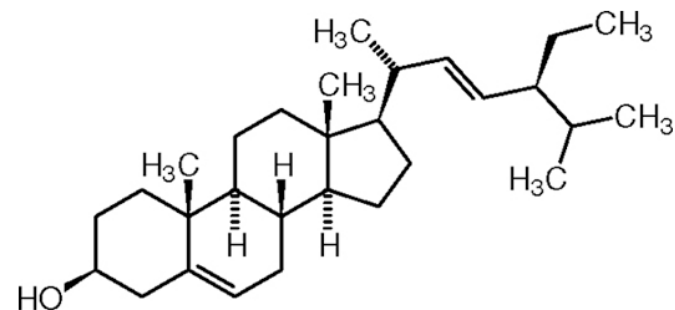


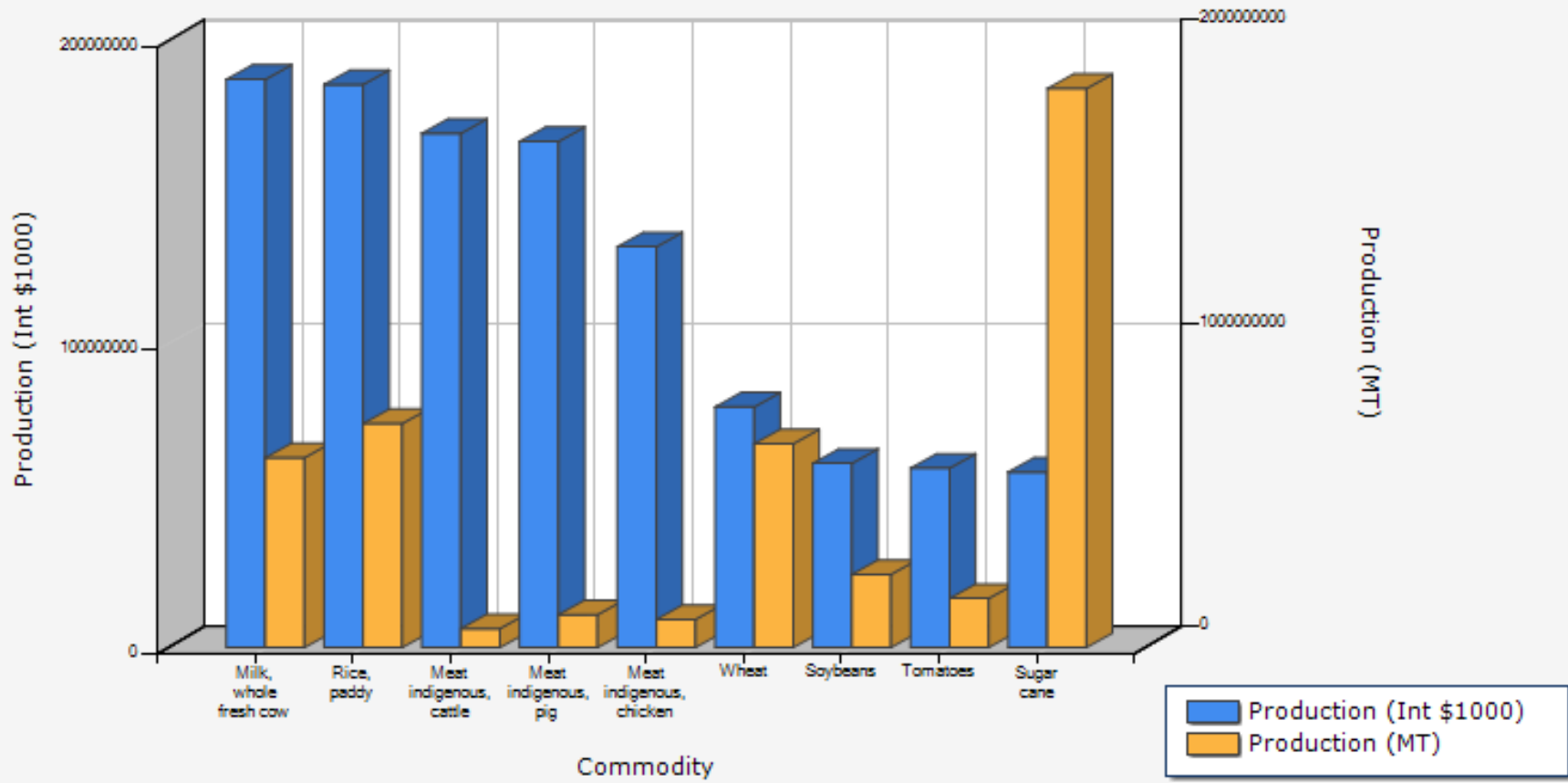
Enginyeria metabòlica d'esterols en tomàquet: Una eina per millorar la qualitat del fruit i la tolerància a condicions ambientals adverses?

Teresa Altabella



Tomato is important as food and in the global economy

Top production - World (Total) - 2012



Tomato is important as food and in the global economy

THE TOP PRODUCERS OF TOMATOES IN 2012

in tons; Source: FAOSTAT



*FAO estimates

Tomato as a model system for studying fleshy fruit ripening



- ✓ commercial importance
- ✓ relatively short development period
- ✓ easy propagation
- ✓ diploid
- ✓ genome: 950 Mb, 12 chromosomes

Sequenced genome (2012)

Sol Genomics Network

<http://solgenomics.net/>



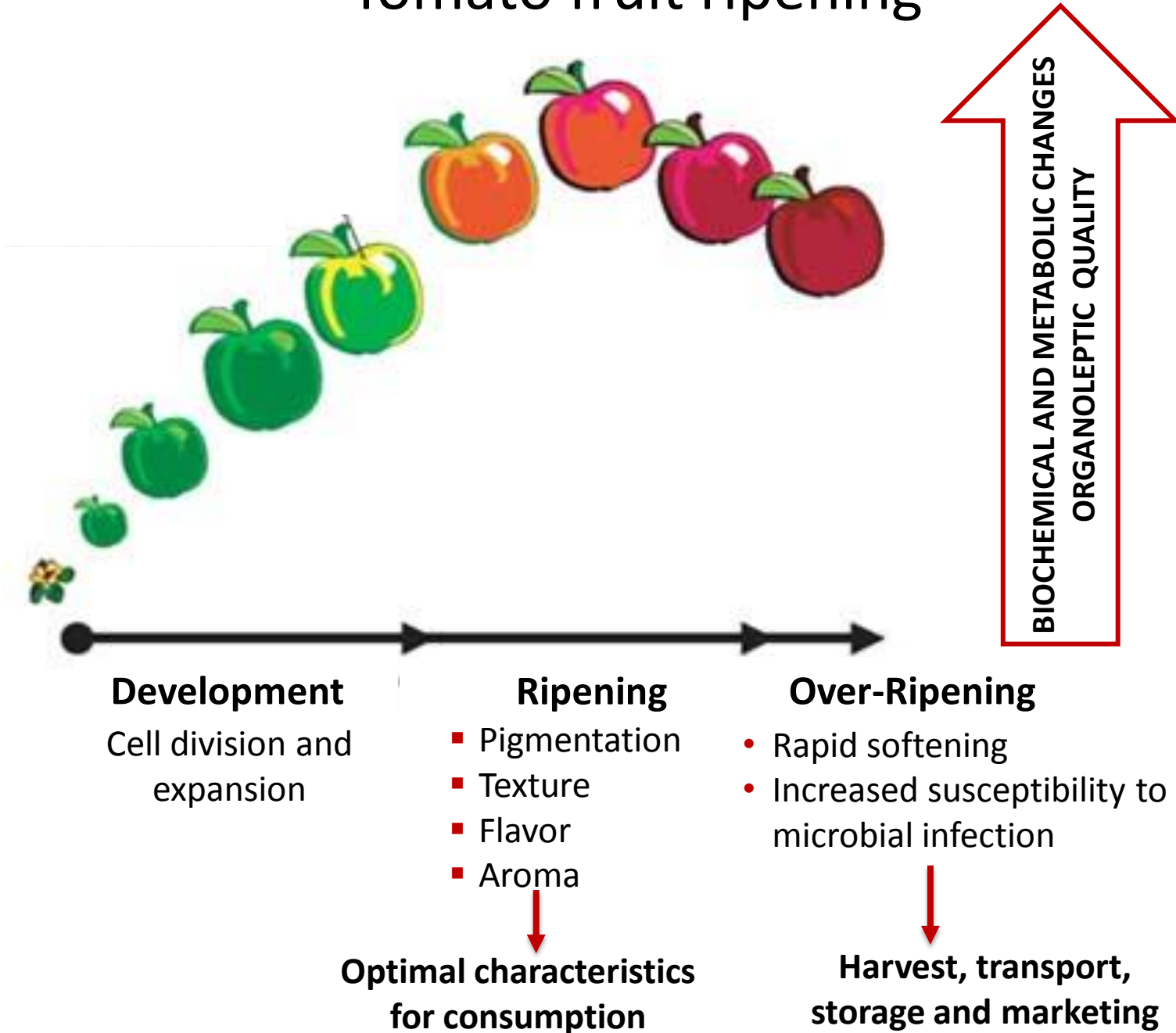
***S. lycopersicum* cv. Micro-Tom**

cv. Florida Basket X cv. Ohio 4013-3

dwarf phenotype: mutations in the recessive genes *dwarf* (*d*) and *miniature* (*mnt*)

