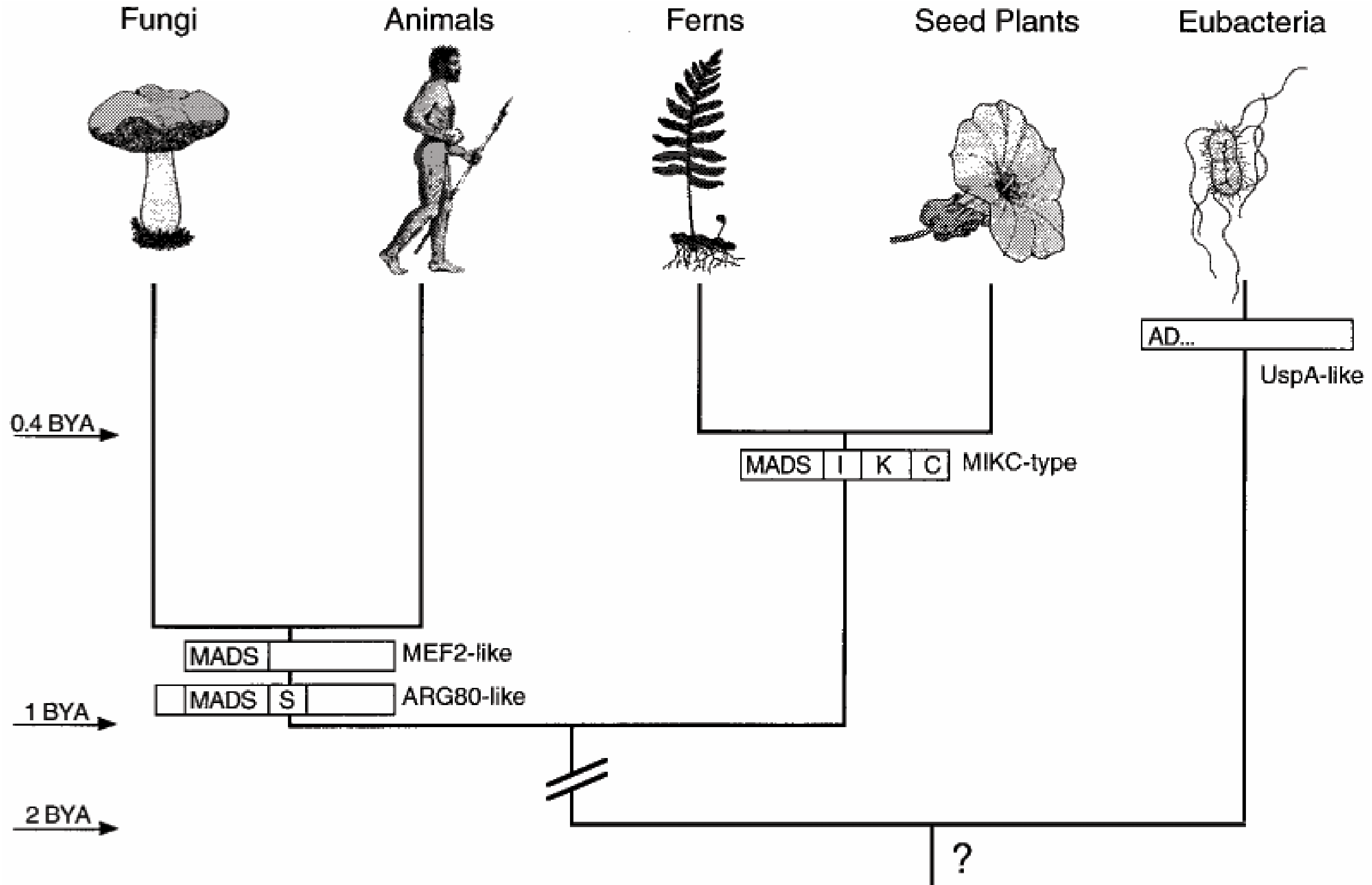
leaf leaf leaf leaf

MADS box transcription factors play important roles in floral development

AP1, AP3, PI, AG are MADS box transcription factors

M : MCM1 yeast
A : Agamous
D : Deficiens, Antirrhinum B function gene
S : serum response factor, humans

