Journées scientifiques du Groupe Céréales à Paille
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Clermont-Ferrand, France

Plant biotic interactions in the epigenomic era

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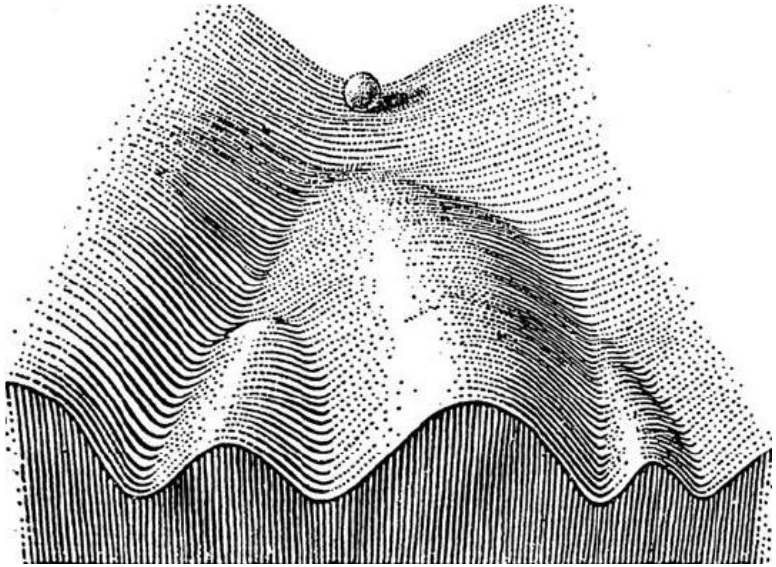
Epigenetics

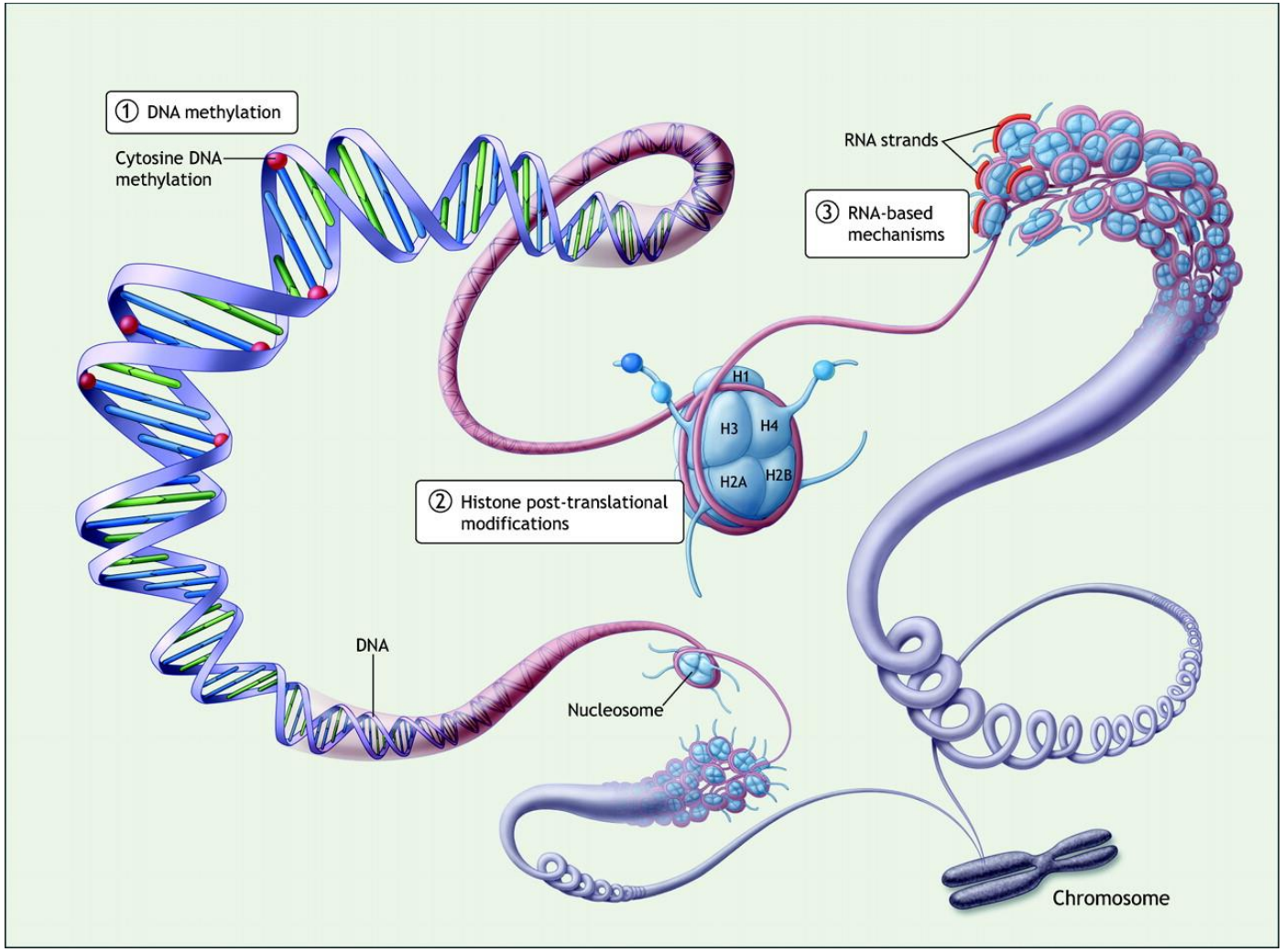
The study of changes in gene function that are mitotically and/or meiotically heritable and that do not entail a change in DNA sequence

