breeding for increased yields – the epigenetic approach

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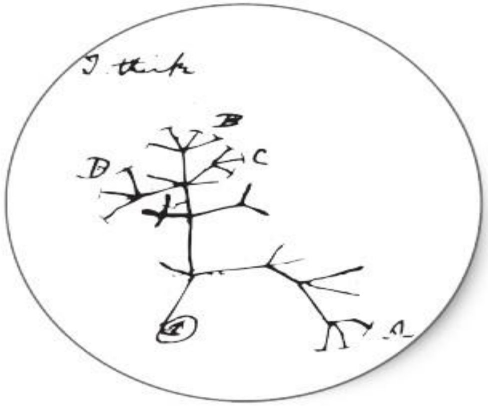
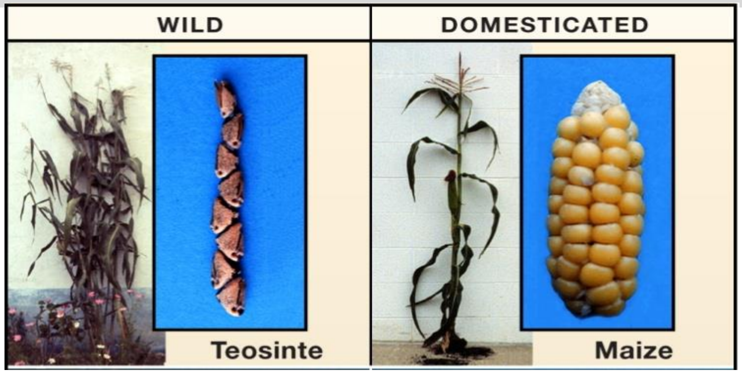
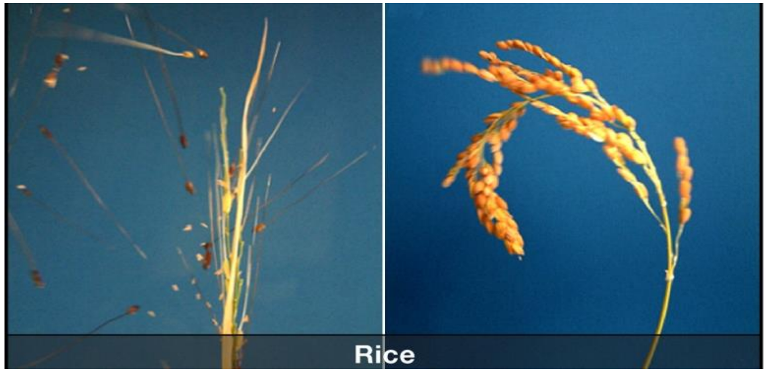
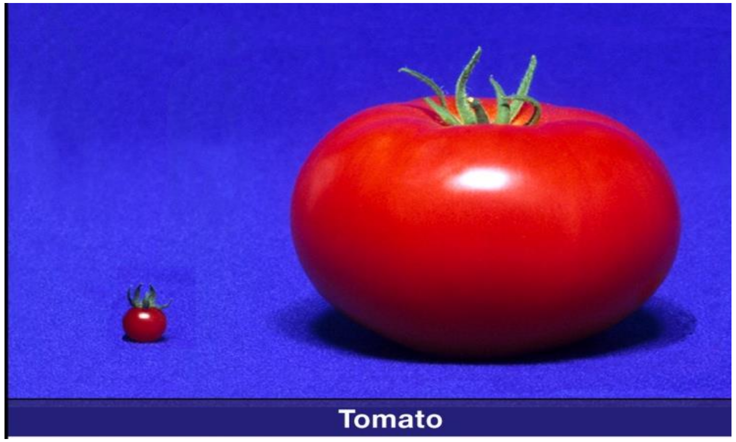


SCI - Breeding Plants for the Future
Reading UK - May 15th 2014

crop domestication vs diversification



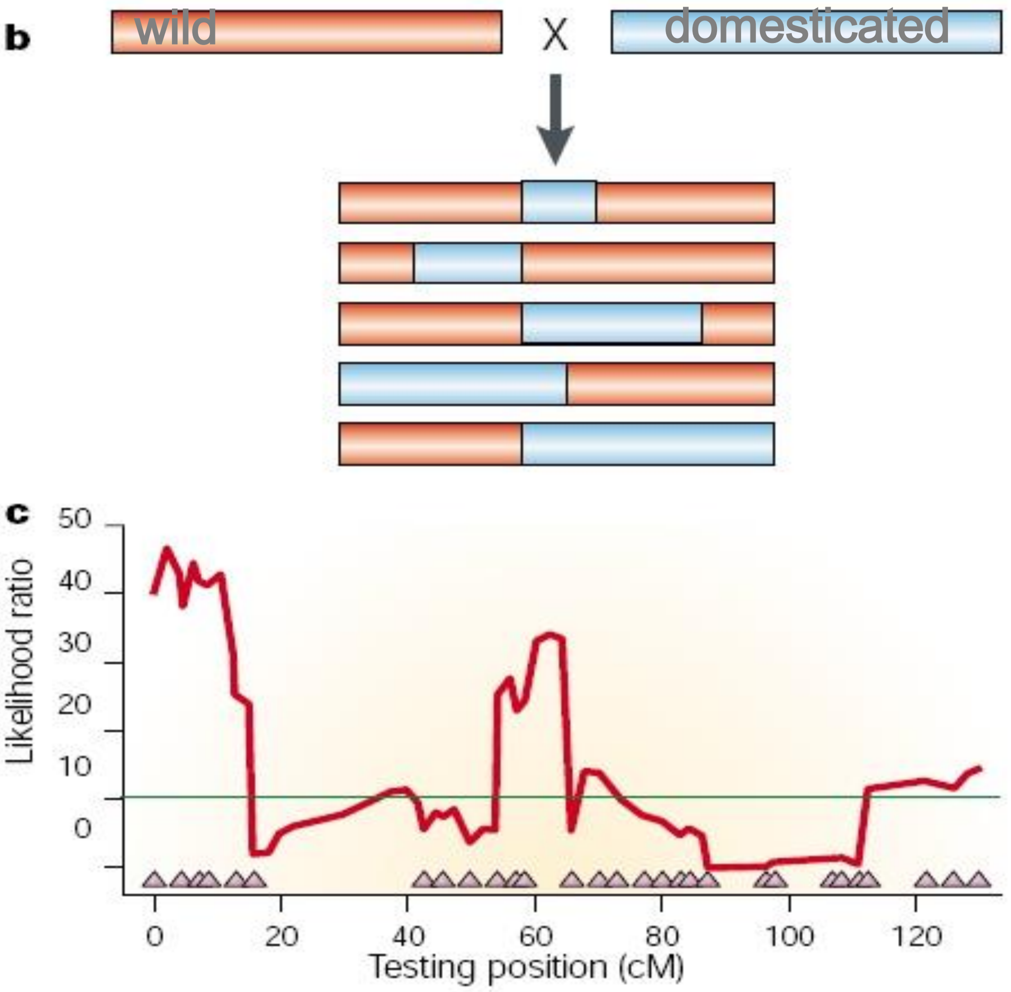




domestication
associated in some examples with selection of few key genes affecting apical dominance, seed shattering, fruit or seed size,
Most examples known affect regulators/transcription factors rather than enzymes

diversification
associated with many genes
normally associated with changes in coding sequence including enzymes

genetic determinants of crop phenotypes



Quantitative traits:

- several genes contribute independently to the trait

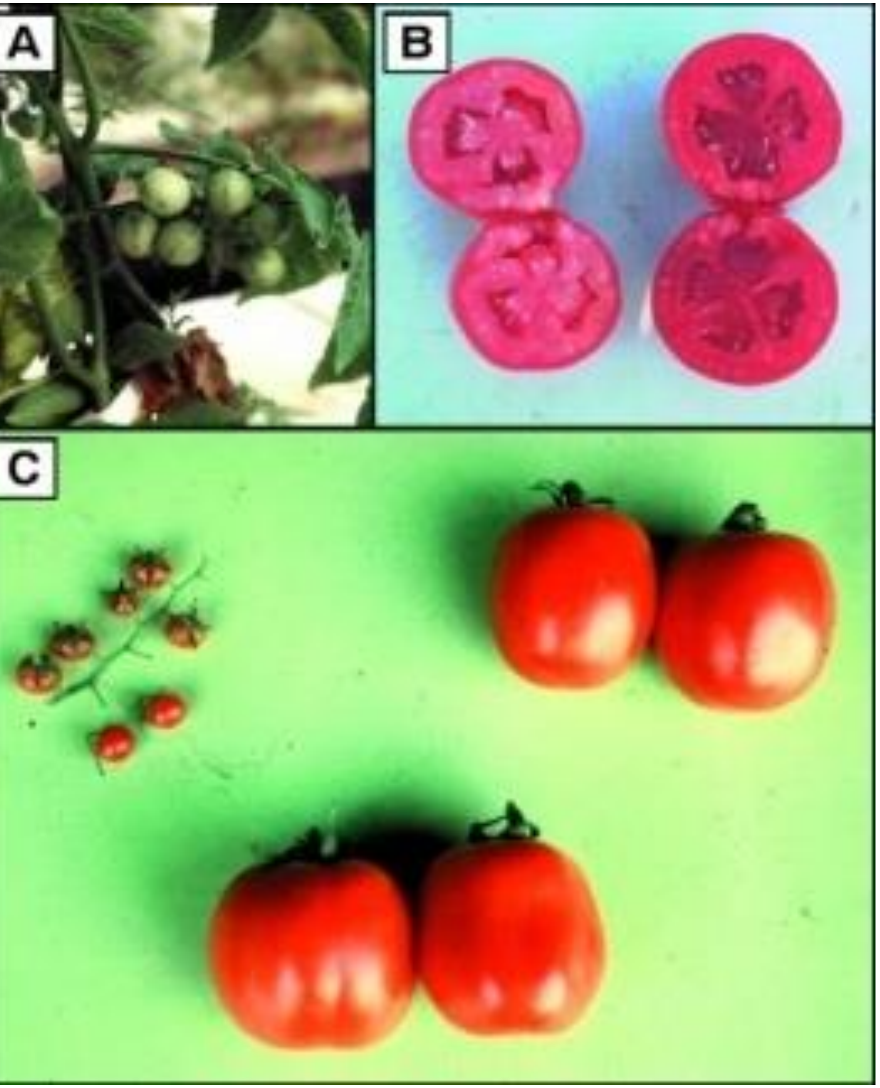
OR

- a single gene accounts for most of the trait but its expression is influenced by other loci or by environmental factors