AP2 - another class of transcription factor

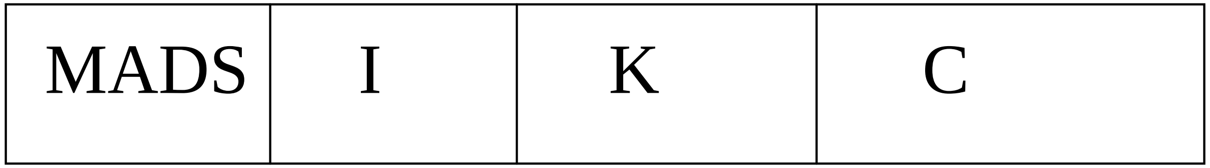


MADS box TFs have been amplified in the plant lineage and AP2-like are plant specific

Genome sequencing programmes allow the number of transcription factors belonging to each family in different organisms to be counted

	MADS	AP2-like
Arabidopsis	82	138
Drosophila	2	0
C. Elegans	2	0
Yeast	4	0

Structure of plant MADS box transcription factors

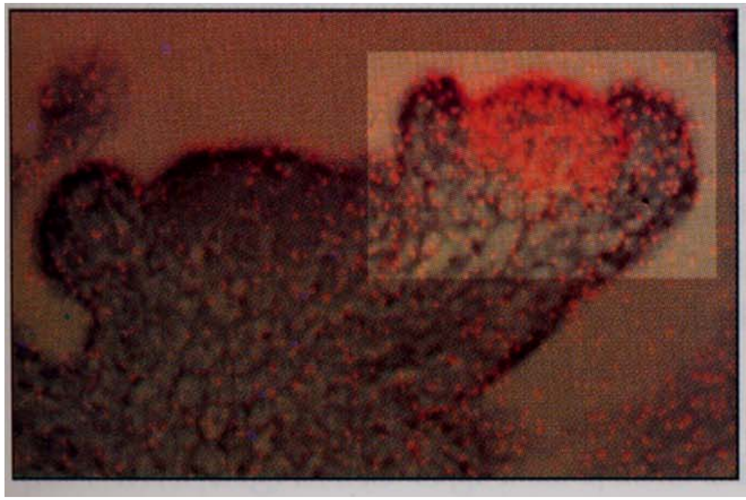


MADS transcription factor

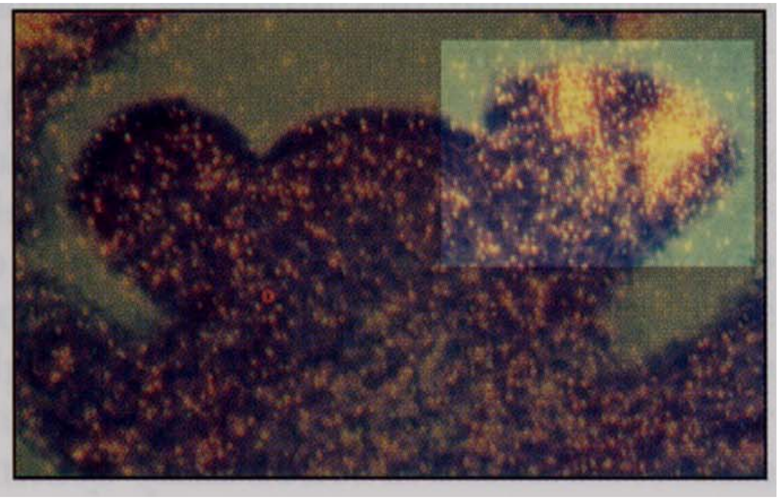
MADS - DNA binding
I - intervening region
K - protein-protein interactions
C - carboxy-terminal domain

Bind DNA through a conserved DNA sequence called CArG Box – $CC(A/T)_6GG$

Patterns of expression indicate that spatial control is regulated mainly at the level of transcription