➔A change in phenotype without a change in genotype



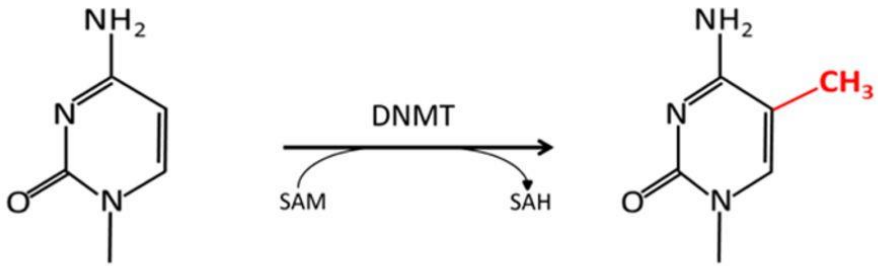
(Waddington, 1957)

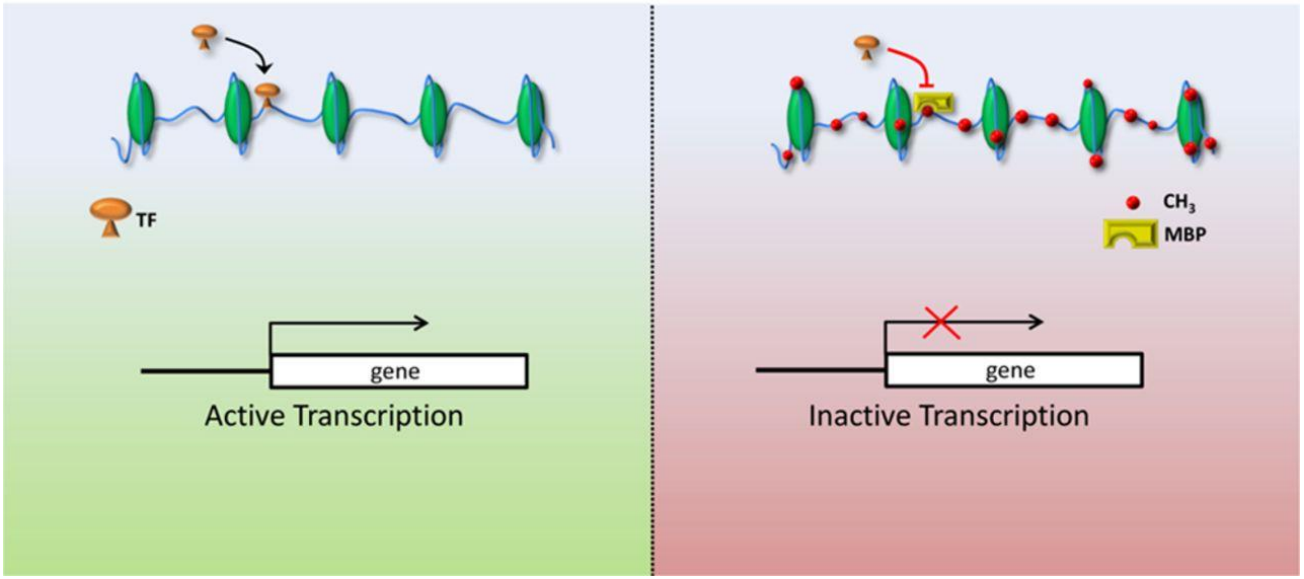
Epigenetic regulations



(Matouk and Marsden, Circ Res 2008)