- ✓ small size (1,357 plants / m²)
- ✓ rapid life cycle (70-90 days from seeds to ripe fruit)
- ✓ easy transformation

Tomato fruit ripening



Tomato fruit ripening



High susceptibility of the plant to different plagues

PESTICIDES

- Increase the production costs
- A risk factor for consumers and the environment



Development of pest resistant varieties is a major challenge in sustainable agriculture



Over-Ripening

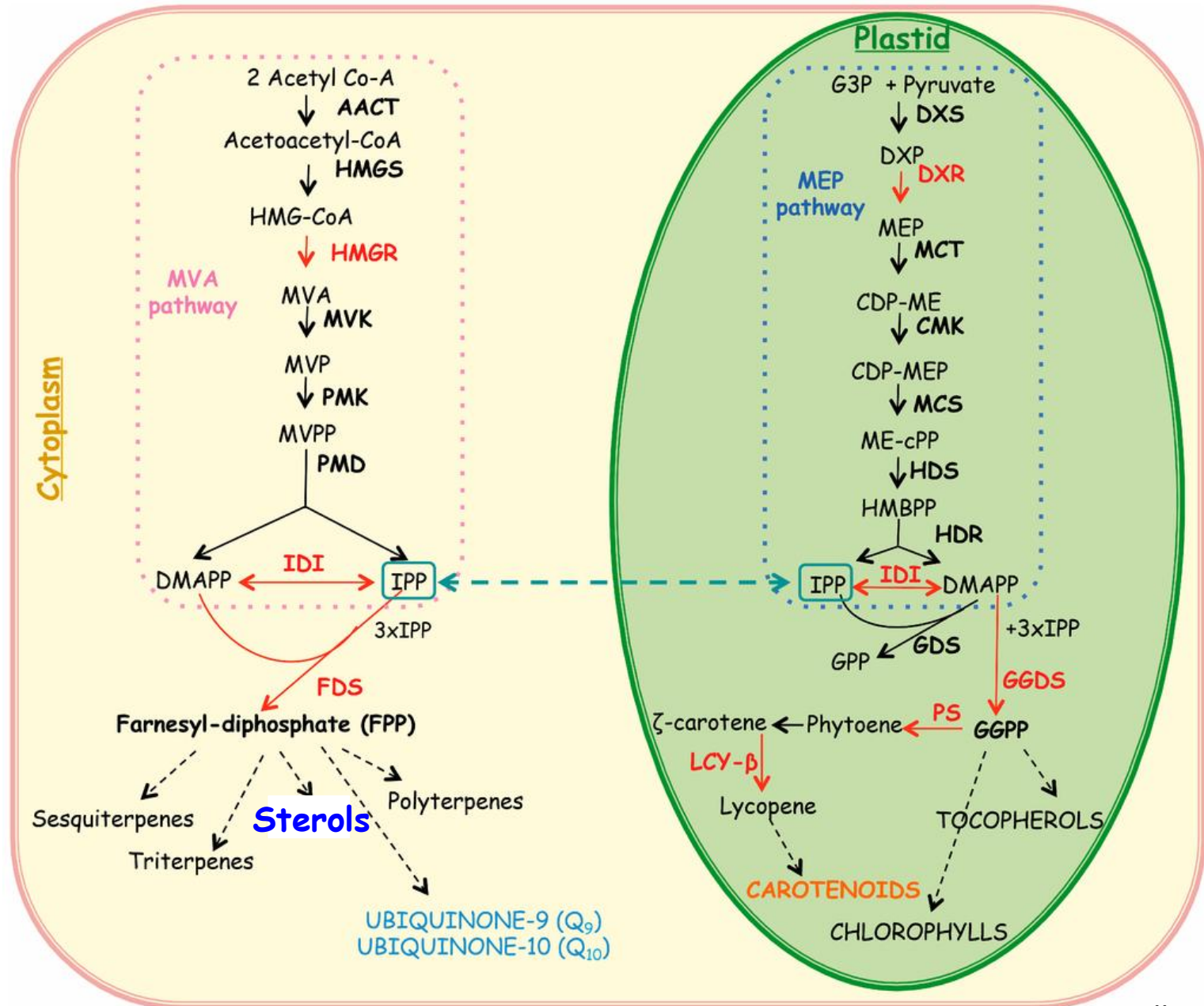
- Rapid softening
- Increased susceptibility to microbial infection



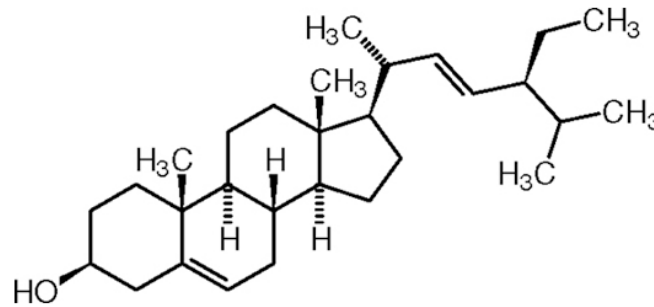
Harvest, transport, storage and marketing

s

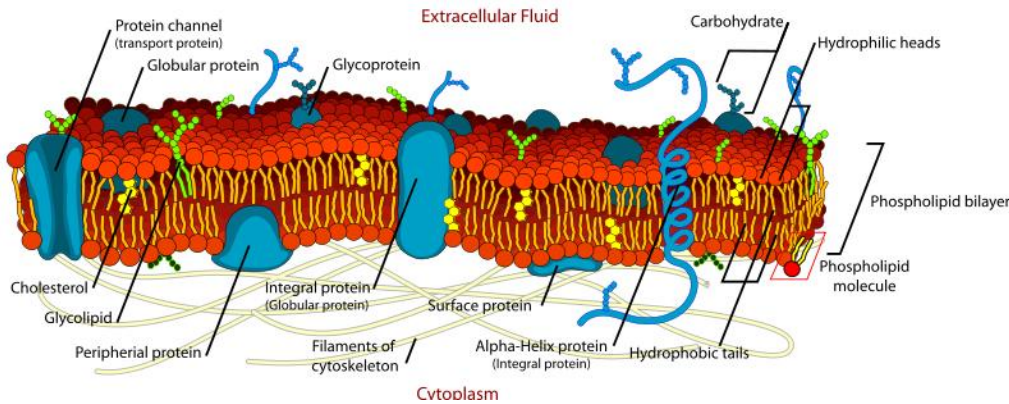
Isoprenoid biosynthesis in plants



Sterols are essential components of cell membranes

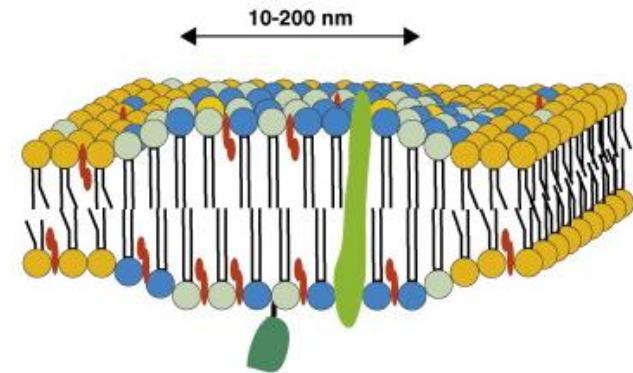


Cell membranes



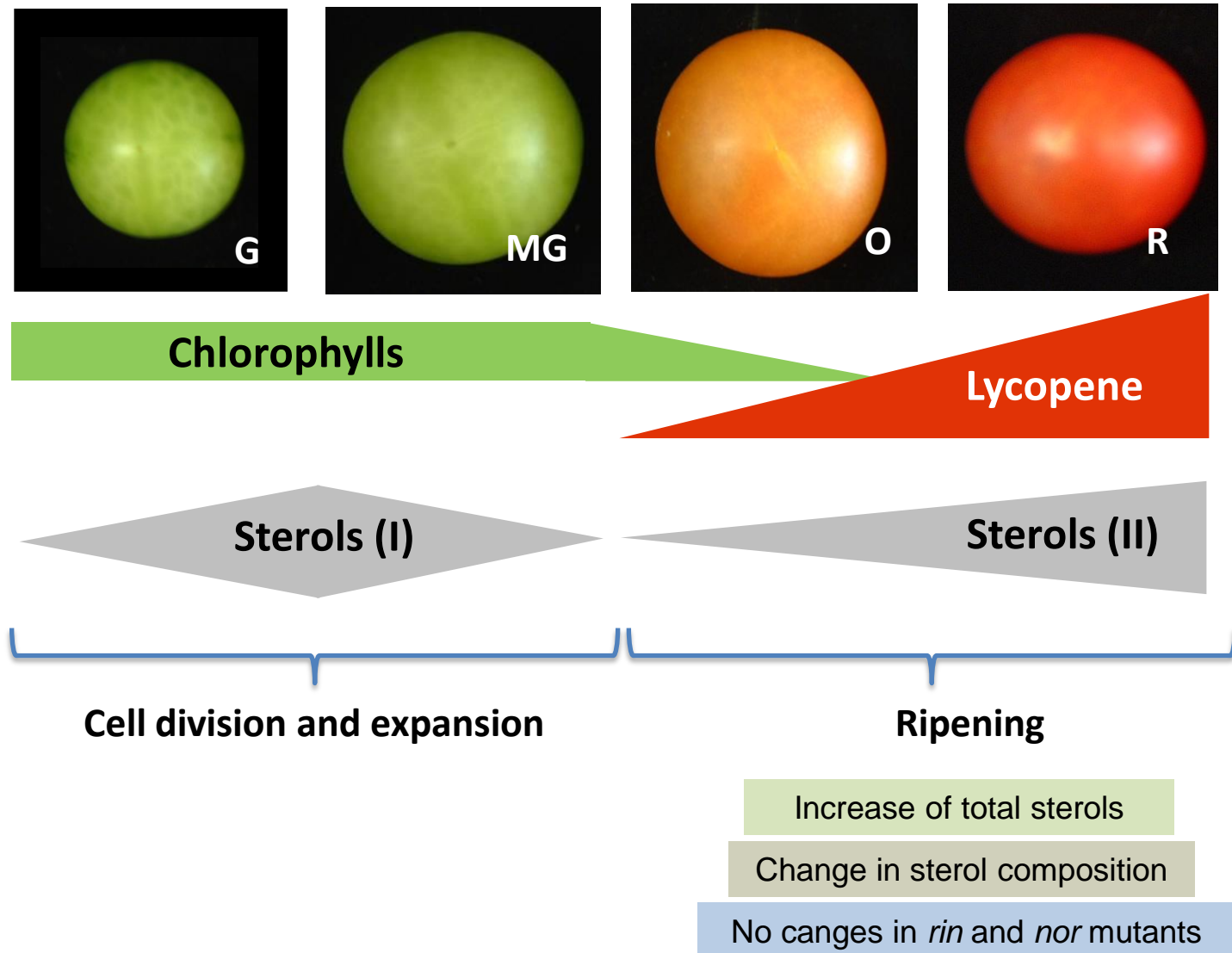
Modulate membrane fluidity and permeability