- QTL analysis requires genetic markers to differentiate the parental chromosomes
  - single nucleotide polymorphism
  - Insertion deletions
  - microsatellites
- Segregation is revealed in the F2
  - Likelihood ratio assesses probability that a marker is associated with a QTL affecting the trait

Citation: Miles, C. & Wayne, M. (2008) Quantitative trait locus (QTL) analysis. *Nature Education* 1(1)

the mysteries of crop diversification (= breeding = artifical evolution)



progessive improvement beyond the range of the parents

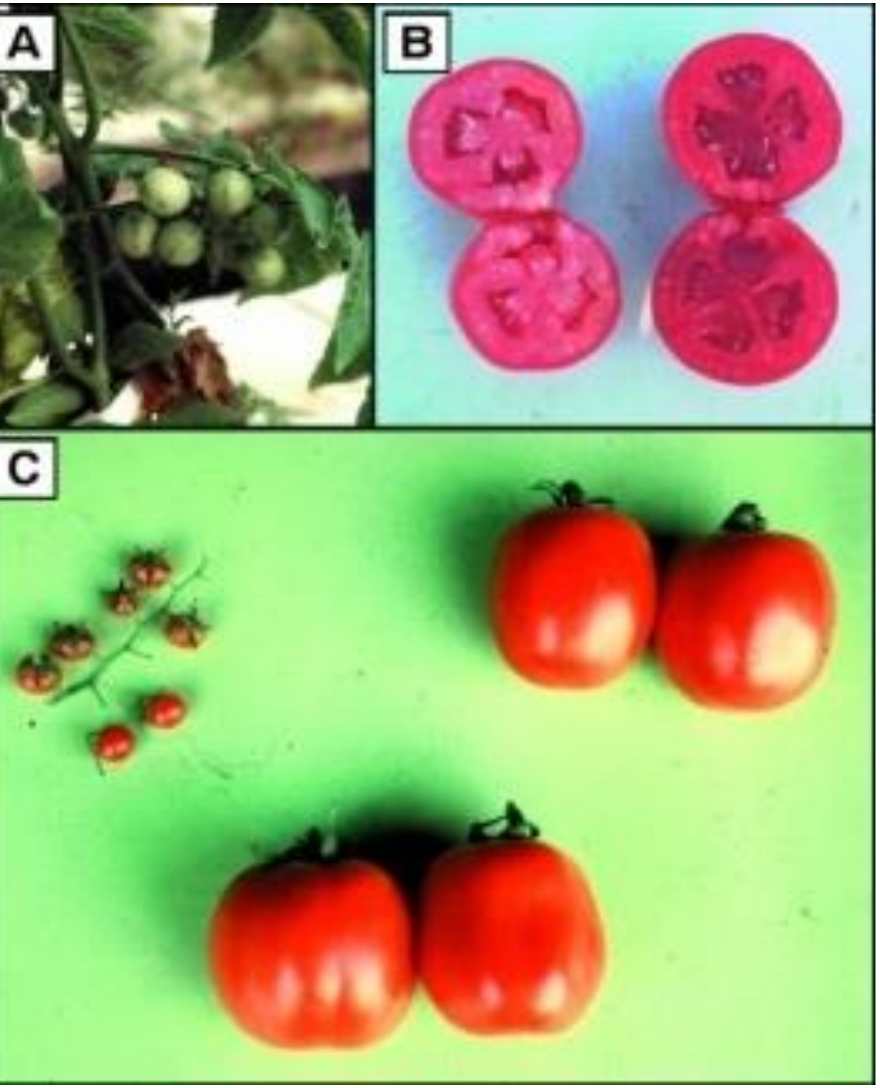
- transgressive segregation
- epistasis

inability to account for all variation at QTL

- multiple minor loci
- ????

Tanksley and McCouch Science 277 (1997) 1063-1066

epigenetics ?????



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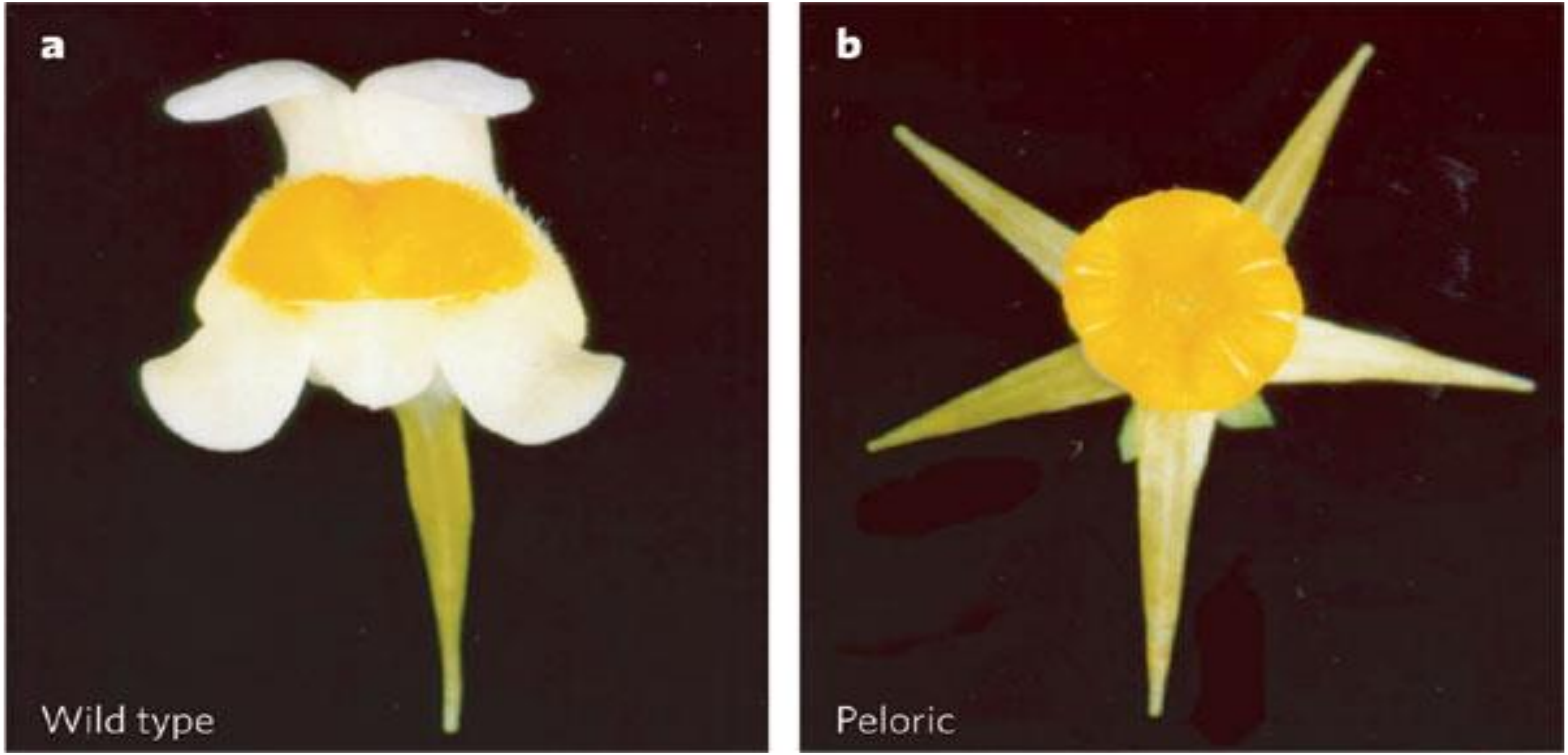
Tanksley and McCouch Science 277 (1997) 1063-1066

peloria/cycloidea affects the shape of toadflax flowers (*Linaria*)