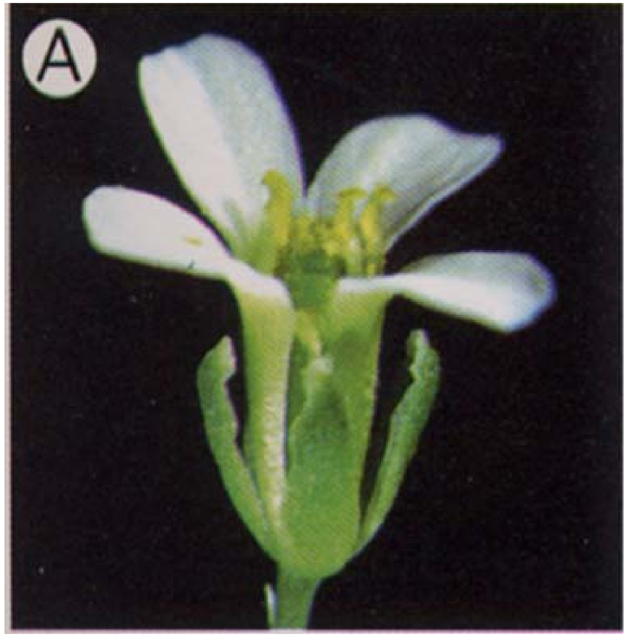
Agamous
C function
Expressed in whorls 3 and 4



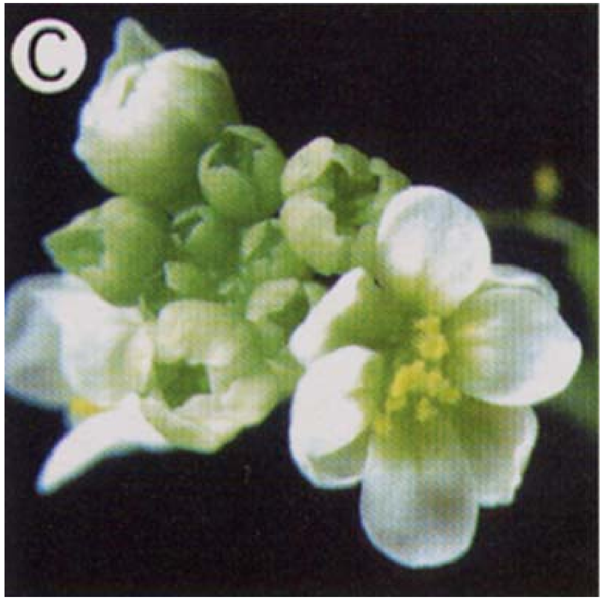
Apetala3
B function
Expressed in whorls 2 and 3

Misexpression from the 35S viral promoter in transgenic plants supports proposed roles of B function genes