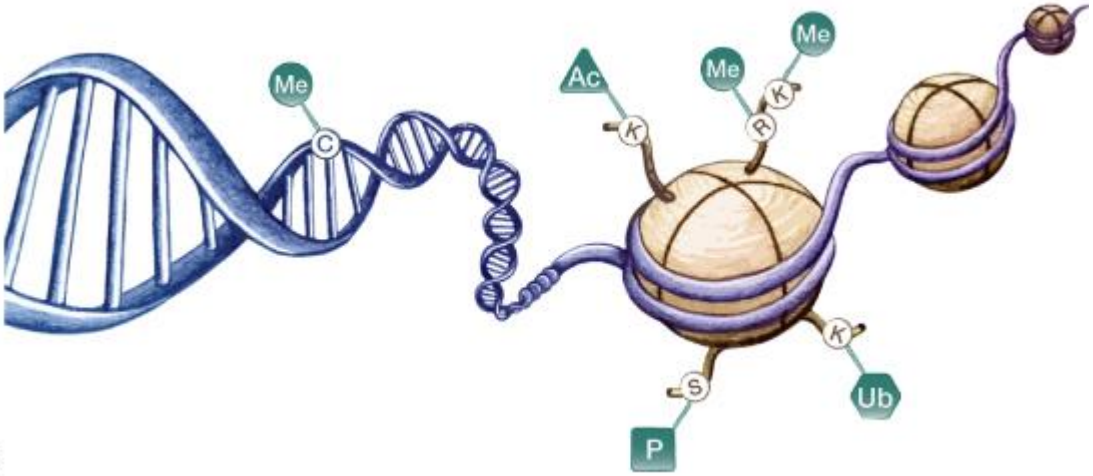
DNA methylation

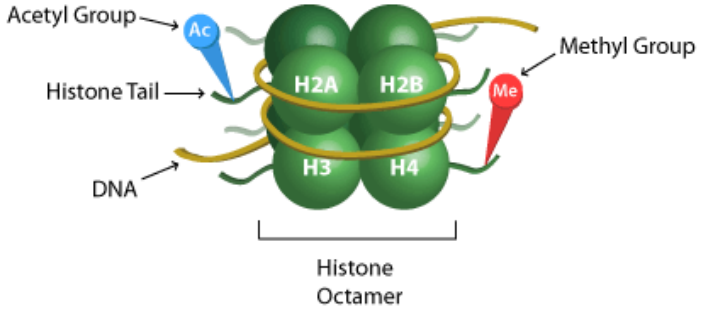


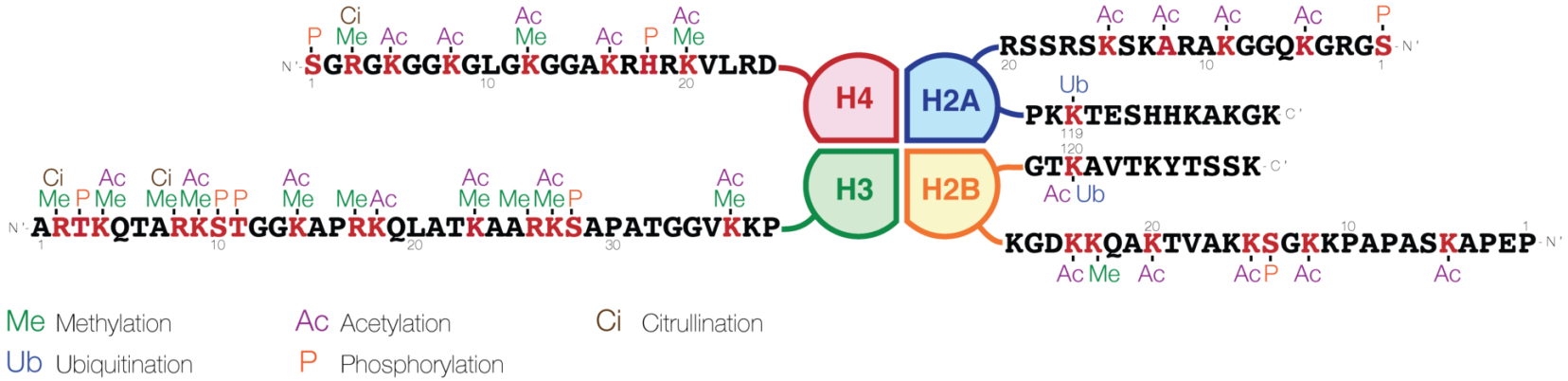


(Zhong et al., Circ Res 2016)