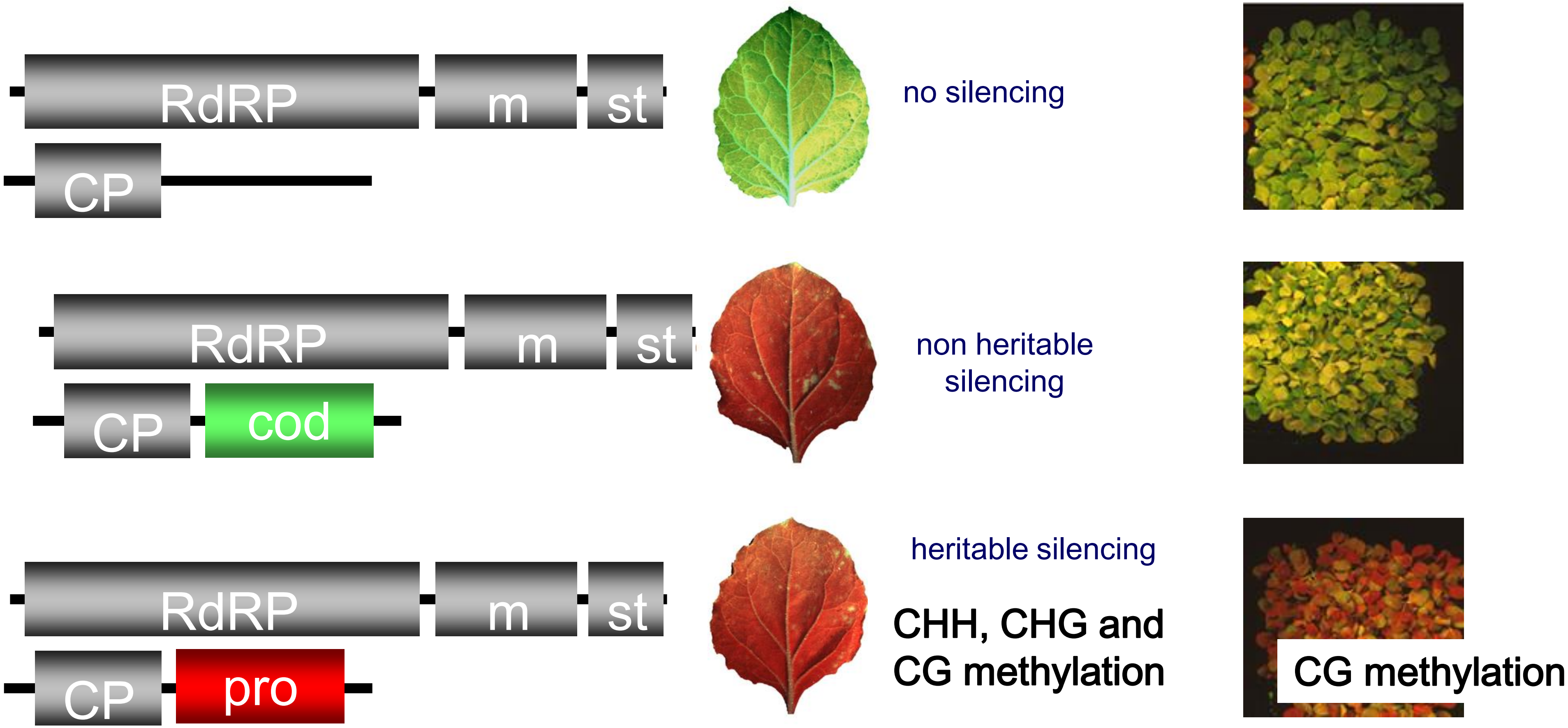
flower shape affected by *cycloidea*
phenotype changes without differences in DNA sequence

a very clear transgenerational epigenetic effect: virus-induced gene silencing = VIGS

virus vector constructs

infected plants

progeny



no silencing

non heritable silencing

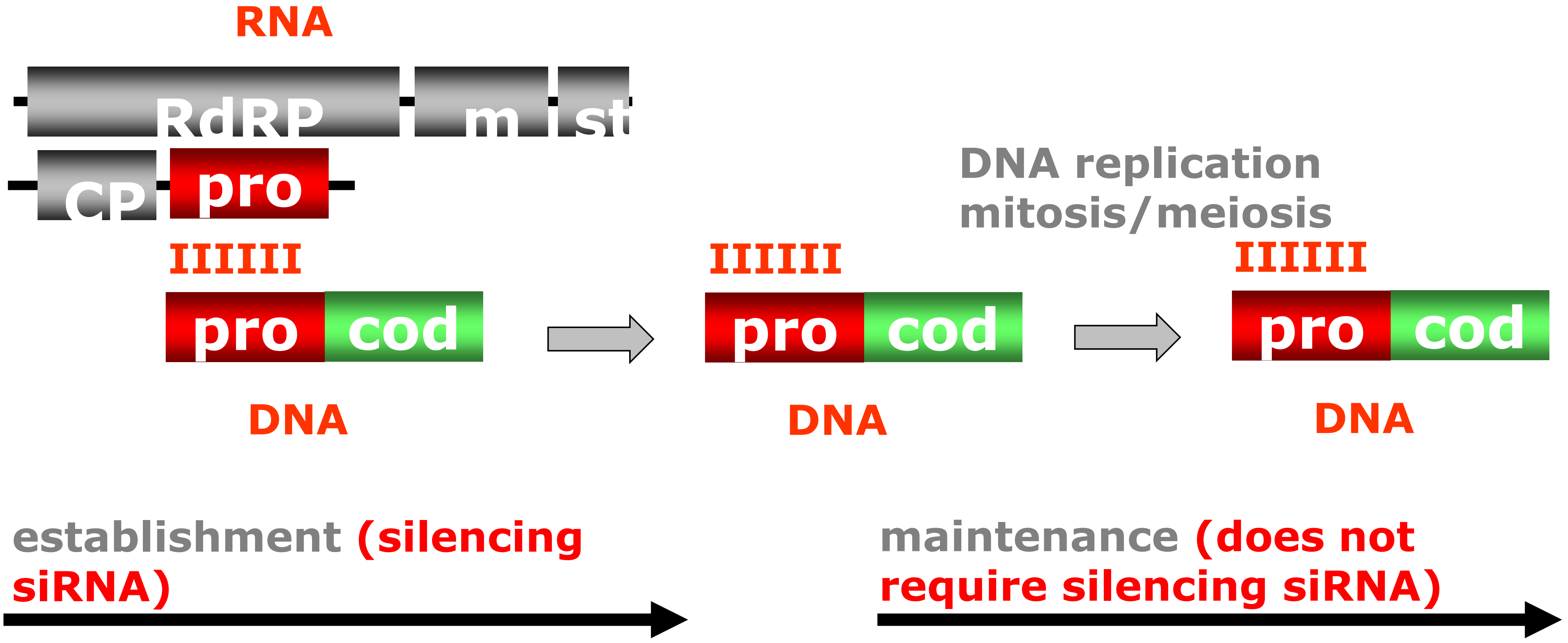
heritable silencing

CHH, CHG and CG methylation

CG methylation

heritable promoter silencing is dependent on promoter DNA methylation

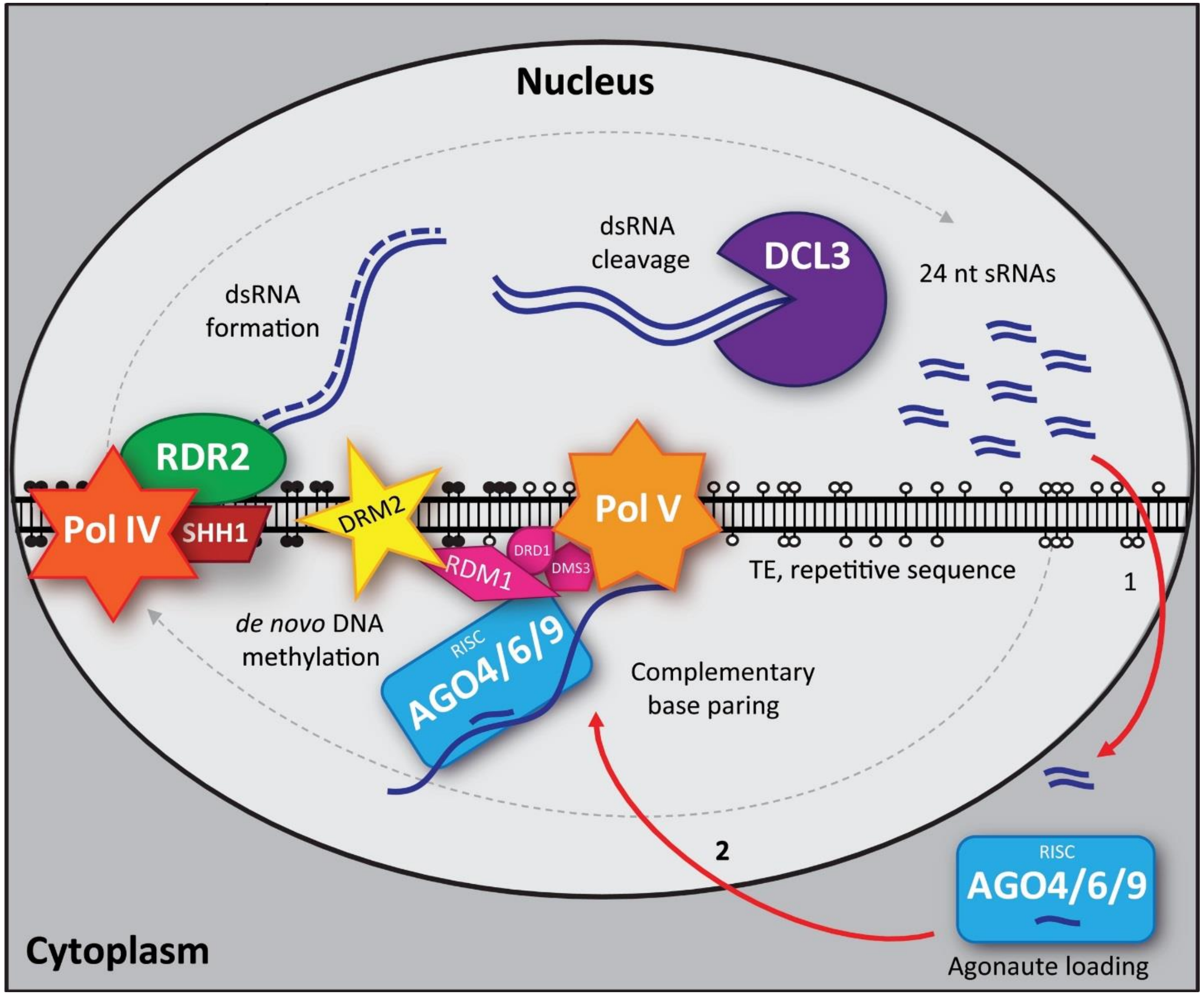
separate establishment and maintenance in heritable epimutation



establishment (silencing siRNA)