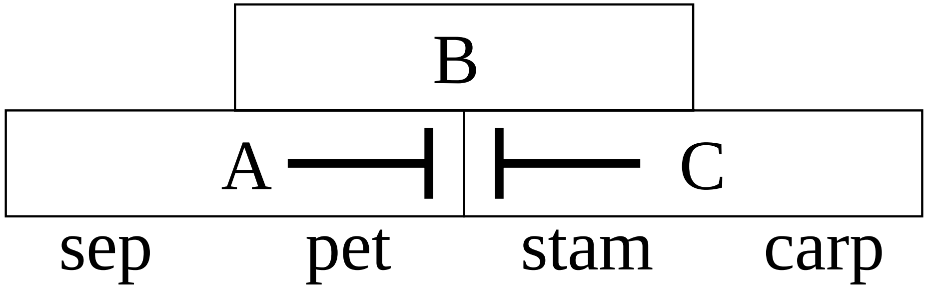
Wild type



35S::AP3 35S::PI



Wild type

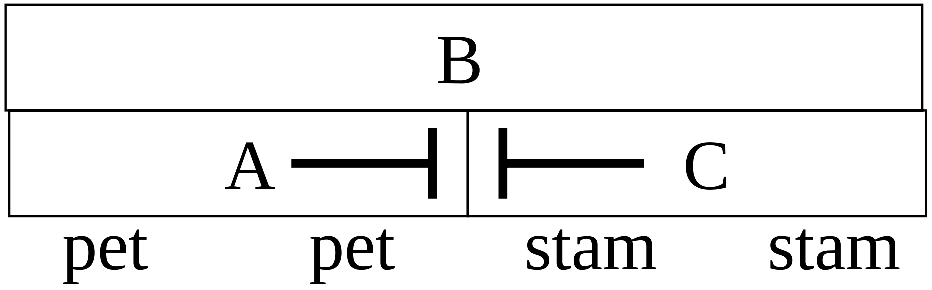


B

A ⊣ ⊢ C

sep pet stam carp

35S::AP3 35S::PI

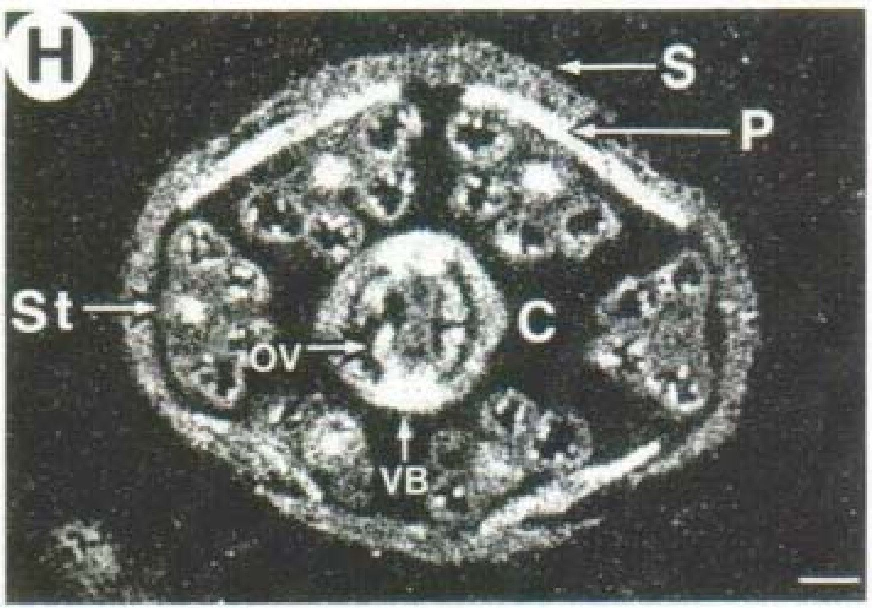


B

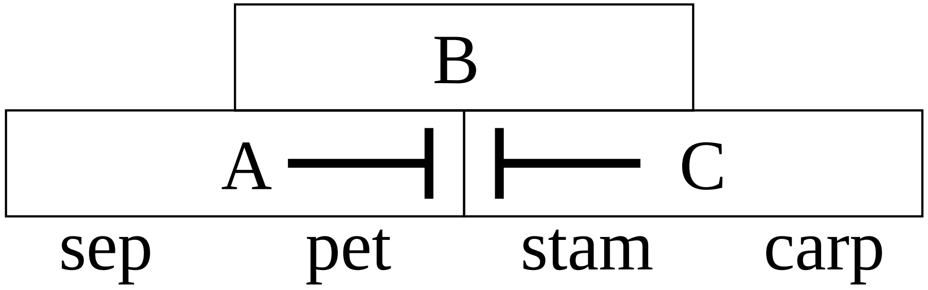
A ⊣ ⊢ C

pet pet stam stam

The A function gene AP2 is an exception: expressed in all whorls but only active in 1 and 2 whorl