Histone modifications

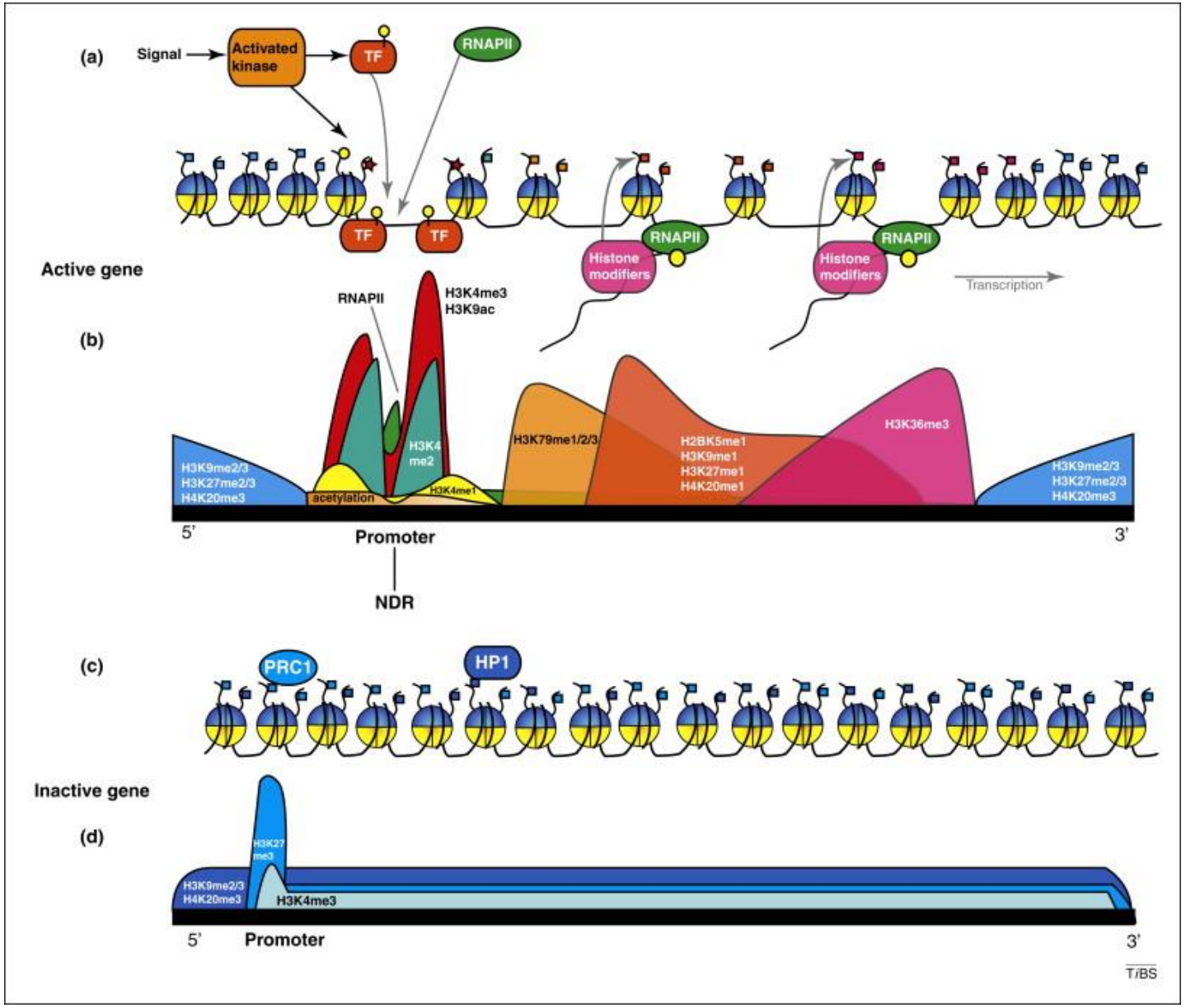






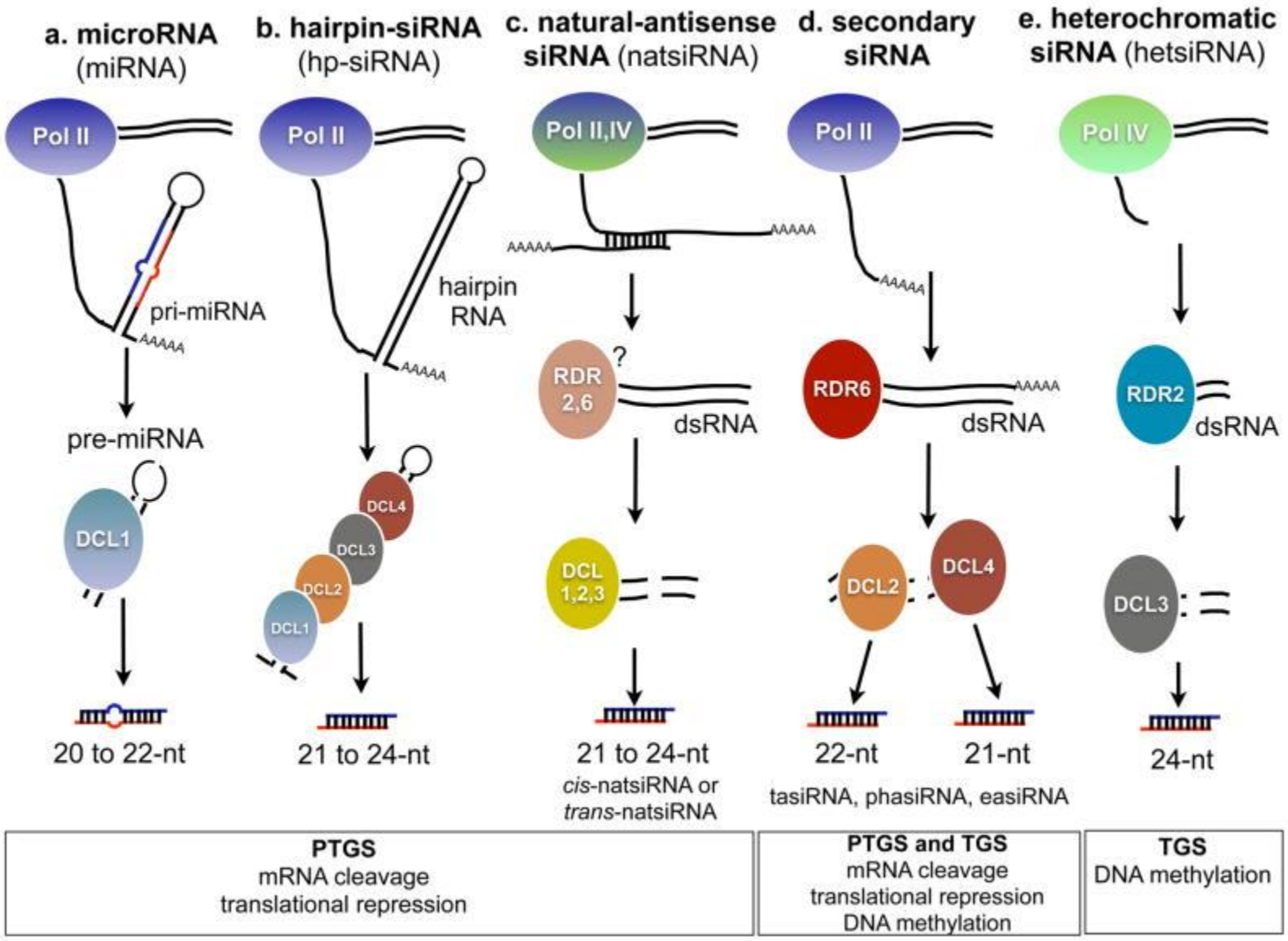
Me Methylation
Ub Ubiquitination
Ac Acetylation
P Phosphorylation
Ci Citrullination