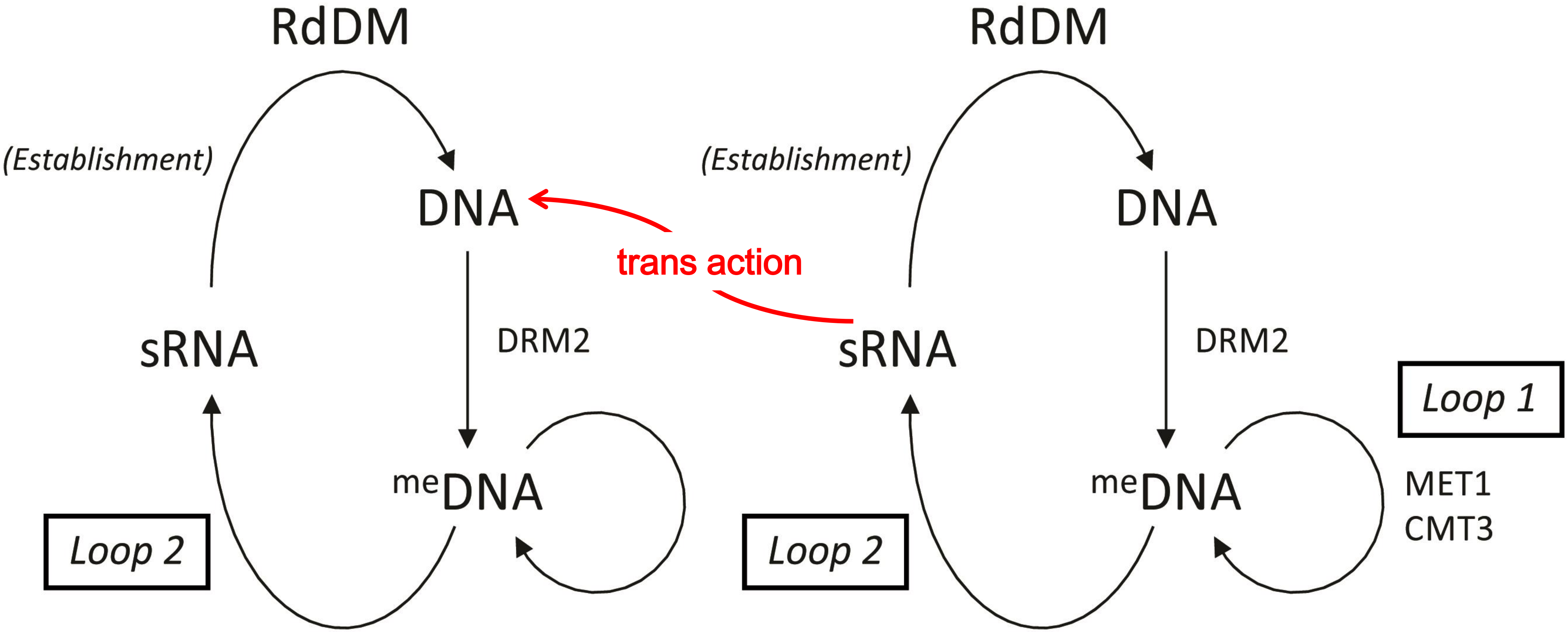
maintenance (does not require silencing siRNA)

establishment – a self reinforcing feedback system – RNA dependent amplification of silencing

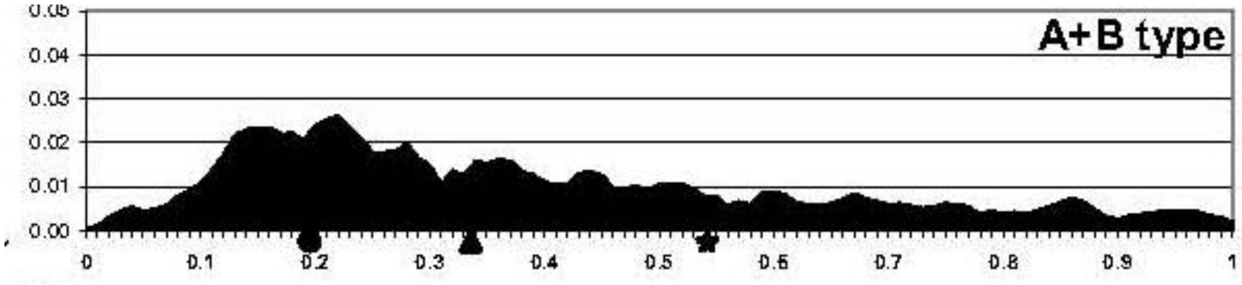


Donna Bond

maintenance of RdDM – a self reinforcing system with amplification and heritability



thousands of sRNA loci are distributed throughout the chromosomes of Arabidopsis and associated with transposable elements

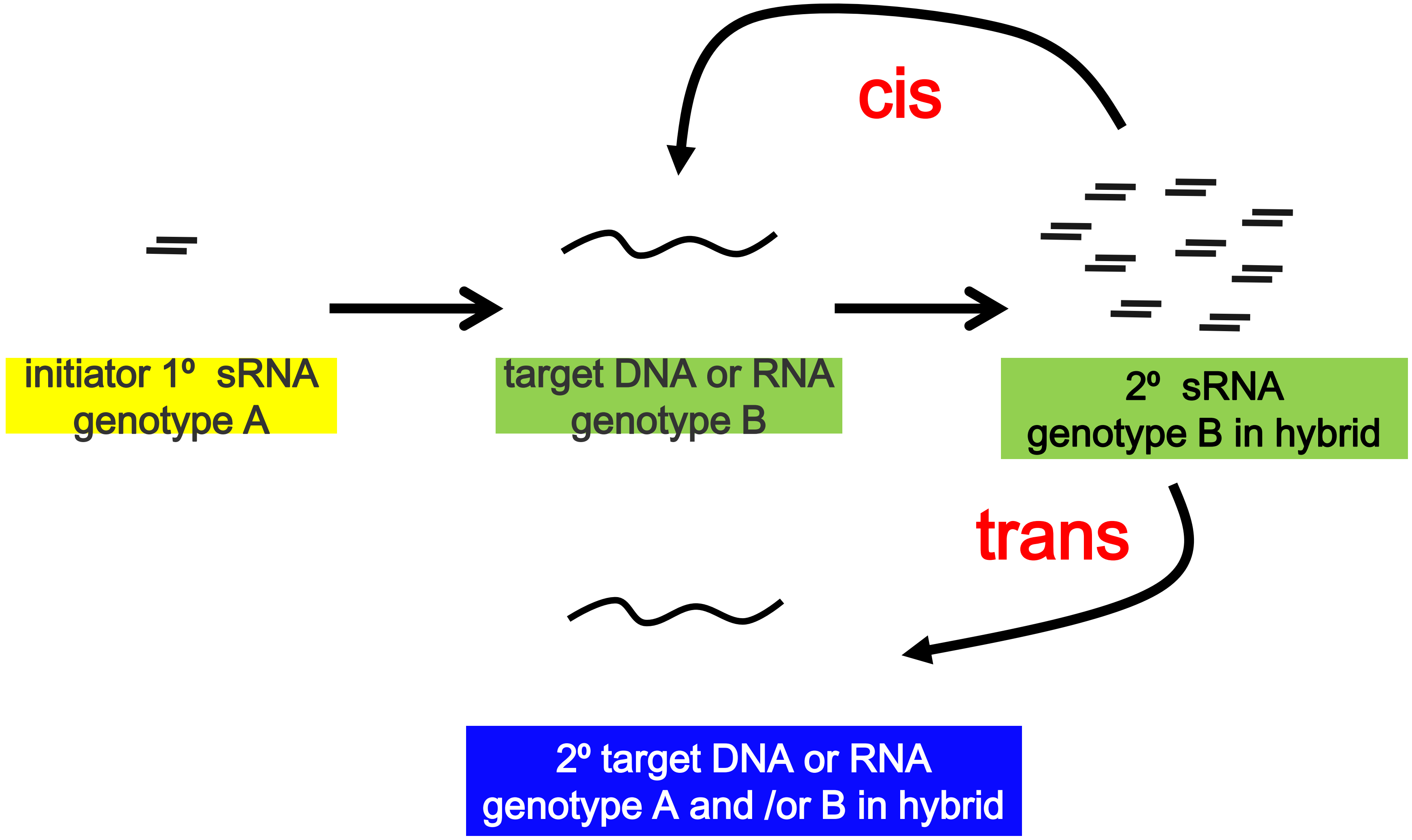


centromere

telomere

Becky Mosher

sRNA and genome interactions ?