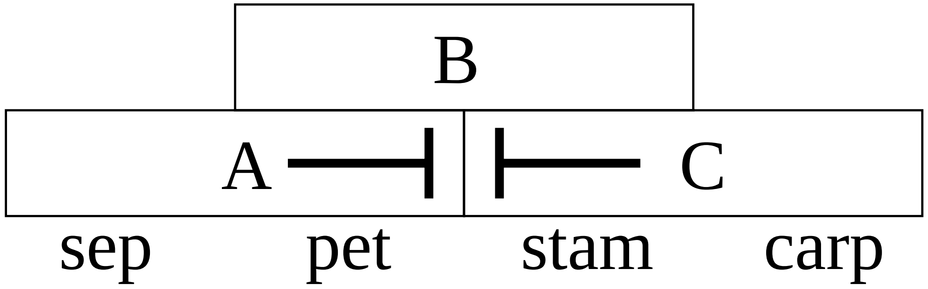
Wild type



Regulation of Floral organ identity gene expression

AP1 (A function) misexpression in ag (C function) mutant

Wild type



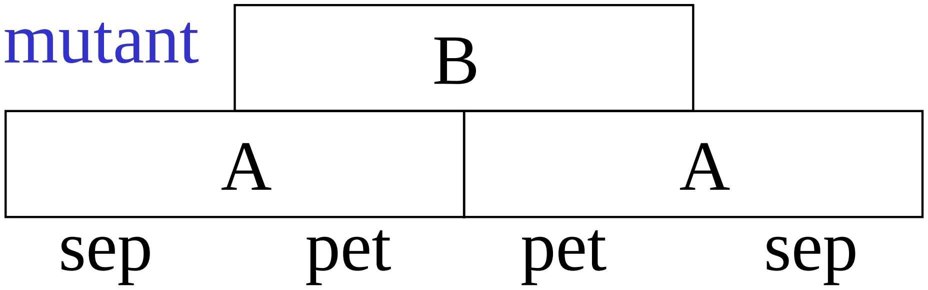
B

A C

sep pet stam carp

ag

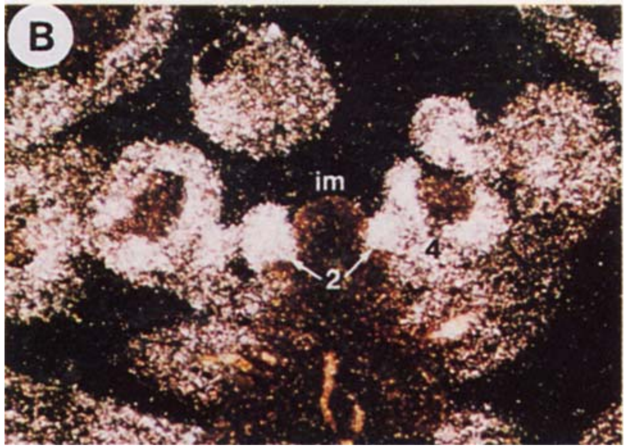
C mutant



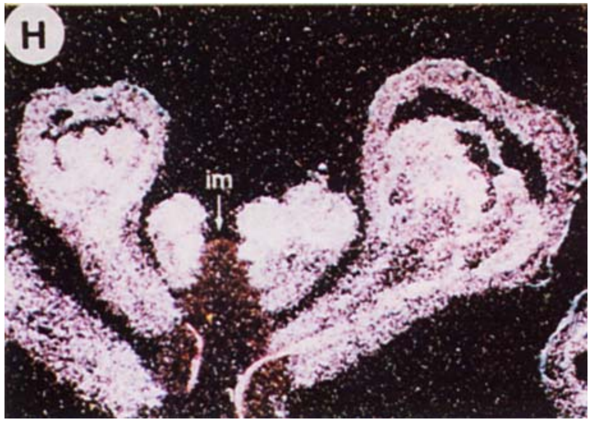
B

A A

sep pet pet sep



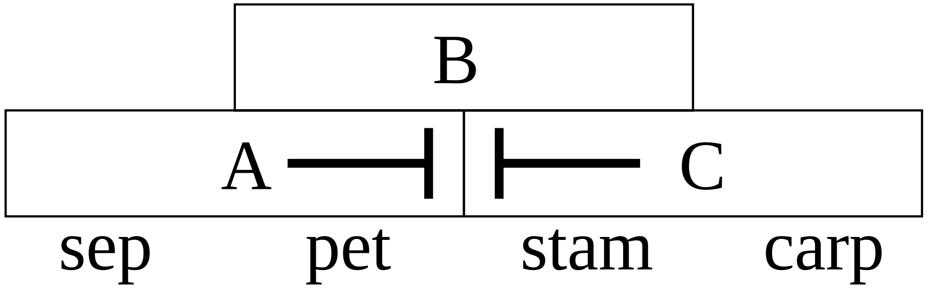
AP1 mRNA in
Wild-type plants
Only in whorl 1 and 2