Lipid rafts

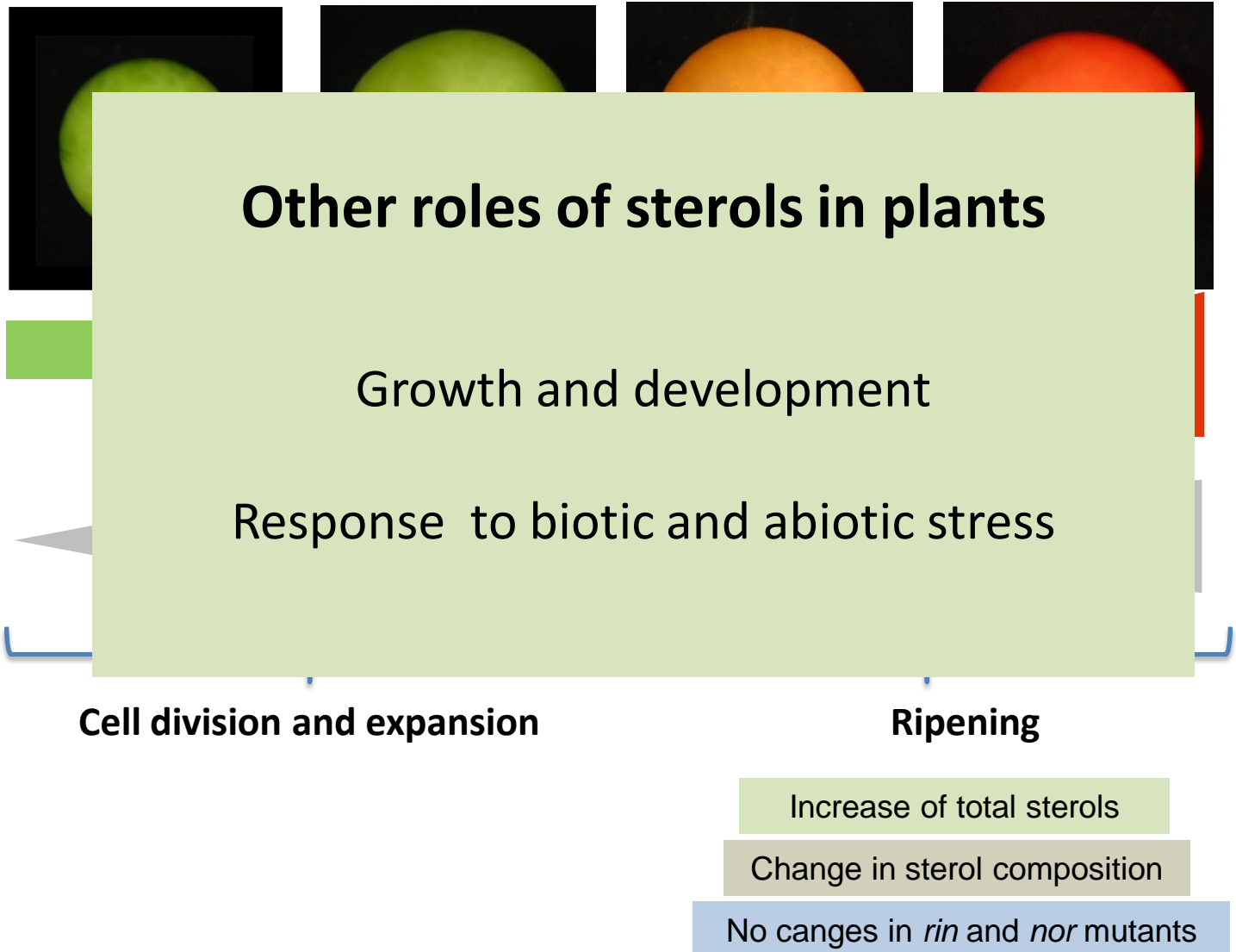


Signaling
Cell polarity
Trafficking
Secretion

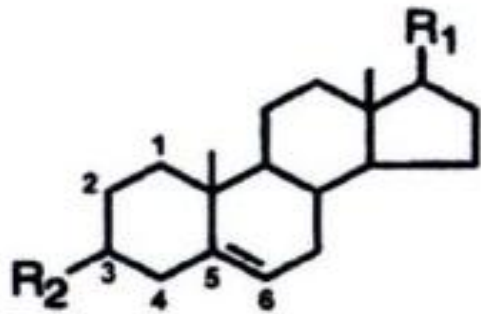
Changes in sterol composition associated to tomato fruit development and ripening



Changes in sterol composition associated to tomato fruit development and ripening



Tomato (like other *Solanum* species) have an unusual sterol composition



Arabidopsis



Tomato



Free sterols	74 %	10 %
Steryl esters	15 %	8 %
Steryl glucosides	8 %	26 %
Acylated steryl glucosides	3 %	56 %

> 80%

Tomato (like other *Solanum* species) have an unusual steryl lipid composition

Arabidopsis

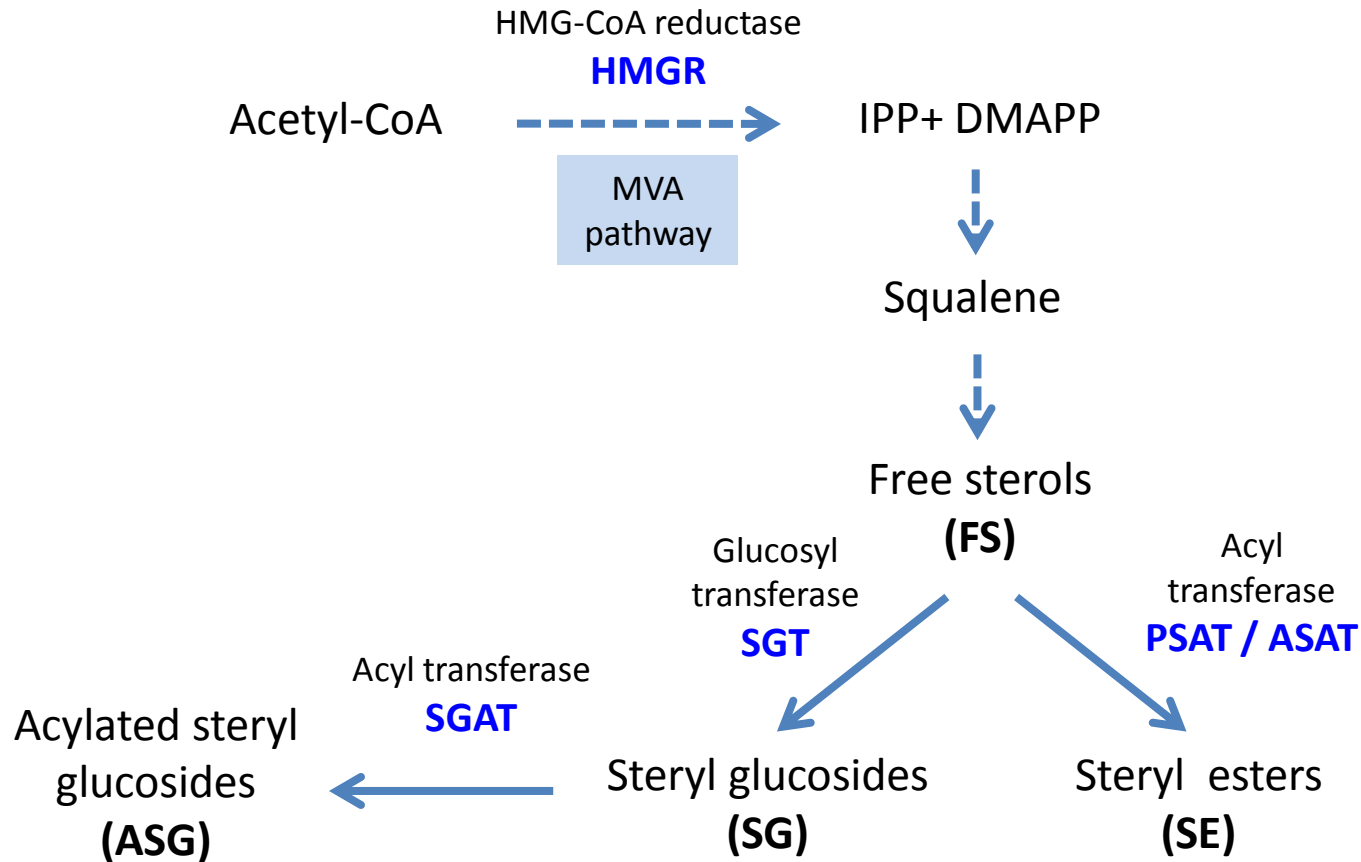
Tomato

The biological and evolutionary significance of this peculiar sterol composition is currently unknown