initiator 1º sRNA
genotype A

target DNA or RNA
genotype B

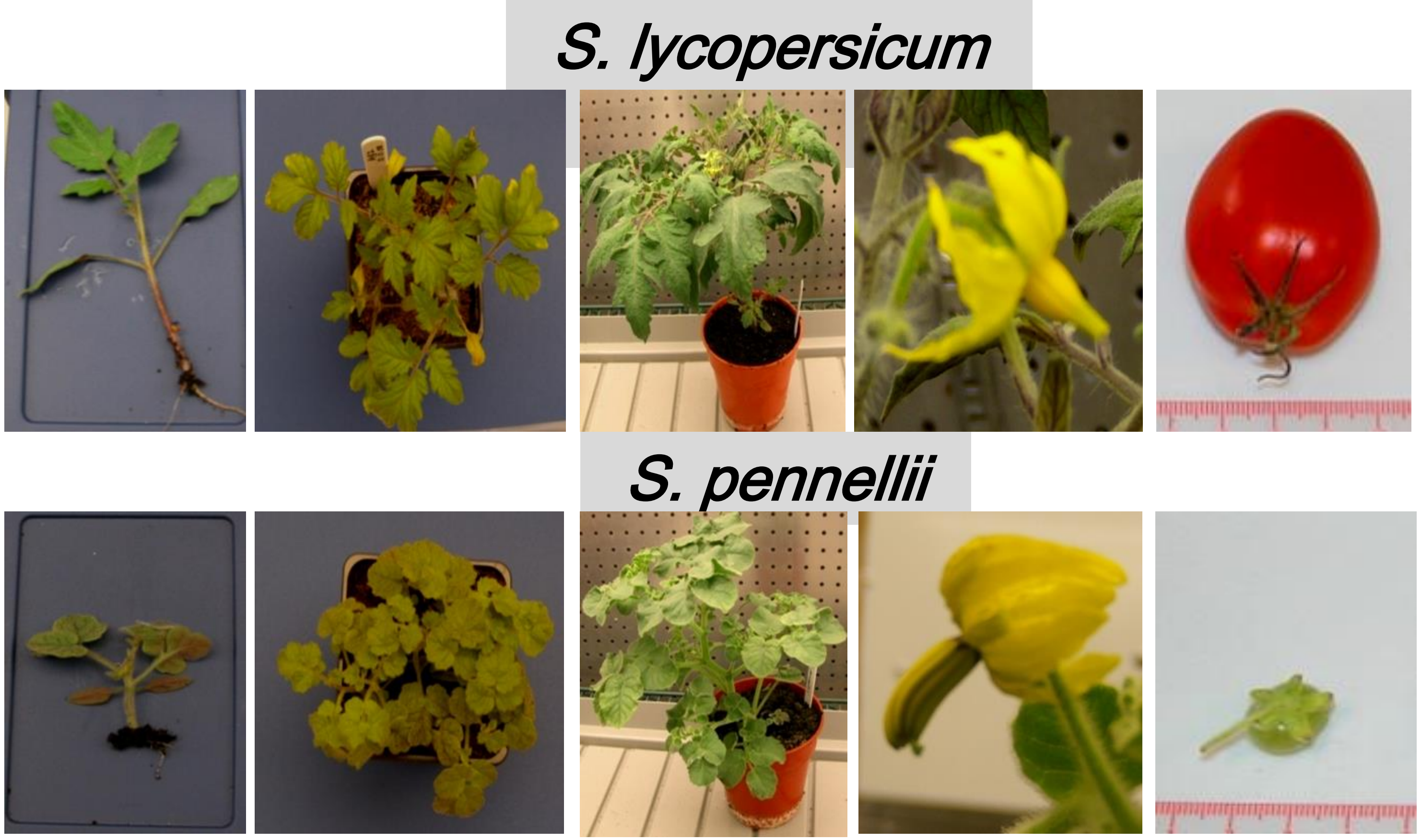
2º sRNA
genotype B in hybrid

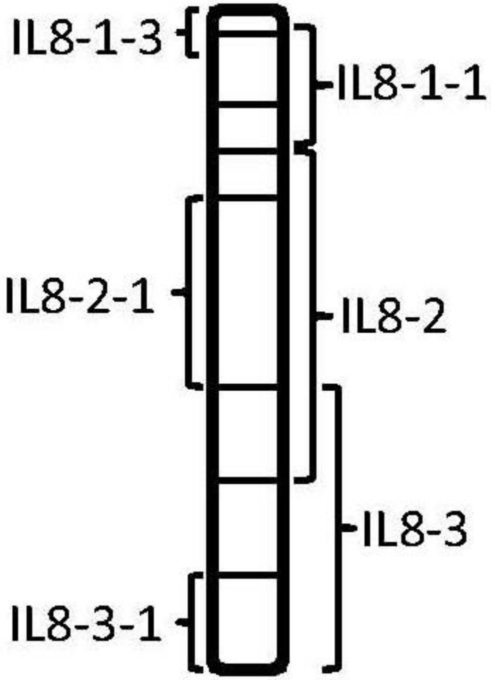
cis

trans

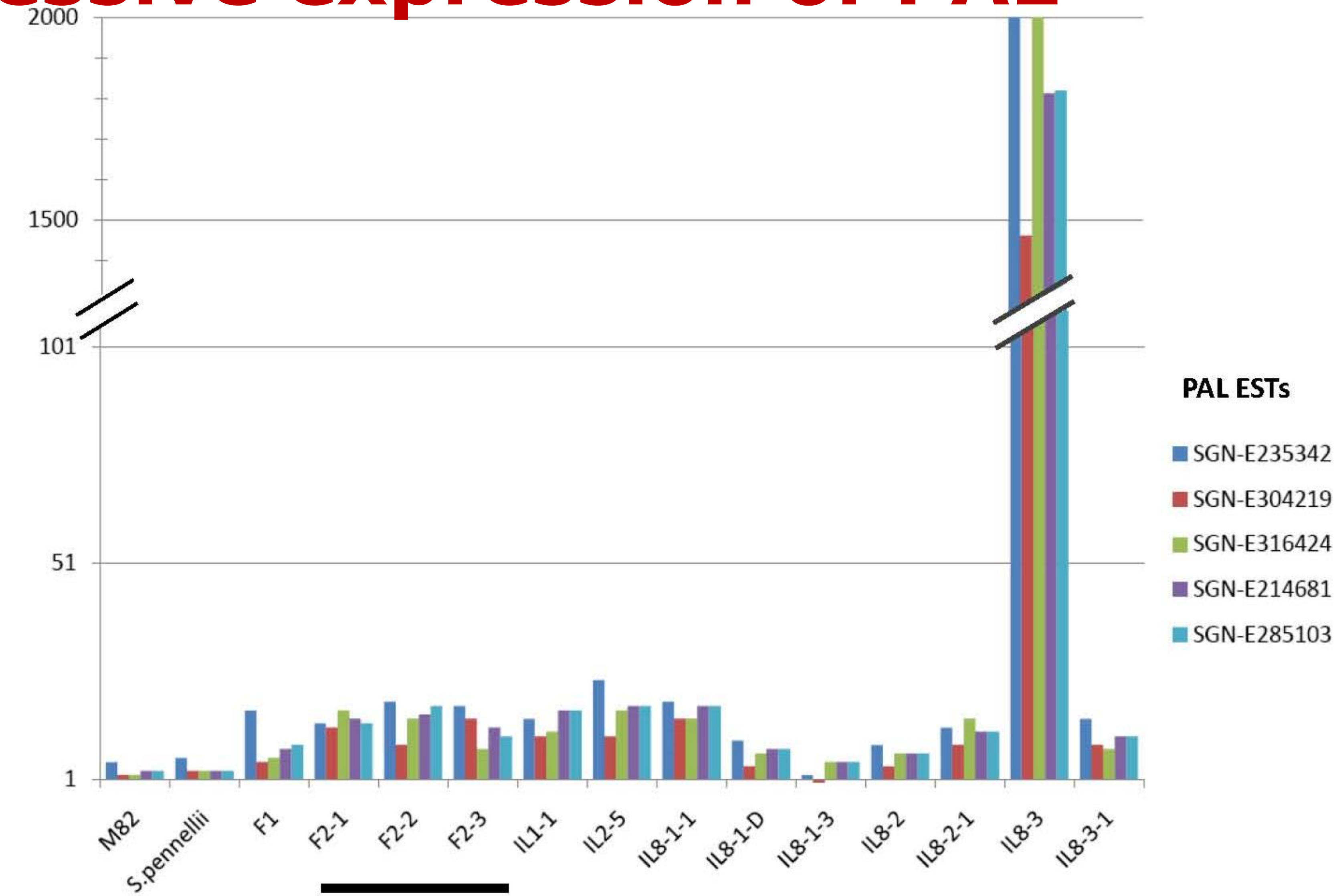
2º target DNA or RNA
genotype A and /or B in hybrid

sRNA and genome interactions in tomato and relatives





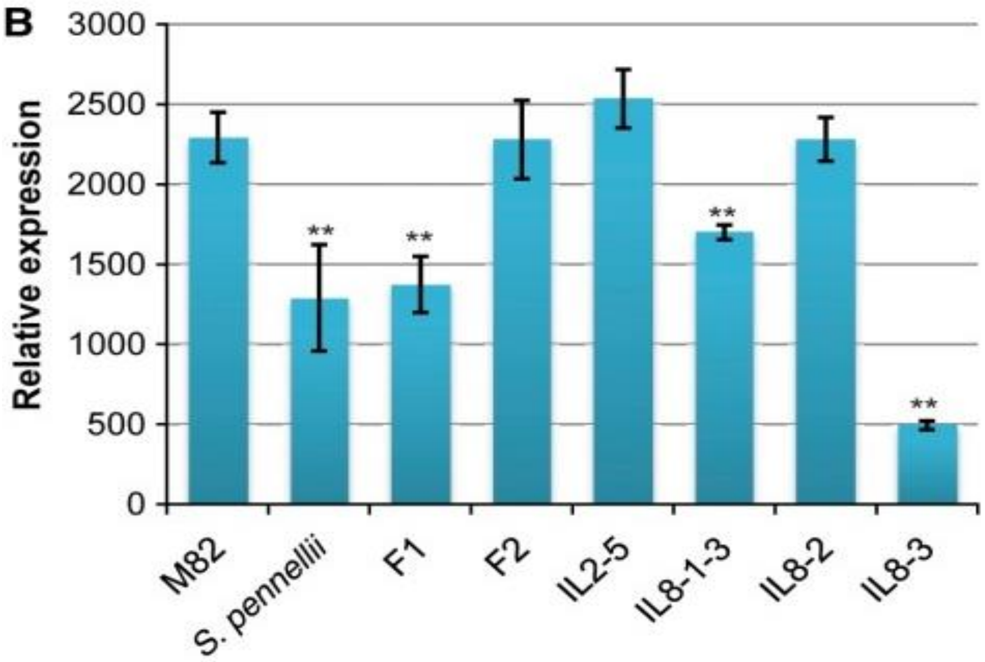
transgressive expression of PAL siRNAs

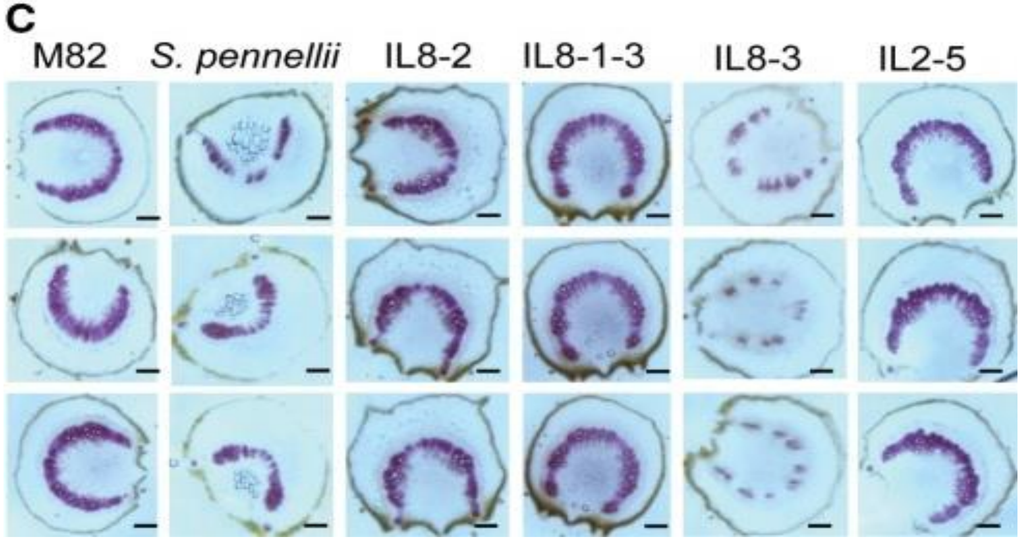


representation of of EST siRNA in Illumina datasets – phenylalanine ammonia lyase in particular