AP1 mRNA in
ag mutant plants
In all whorls

Further additions to the ABC model : SUPERMAN

Wild type

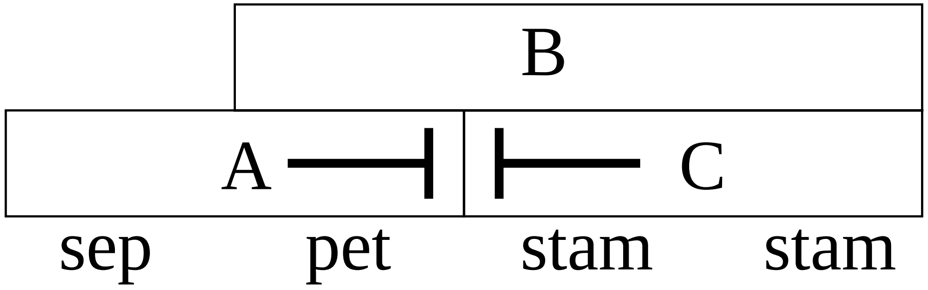


B

A ⊣ ⊢ C

sep pet stam carp

superman



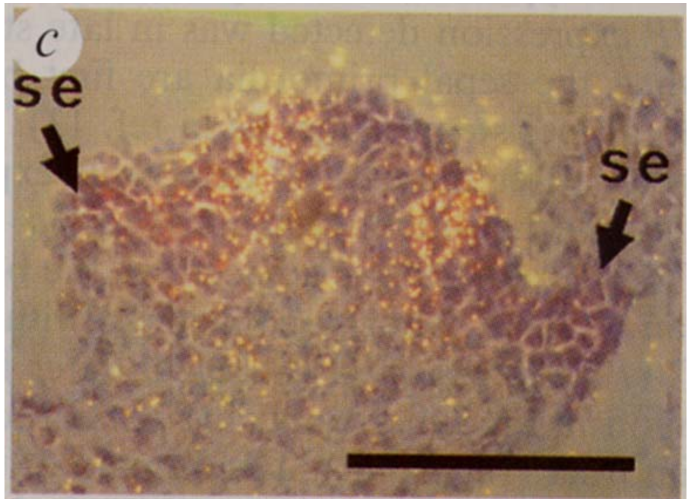
B

A ⊣ ⊢ C

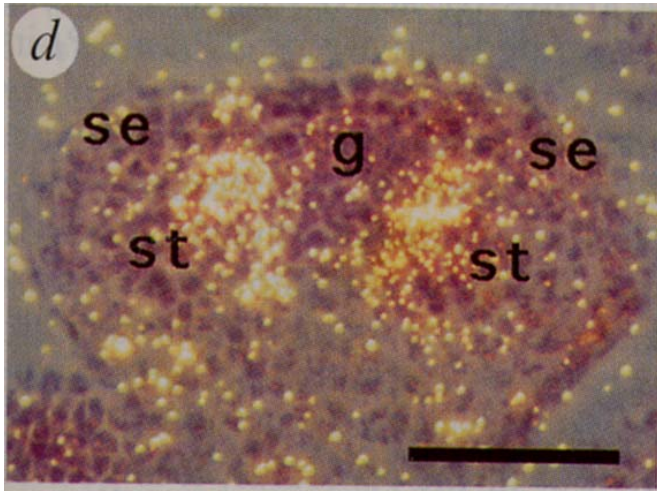
sep pet stam stam

SUPERMAN is expressed at the boundary between the third and fourth whorl

Stage 3



Stage 4

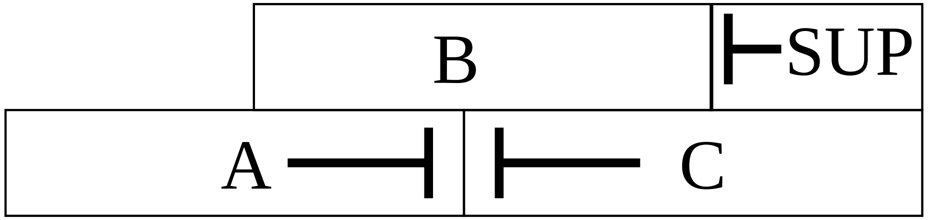


SUP encodes a likely zinc-finger DNA-binding protein containing Cys2 His2 type zinc fingers and a Serine/proline rich activation domain.