Free sterols	74 %	10 %
Steryl esters	15 %	8 %
Steryl glucosides	8 %	26 %
Acylated steryl glucosides	3 %	56 %

> 80%

Schematic representation of sterol metabolism in tomato



Objectives

1. Identification and characterization of the genes and enzymes involved in the biosynthesis of conjugated sterols in tomato.
2. Generation of genetically modified tomato lines with altered profiles of free and conjugated sterols (plant and/or fruit).
3. Evaluation of the effects of the perturbations in sterols metabolism on plant development, fruit development and ripening, and resistance to biotic and abiotic stresses.
4. Identification and characterization of mutant and allelic variants of genes involved in sterol metabolism using TILLING and EcoTILLING.

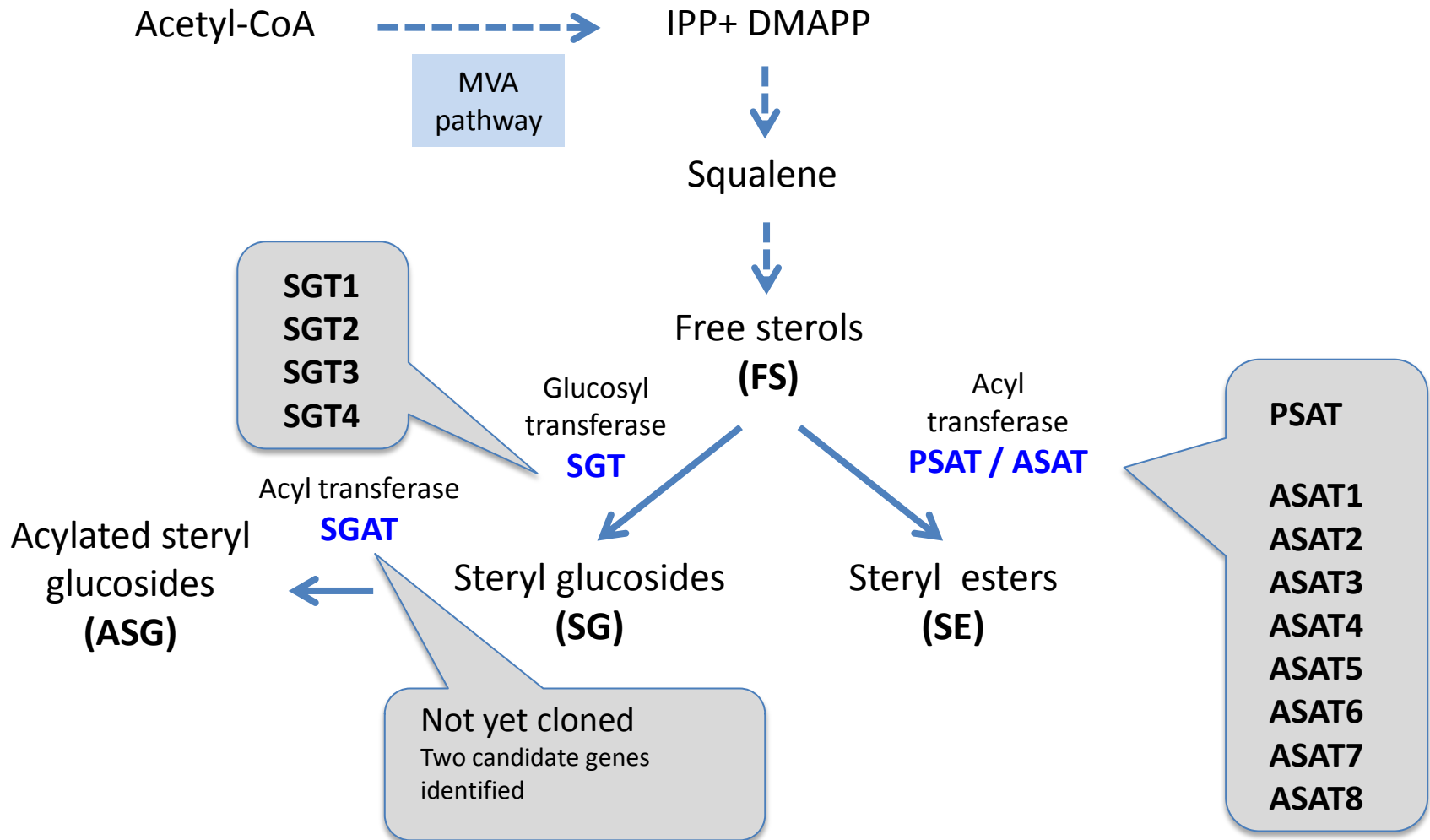
Objective 1: Identification and characterization of the genes and enzymes involved in the biosynthesis of conjugated sterols in tomato

1.1. Cloning and Functional validation of candidates enzymes (PSAT, ASAT, SGT)

1.2. Study of the expression pattern of the corresponding genes

1.3. Study of the subcellular localization of the enzymes

Enzymes involved in sterol metabolism in tomato are encoded by gene families



Cloning and characterization of *PSAT* from *S. lycopersicum* (cv. Micro-Tom)

The *PSAT* cDNA cloned from mature green fruit RNA of *S. lycopersicum* cv. Micro-Tom (*SIPSAT*), encodes a 630 aa protein that is 77% identical to the Arabidopsis *PSAT1*

tomato	1	MRG-----CHVGEVVIIFILLA---TAGNLGGEPAGDYSKLSGIIIPGFASTQLRAWSII
arabidopsis	1	MGANSKSVTASFTVIVAFELICGGRTAVEDETEFHGDYSKLSGIIIPGFASTQLRAWSII
tomato	52	DCPYSPPLDFNPLDLVWLDTTKLLSAVNCWFKCMVLDPNQTDHNECKSRPDSGLSAITEL
arabidopsis	61	DCPYTPLDFNPLDLVWLDTTKLLSAVNCWFKCMVLDPNQTDHPECKSRPDSGLSAITEL
tomato	112	DPGYITGPLSSVWKEWIKWCIEFGIEANAIIVAPYDWRLSPSKLEERDLYFHKLKLTFTET
arabidopsis	121	DPGYITGPLSTVWKEWLKWCVEFGIEANAIIVAPYDWRLSPKLEERDLYFHKLKLTFTET
tomato	172	ALKLRGGPSSIVFAHSLGNNVFRYFLEWLKLEIAPKEYGRWLDCHI HAYFAVGAPLLGAIET
arabidopsis	181	ALKLRGGPSSIVFAHSMGNNVFRYFLEWLRLLEIAPKHYLKWLDCHI HAYFAVGAPLLGSVE
tomato	232	TVKATLSGSTFGLPVSEGTVRLMFTNIFGSSIWMLPFSKYCTTDNVYRRHFSGG-NRKYHH
arabidopsis	241	AIKSTLSGVTFTGLPVSEGTARLLSNSFASLLM-PFSKNCKGDNTEWTFHSGGAARKDKR
tomato	291	AYHCDEHELKSKYSGWPTNIIINIEVPSNRGNEVYPSVVETPQTNLSGKECGEPTQLSFSFA
arabidopsis	300	VYHCDEEYEQSKYSGWPTNIIINIEIIPST-----SVTETALVNMTSMCEGLPTLLSFTA
tomato	351	REVS DGTFFKAIKNYDPDSEERL FHL LKKS YHDDPILNPLTPWERPPIKNI FCIYGVDSKT
arabidopsis	353	RELADGTLFKAIEDYDPDSKRLHLQL-KLYHDDPVENPLTPWERPPIKNVFCIYGAHLKT
tomato	411	EVGYFAPSGKPYPDNWIITDVIYEIEGSLYSRSGNLVEGNPGATSGDETVPYHSLSWCK
arabidopsis	412	EVGYFAPSGKPYPDNWIITDVIYEIEGSLVSRSGTVVDGNAGPI TGDETVPYHSLSWCK
tomato	471	NWLGPKVNI TRT PQSEHDGSDVQVHLNIEHQHGEDIIPNMTKLPTMKYITYYEDSESEFPG
arabidopsis	472	NWLGPKVNI TMA PQPEHDGSDVHVELNVDHEHGSDI IANMTRAPRVKYITFYEDSESI PG
tomato	531	TRTAVWELDKANHRNIVRSPALMRELWLDMWHDIEHPDKKSKFVTKAKRGPLRDEDCYWDY
arabidopsis	532	KRTAVWELDKTNHRNIVRSEVLMRELWLDMWHDIQPGAKSKFVTKAKRGPLRDADCYWDY
tomato	591	GKARCAWAHEHCYRYVFGDVHLGQSCRLKSSSTSHILSHYV
arabidopsis	592	GKACCAWCEYCEYRYSFGDVHLGQSCRLNNTSANMLLQYI