Padubidri Shivaprasad

…………and transgressive silencing of PAL





Phloroglucinol staining for total lignin

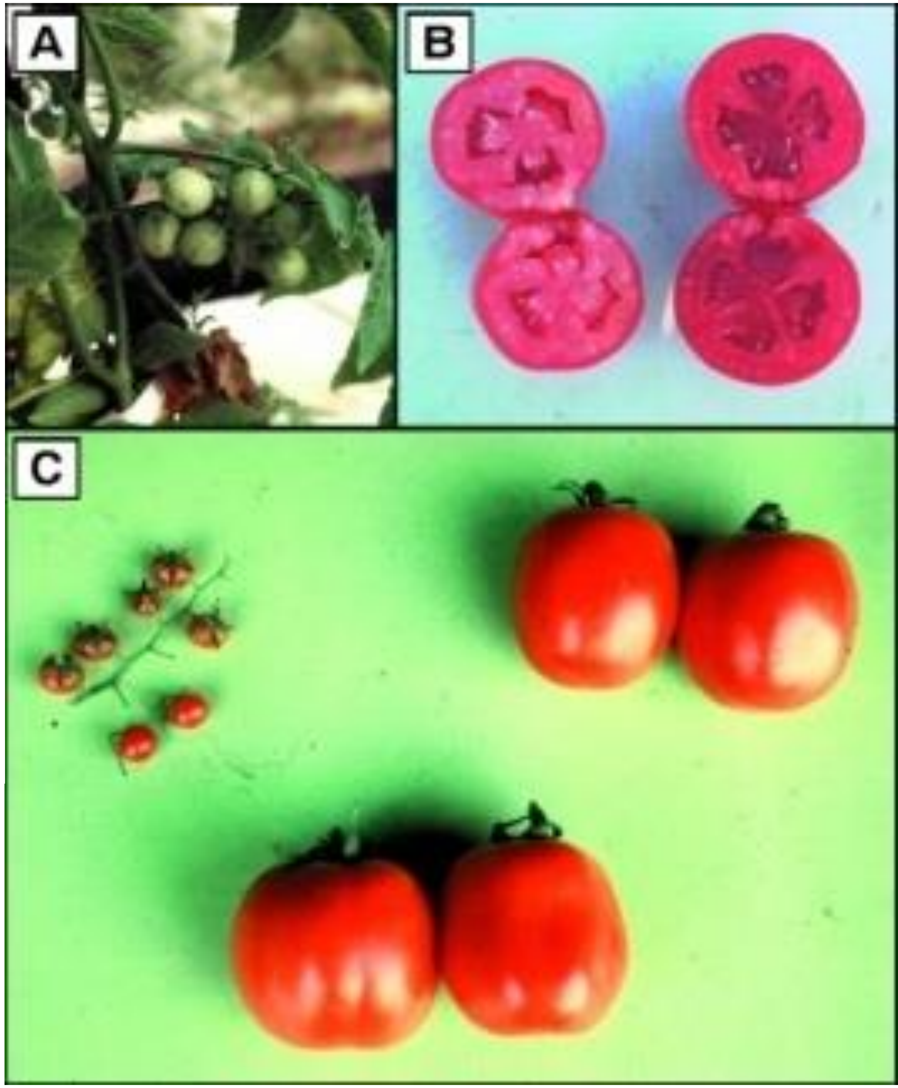
epigenetics in (interspecific) hybrids

Tanksley and McCouch
Science 277 (1997) 1063-1066

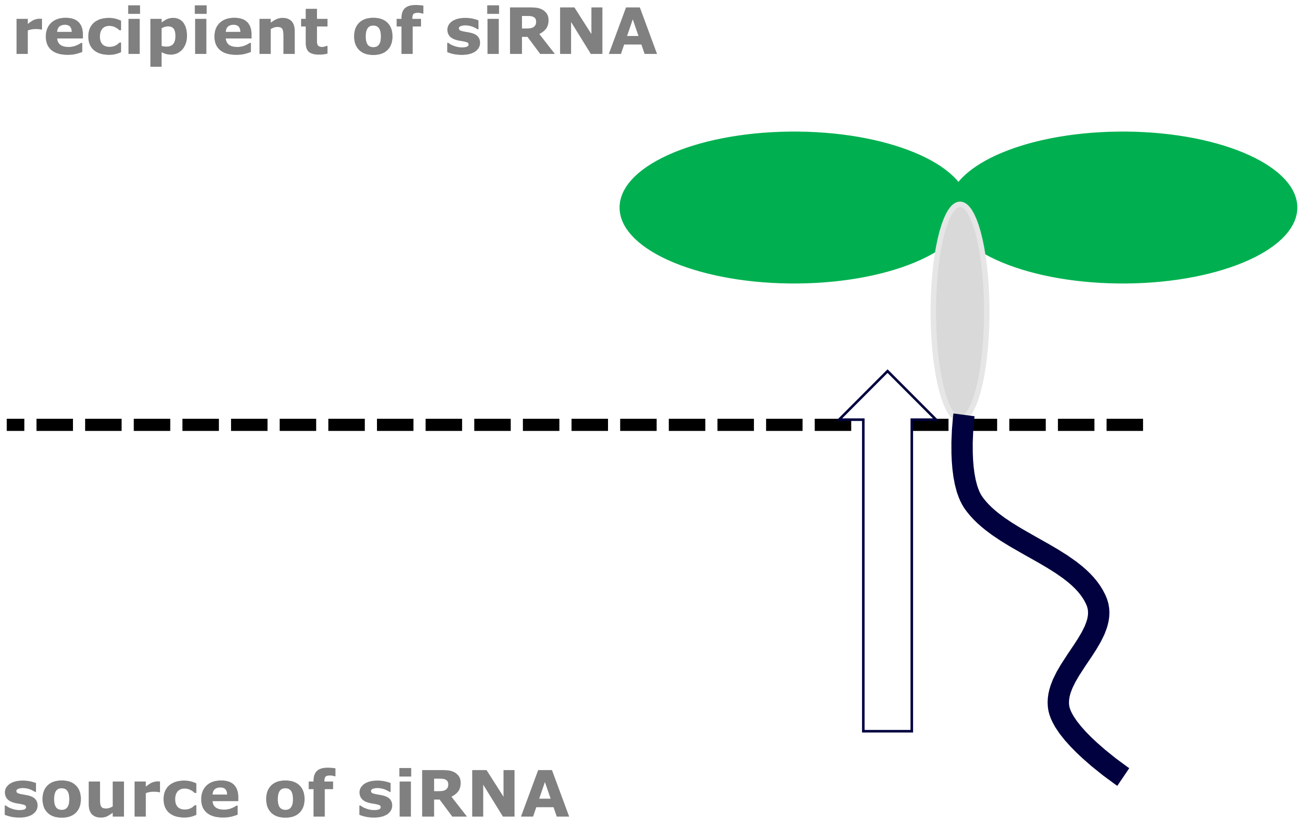
- **transgressive gene expression in interspecific *Solanum* hybrids associated with RNA and epigenetics**

- **hybridisation may be important not only because it initiates new heritable patterns of gene expression**

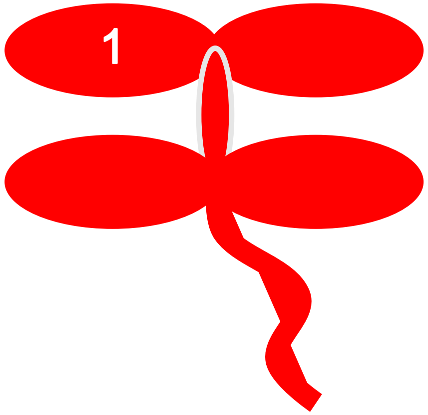
- **heritable variation between varieties or individuals will be due to epigenetic as well as genetic differences** ←



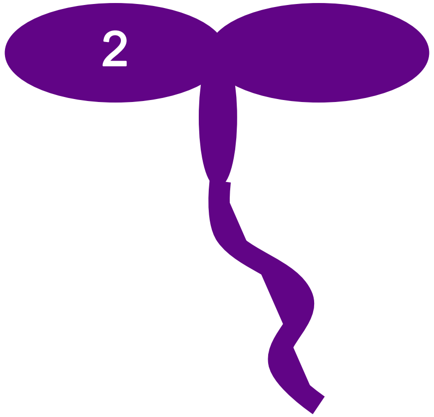
sRNA mobility for initiation of epigenetic change