The dynamics of histone modifications



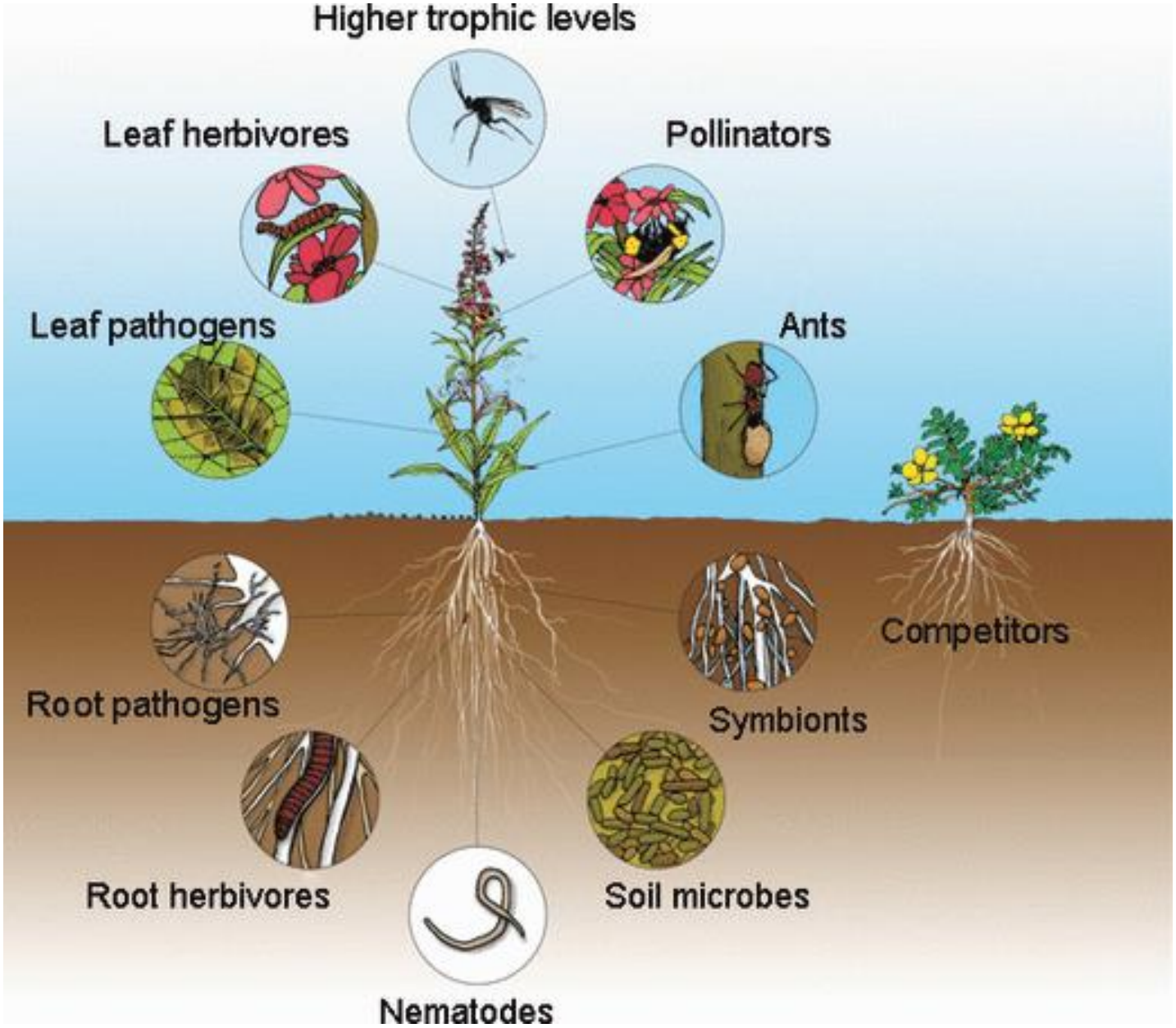
(Barth and Imhof, Trends Biochem Sci 2010)