PINK

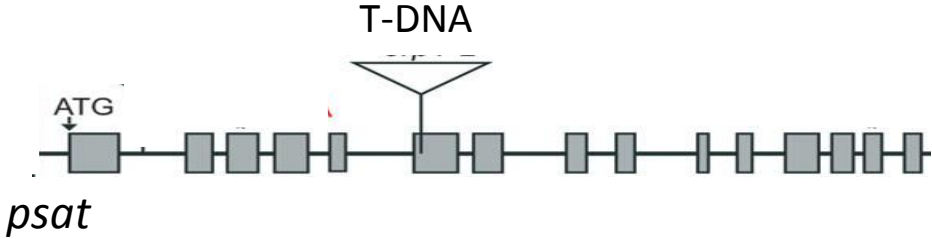
characteristic conserved domains in mammalian LCAT-type enzymes

BLUE

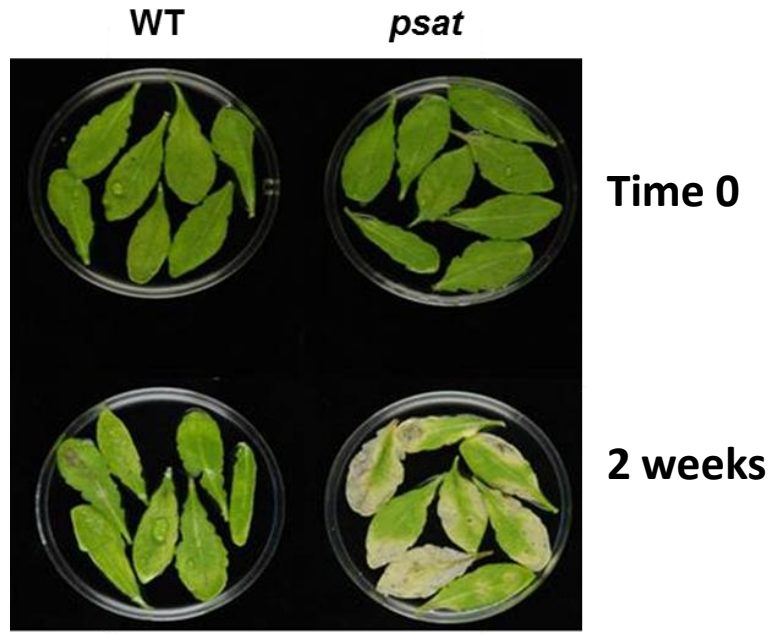
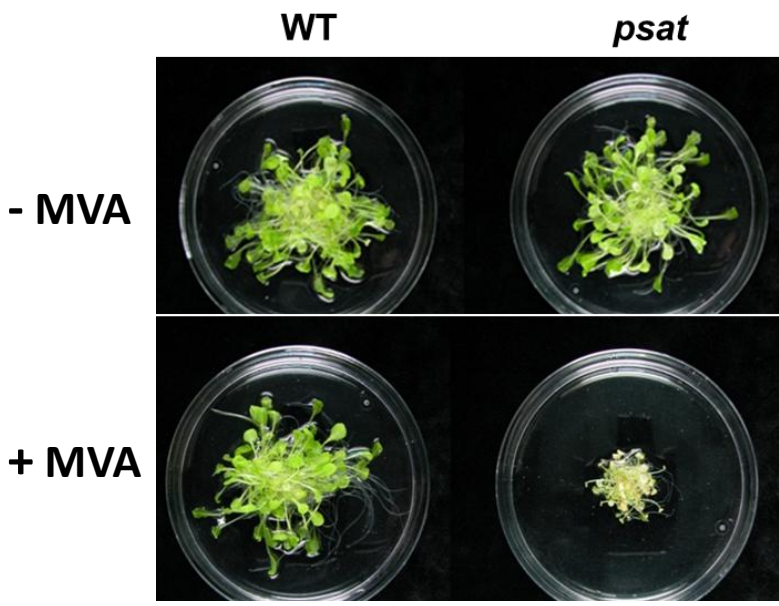
catalytic triad
S-D-H

Functional validation of the candidate SIPSAT enzyme

Complementation of the *Arabidopsis psat* knock-out mutant

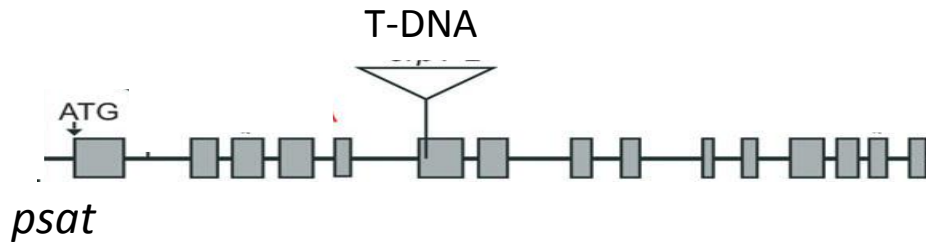


- PHENOTYPE ALTERATIONS**
- Toxicity of MVA treatment
 - Premature senescence



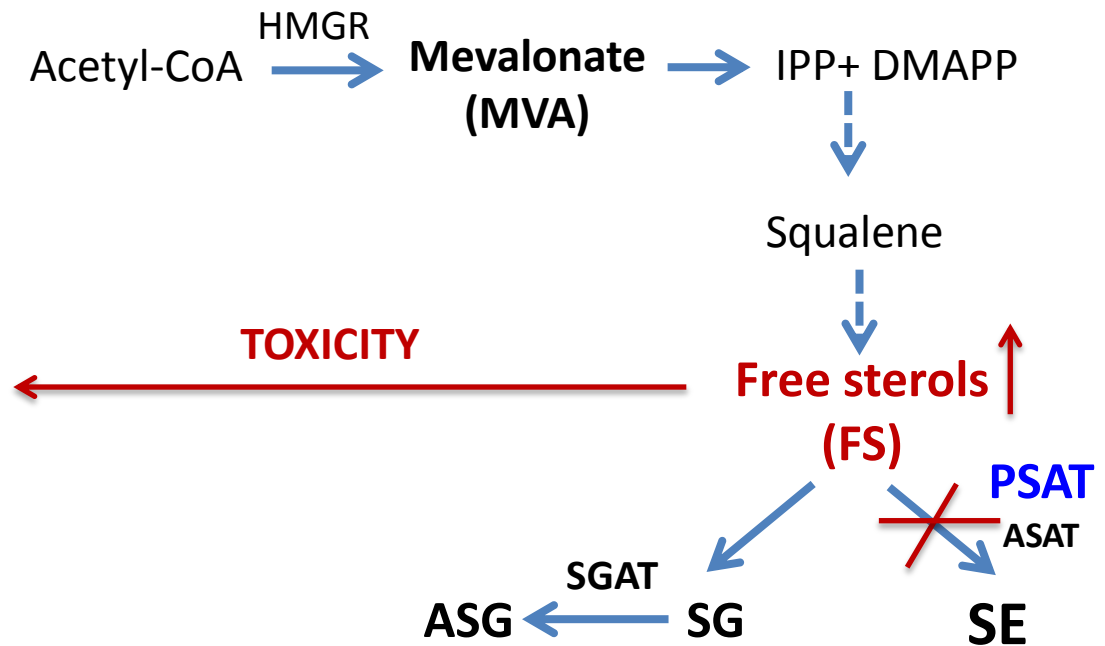
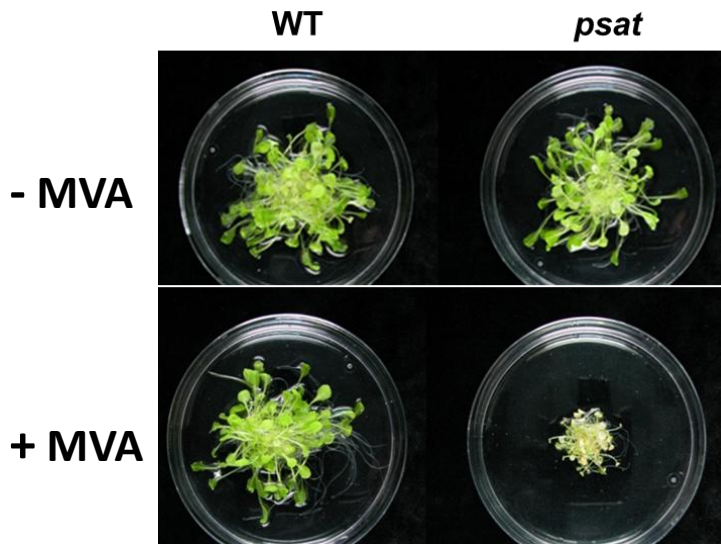
Functional validation of the candidate SIPSAT enzyme