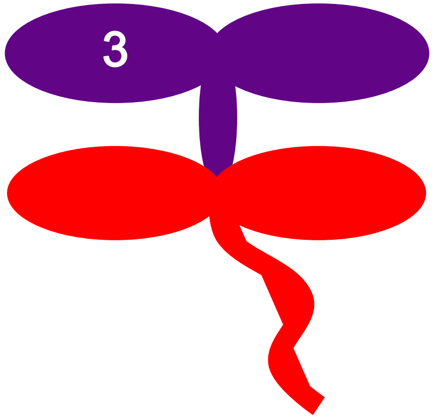
how to make an epigenetically modified plant



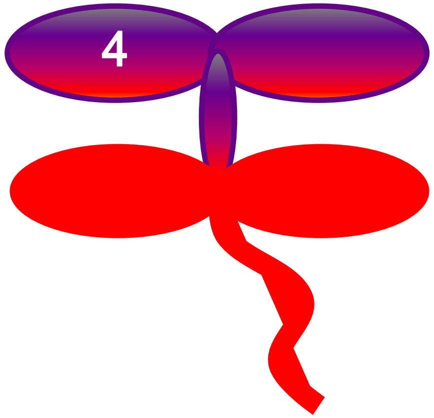
variety producing silencing signal: target gene affecting seed quality



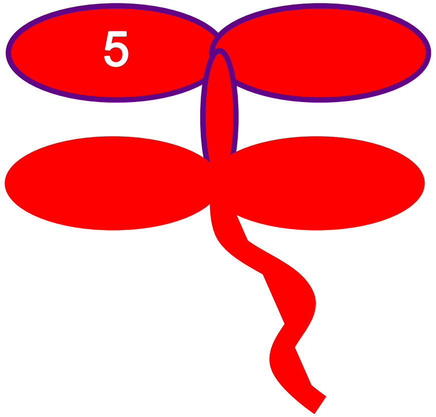
variety with reduced seed quality due to target gene overexpression



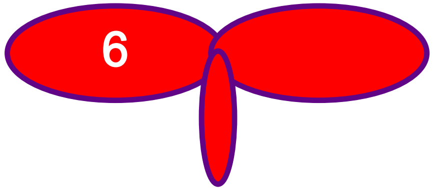
grafted chimaera



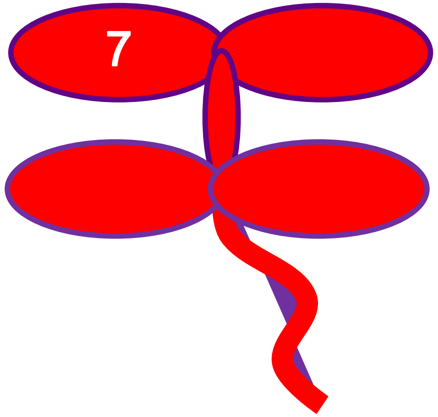
spread of silencing signal across graft union



Full silencing of target gene in grafted plant

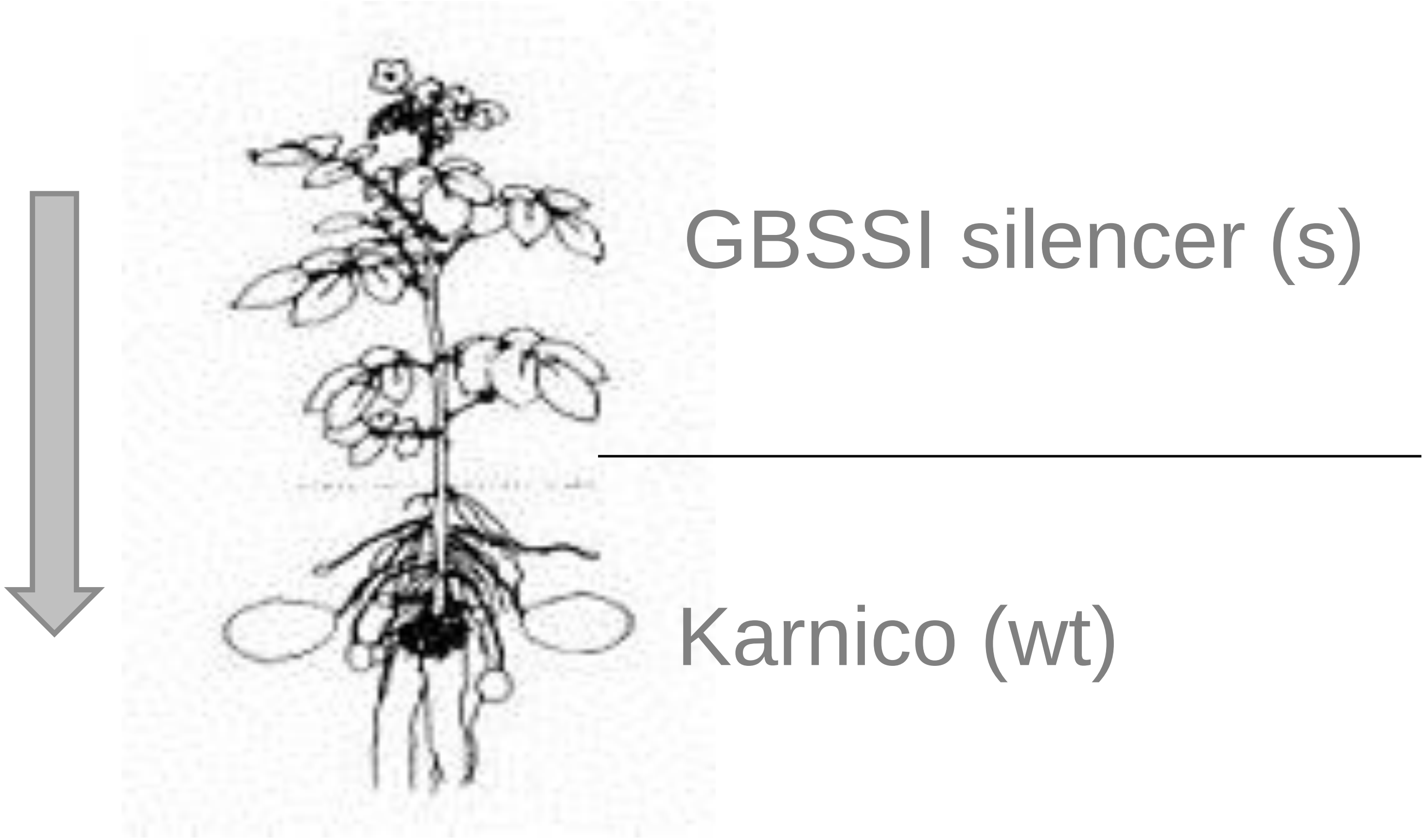


removal of stock



regeneration of root and persistent silencing

TGS of GBSSI in wild type tuber by mobile sRNAs using a GBSSI silenced transgenic scion as a grafting partner



movement of the silencing signal

GBSSI silencer (s)

Karnico (wt)

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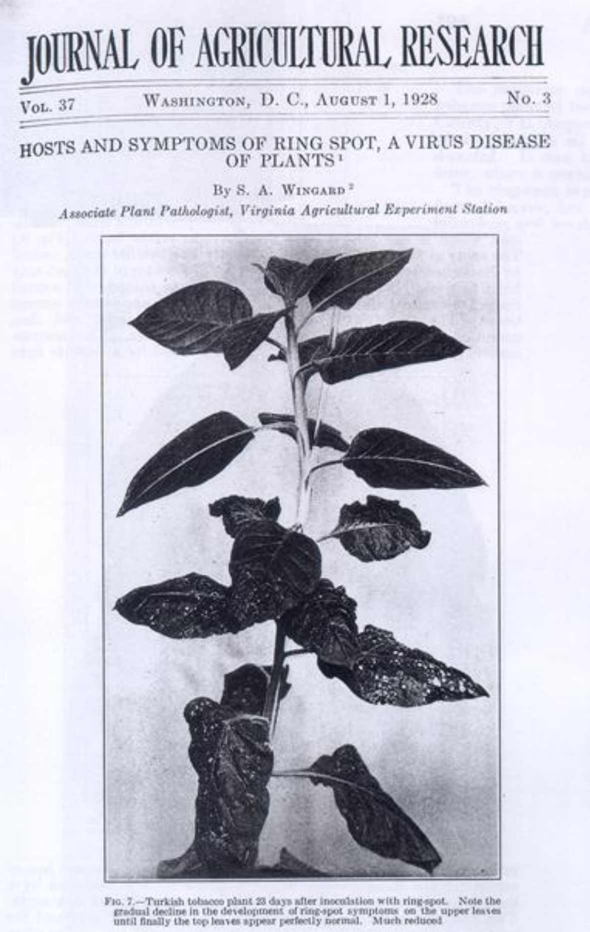
RNA silencing is a virus defense mechanism



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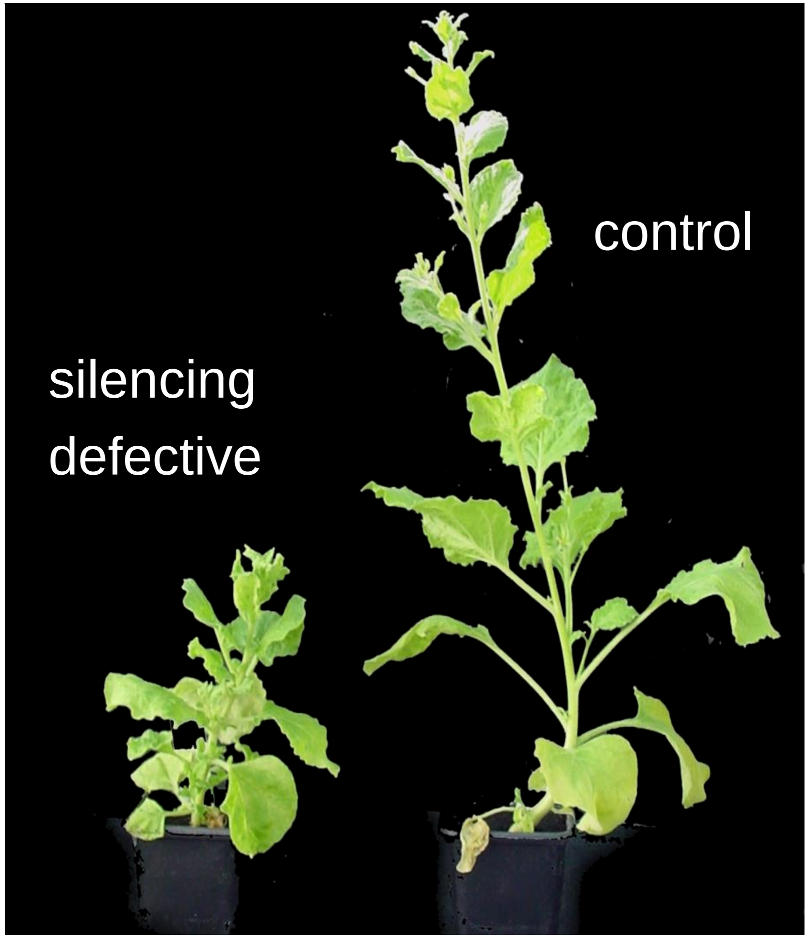
Vol. 37 Washington, D. C., August 1, 1928 No. 3