ABC model

Summary

Wild type



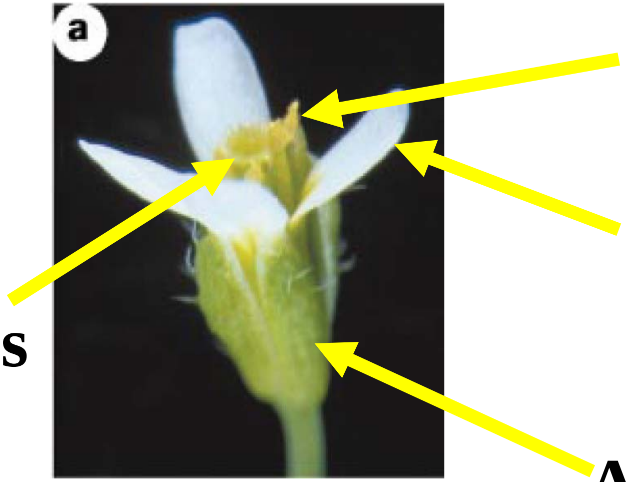
B

⊢SUP

A ⊣

⊢ C

sep pet stam carp



C: Stamens

B: Petals

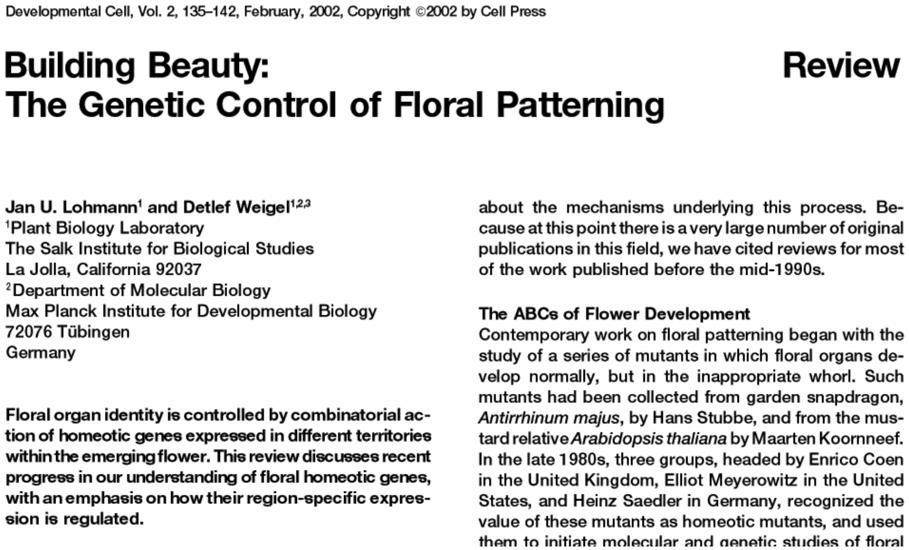
C: Carpels

A: Sepals

Web site

- this presentation

- PDFs



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Building Beauty:
The Genetic Control of Floral Patterning

Review

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Floral organ identity is controlled by combinatorial action of homeotic genes expressed in different territories within the emerging flower. This review discusses recent progress in our understanding of floral homeotic genes, with an emphasis on how their region-specific expression is regulated.

about the mechanisms underlying this process. Because at this point there is a very large number of original publications in this field, we have cited reviews for most of the work published before the mid-1990s.

The ABCs of Flower Development

Contemporary work on floral patterning began with the study of a series of mutants in which floral organs develop normally, but in the inappropriate whorl. Such mutants had been collected from garden snapdragon, *Antirrhinum majus*, by Hans Stubbe, and from the mustard relative *Arabidopsis thaliana* by Maarten Koornneef. In the late 1980s, three groups, headed by Enrico Coen in the United Kingdom, Elliot Meyerowitz in the United States, and Heinz Saedler in Germany, recognized the value of these mutants as homeotic mutants, and used them to initiate molecular and genetic studies of floral

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Forschung

Abt. Entwicklungsbiologie de Pflanzen

George Coupland