Complementation of the *Arabidopsis psat* knock-out mutant



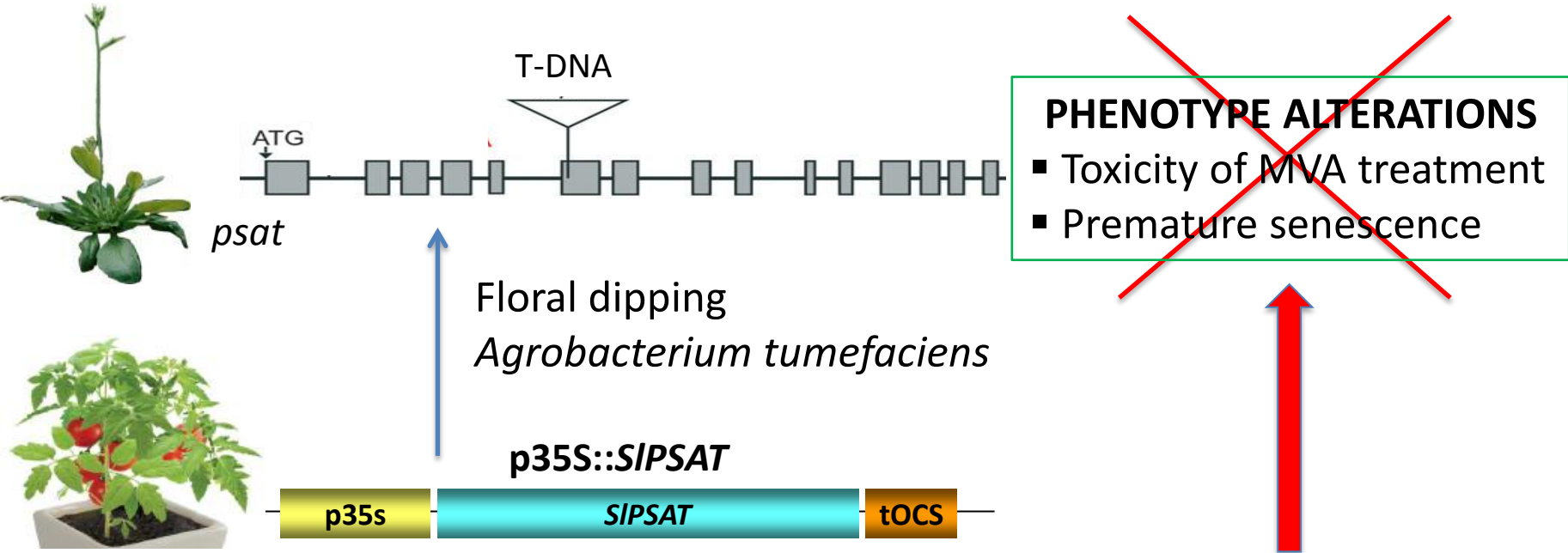
PHENOTYPE ALTERATIONS

- Toxicity of MVA treatment
- Premature senescence



Functional validation of the candidate SIPSAT enzyme

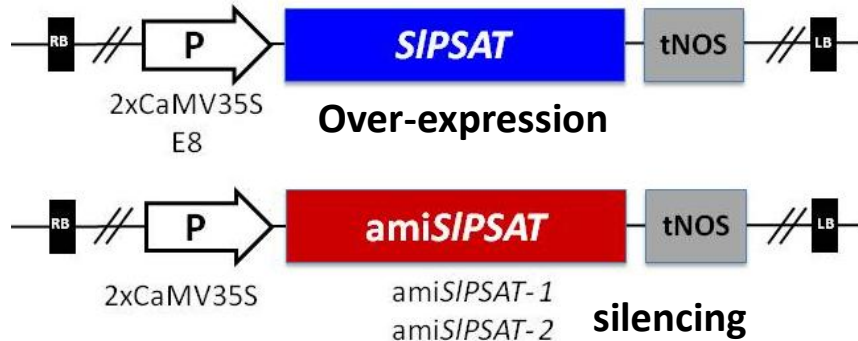
Complementation of the *Arabidopsis psat* knock-out mutant



Basta selection



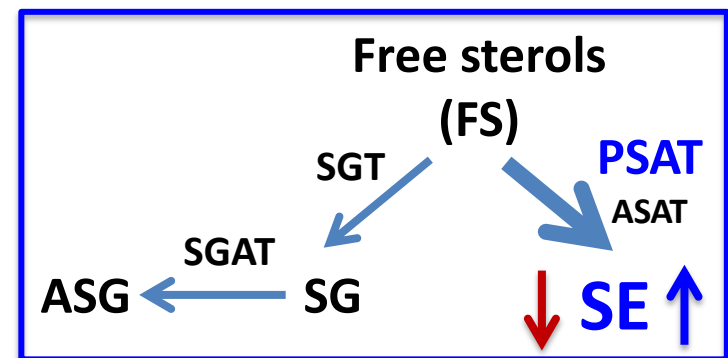
Generation of genetically modified tomato lines with altered profiles of free and conjugated sterols (plant and/or fruit)



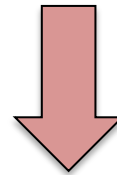
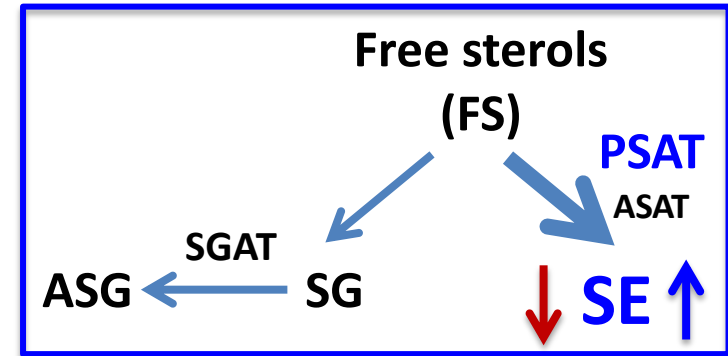
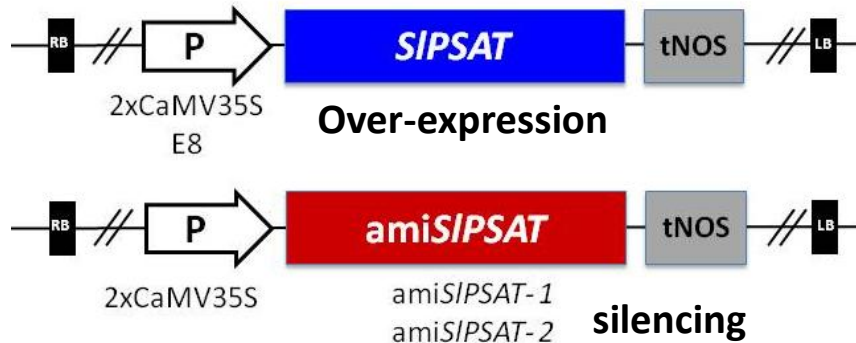
Tomato cotyledons
A. tumefaciens



- Presence of the transgen
- Copy number (1 copy plants)
- *SIPSAT* expression level
- Homozygous selection
- Sterol levels



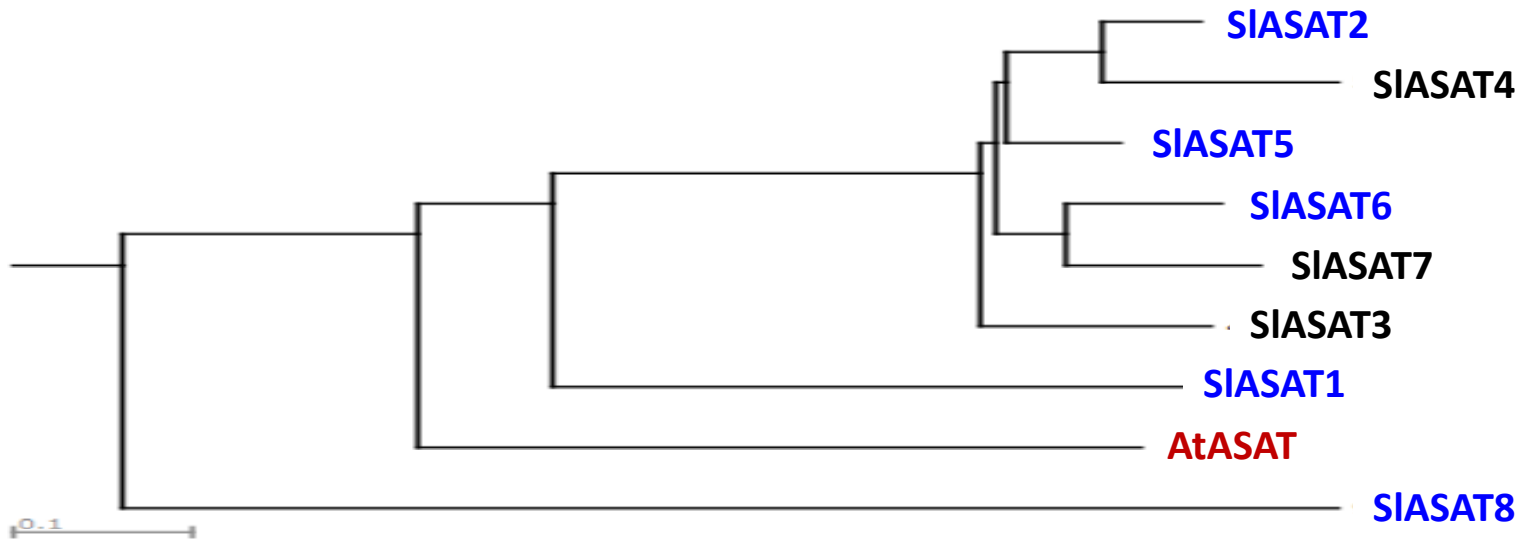
Evaluation of the effects of the perturbations in sterols metabolism on plant development, fruit development and ripening, and resistance to biotic and abiotic stresses.