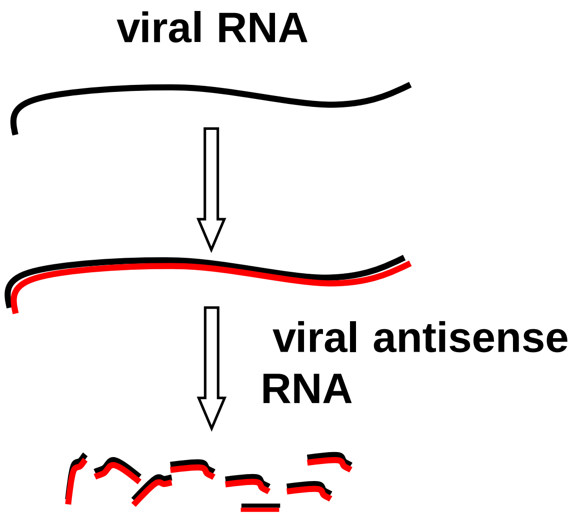
HOSTS AND SYMPTOMS OF RING SPOT, A VIRUS DISEASE OF PLANTS[1]

By S. A. Wingard[2]

Associate Plant Pathologist, Virginia Agricultural Experiment Station

Fig. 7.—Turkish tobacco plant 23 days after inoculation with ring-spot. Note the gradual decline in the development of ring-spot symptoms on the upper leaves until finally the top leaves appear perfectly normal. Much reduced

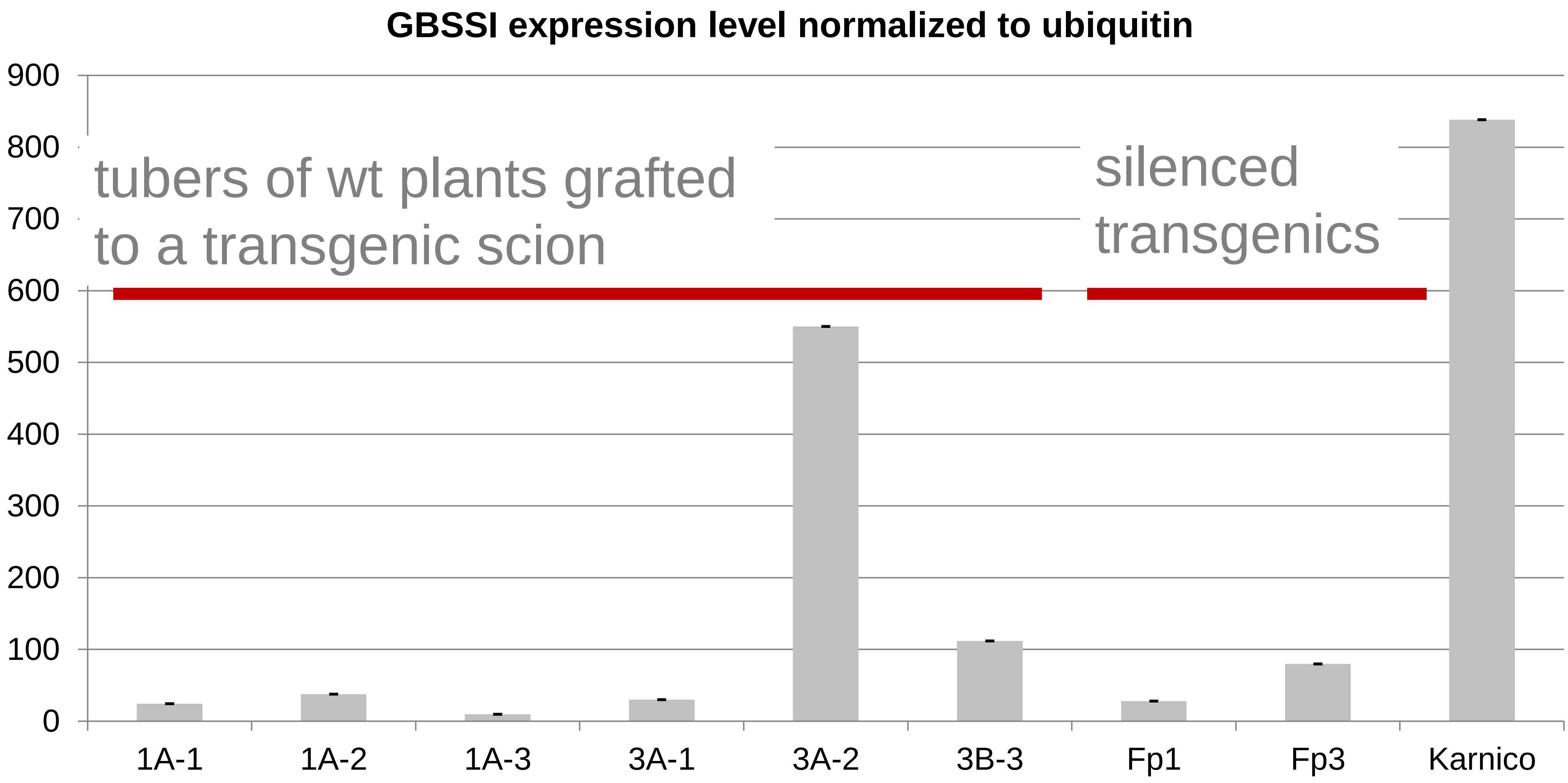




viral RNA

viral antisense RNA

TGS of GBSS by grafting



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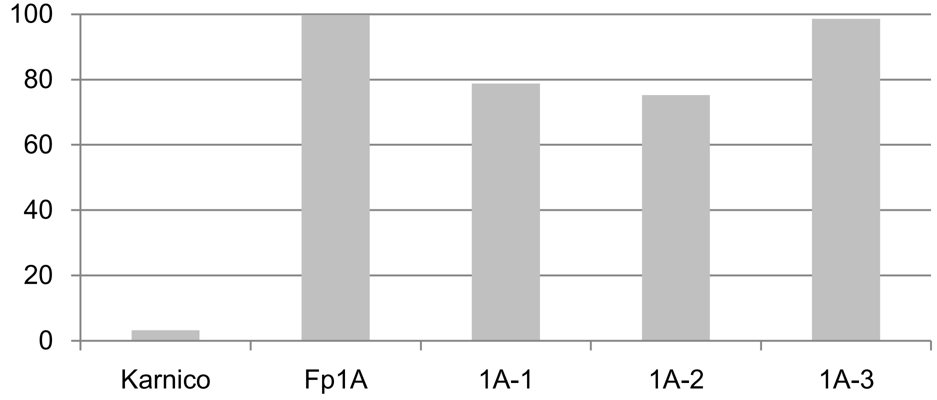
GBSS promoter methylation by grafting

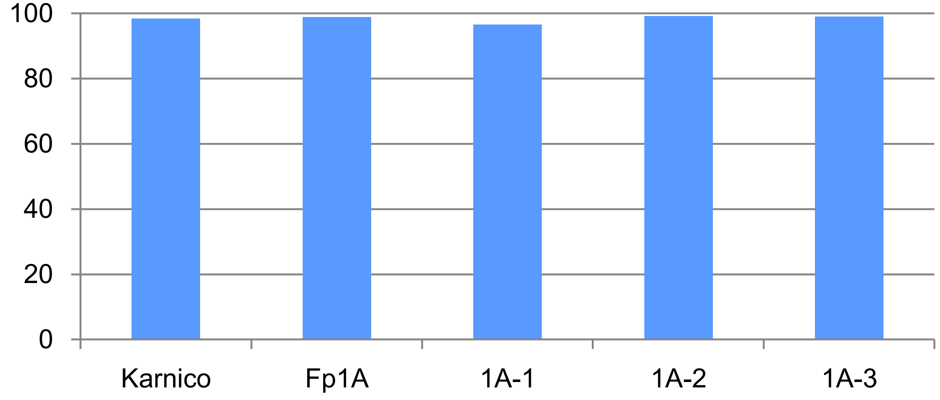
-   +

tubers of wt plants grafted
to a transgenic scion

Methylation %-Potato GBSSI promoter



Methylation % - Potato Mite (+ Control)



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targeted epimutation

- epigenetically modified plants
- delivery method for siRNAs – grafting, virus, transgene
- factors affecting targeting of promoter (including cis and trans-acting factors)
- factors affecting stability of silenced state

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epigenetics in plant breeding

- epigenetic marks affect gene expression
  - heritable
  - induced by hybridisation
  - other types of genome shock
- plant breeders may have been unwittingly selecting for epiQTL
- understanding of epigenetics may allow efficient exploitation of epiQTL in conventional breeding and Epigenetically Modified Plants

Attila Molnar
Charles Melnyk
Donna Bond

Padubidri Shivaprasad
Quentin Gouil

Krys Kelly
Tom Hardcastle

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