- ✓ **Tolerance to pathogens:** *Botritis cinerea*, *Pseudomonas syringe*, *Phytophthora infestans*
- ✓ **Abiotic stress tolerance :** cold, drought
- ✓ **Plant productivity and fruit quality:** number and size of fruits, softening, sugars, acidity

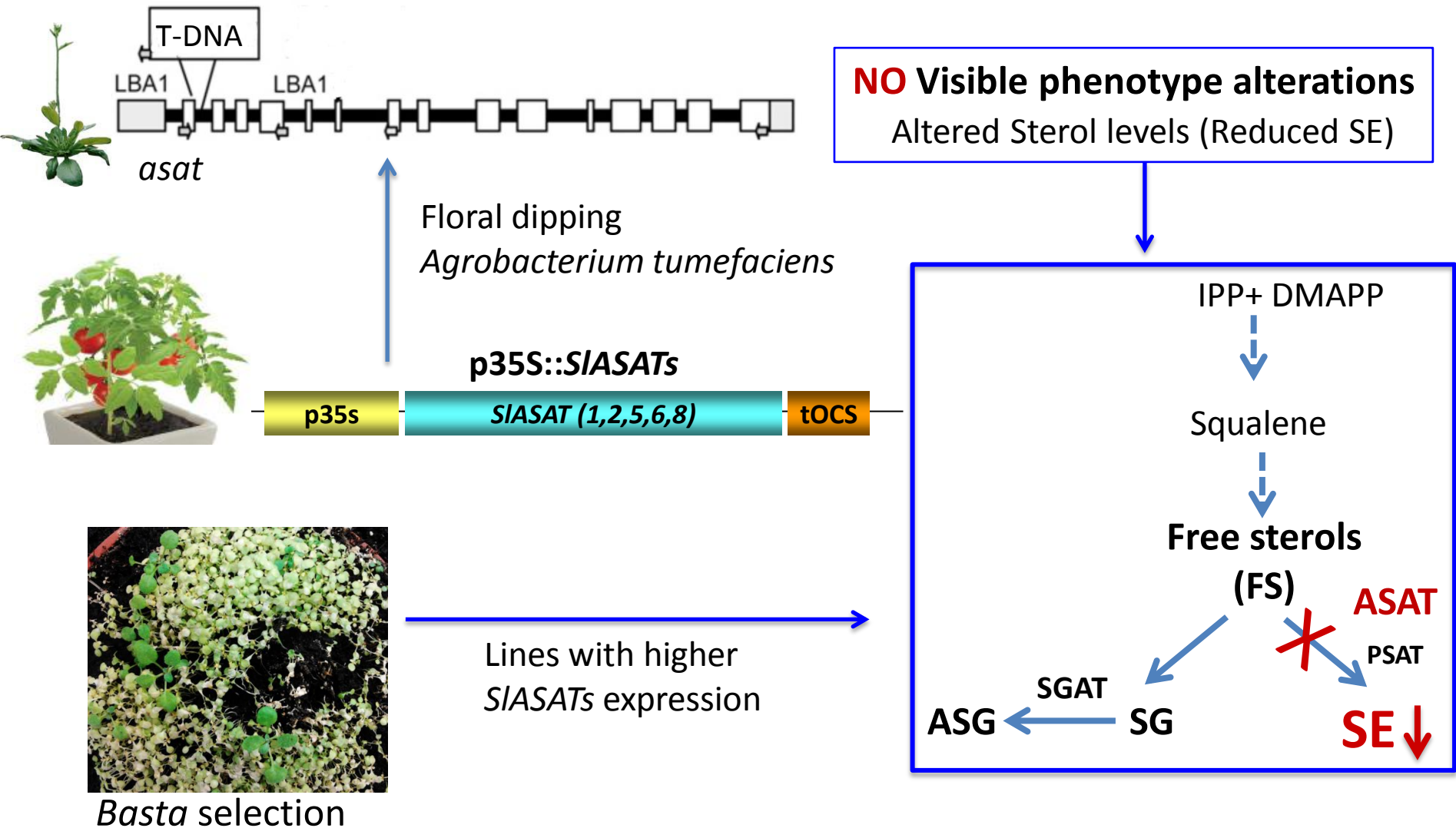
Cloning and characterization of ASAT from *S. lycopersicum* (cv. Micro-Tom)

	AtASAT	SIASAT1	SIASAT2	SIASAT3	SIASAT4	SIASAT5	SIASAT6	SIASAT7	SIASAT8
AtASAT		49	43	42	45	45	43	44	33
SIASAT1	67		47	43	49	49	47	47	33
SIASAT2	76	66		82	75	82	75	72	34
SIASAT3	73	66	84		73	78	71.	69	32
SIASAT4	74	77	88	85		80	72	72	32
SIASAT5	70	68	87	87	85		78	78	34
SIASAT6	68	84	82	81	80	83		79	31
SIASAT7	73	70	81	81	79	82	83		33
SIASAT8	69	75	91	92	91	85	75	86	

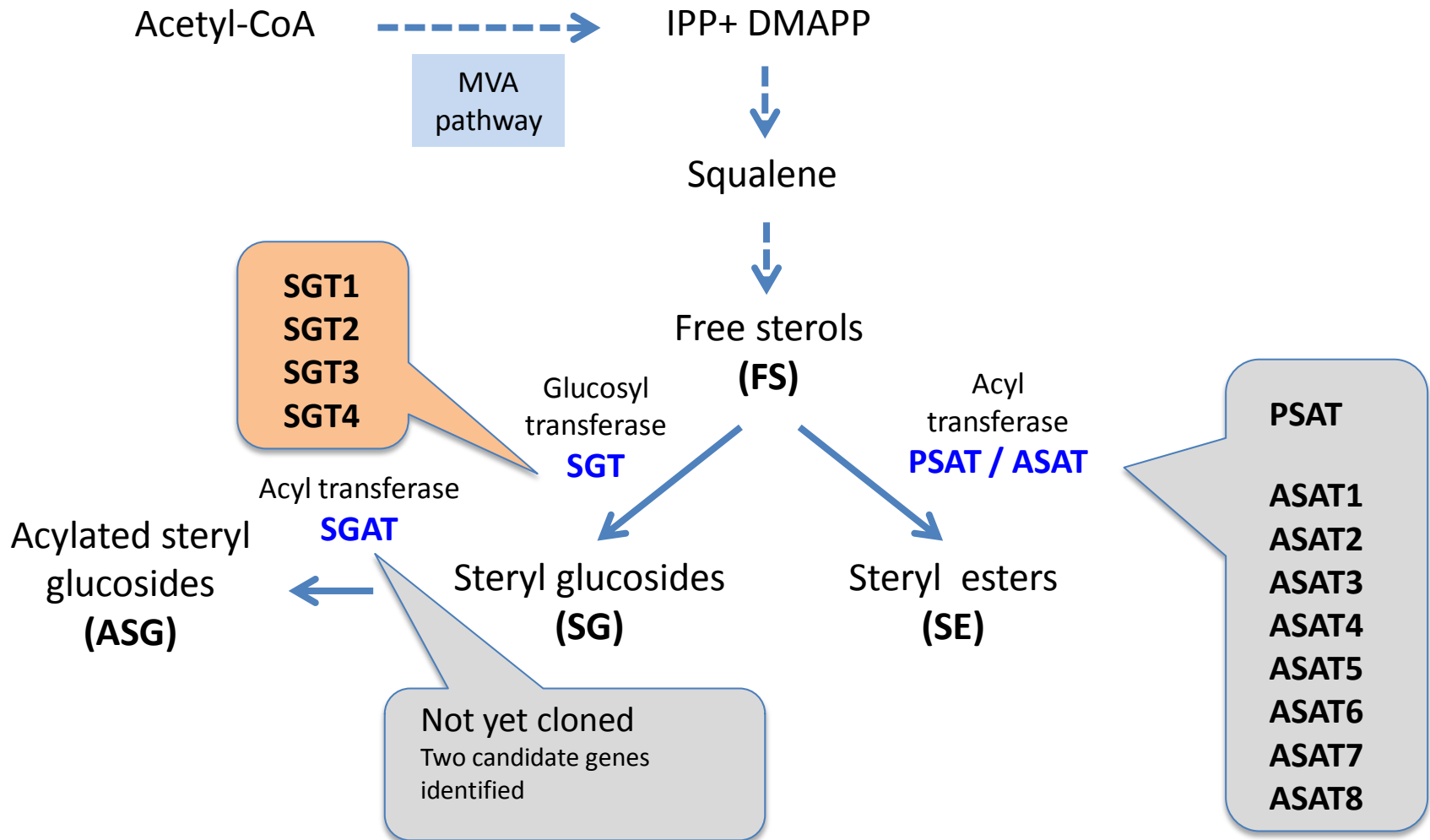


Functional validation of the candidate SIASAT enzymes

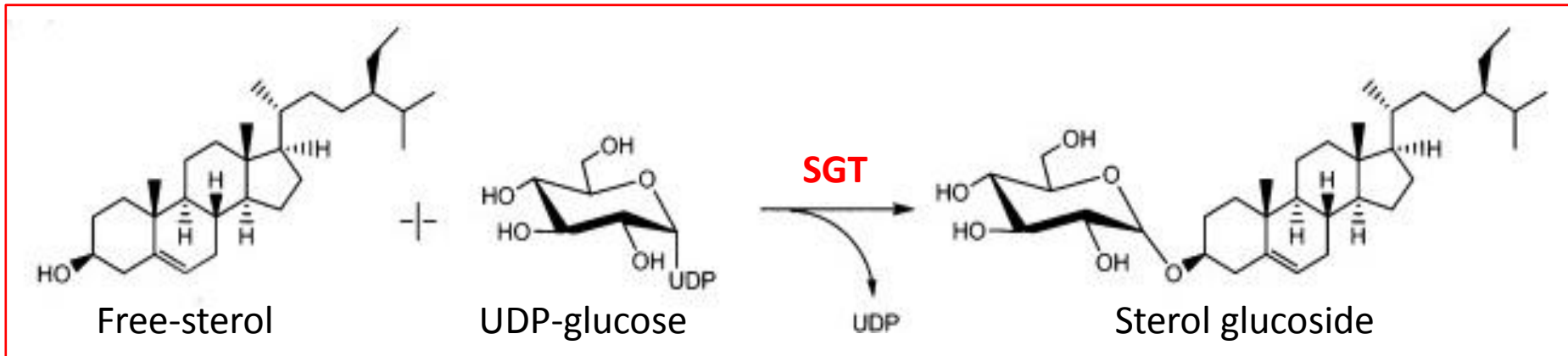
Complementation of the *Arabidopsis asat* knock-out mutant



Enzymes involved in sterol metabolism in tomato are encoded by gene families



Identification of 4 candidate genes encoding SGTs in tomato



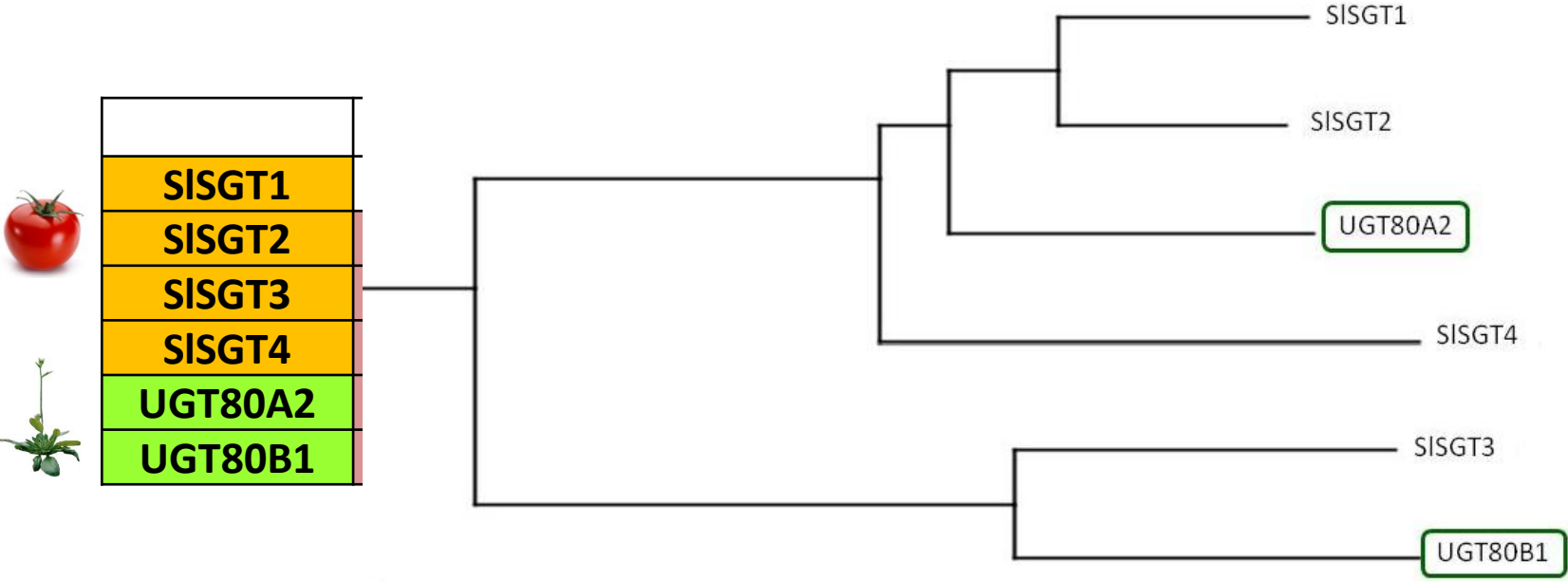
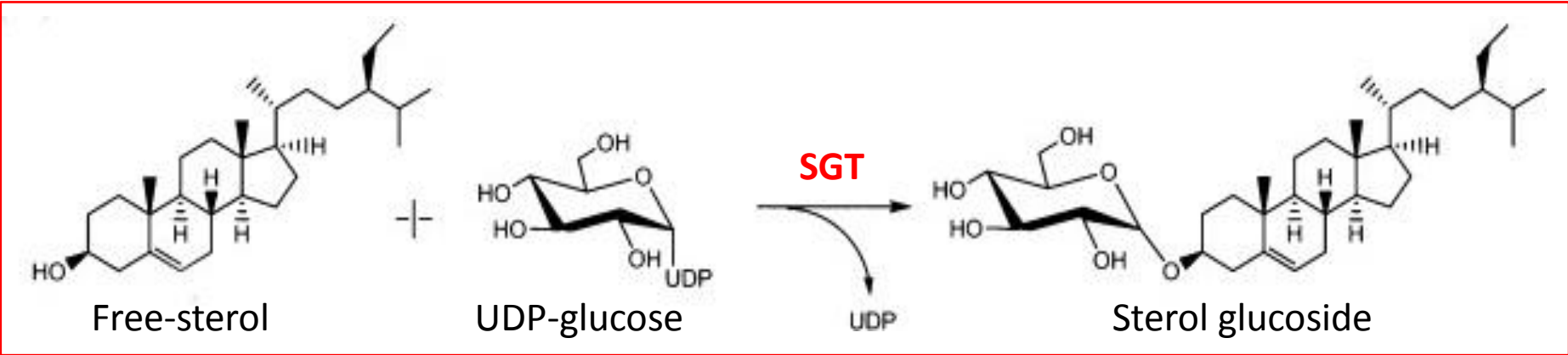
% identity

	SISGT1	SISGT2	SISGT3	SISGT4	UGT80A2	UGT80B1
SISGT1		80	59	65	70	58
SISGT2	85		59	74	74	59
SISGT3	73	75		50	56	69
SISGT4	77	85	64		67	51
UGT80A2	79	82	73	76		57
UGT80B1	73	74	79	68	74	

% similitude

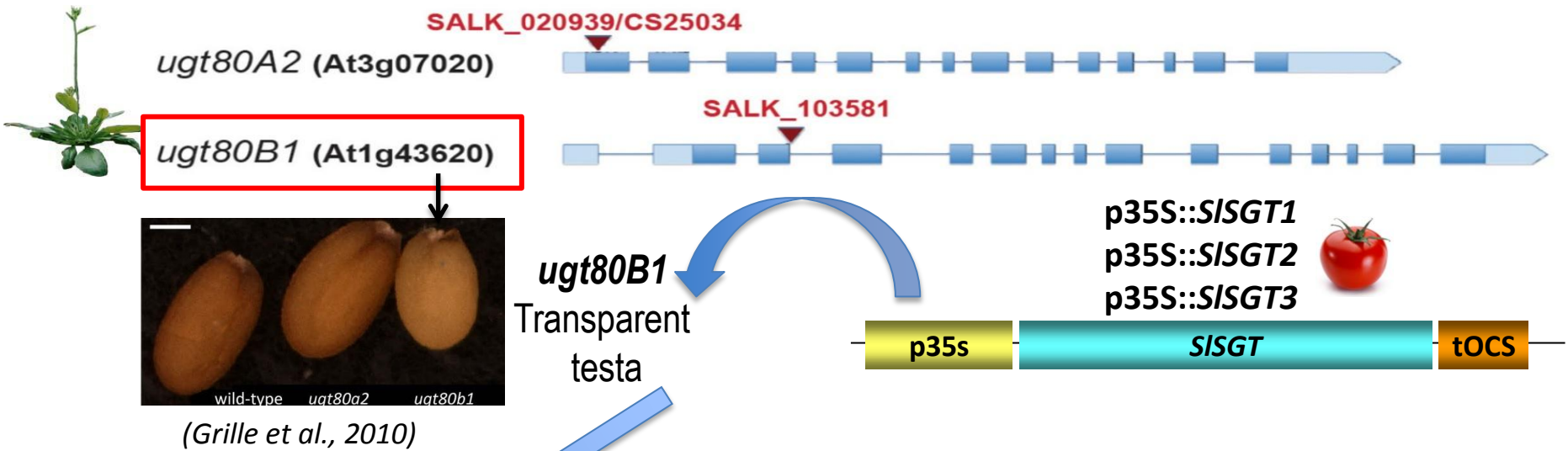


Identification of 4 candidate genes encoding SGTs in tomato



Functional validation of the candidate SISGT enzymes

Complementation of the Arabidopsis *ugt80B1* knock-out mutant



Basta selection

Presence and
 expression of
SISGTs



**Phenotype
 analysis**

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