The expanding world of small RNAs in plants



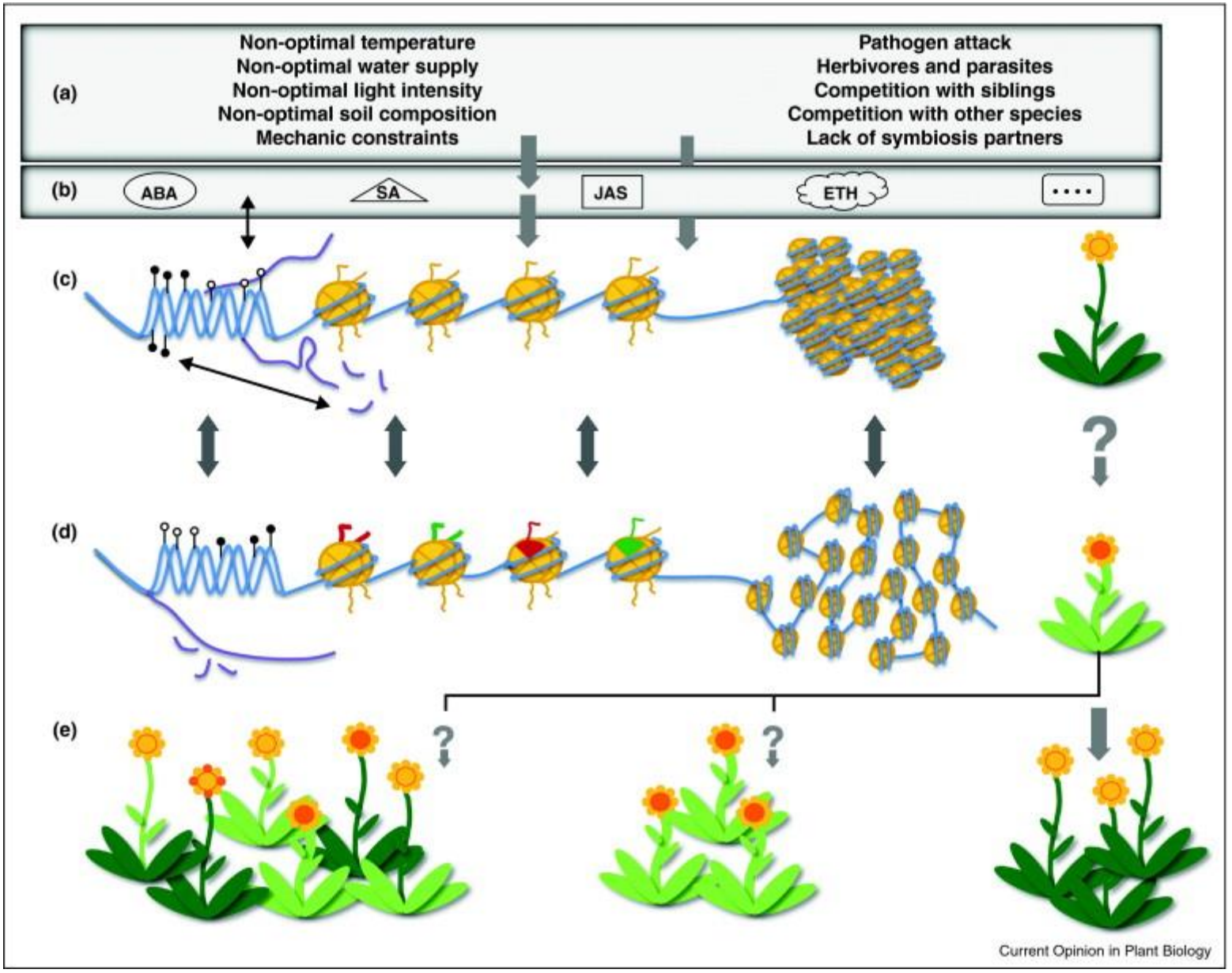
(Borges and Martienssen, Nat Rev Mol Cell Biol 2015)

How plants cope with biotic interactions



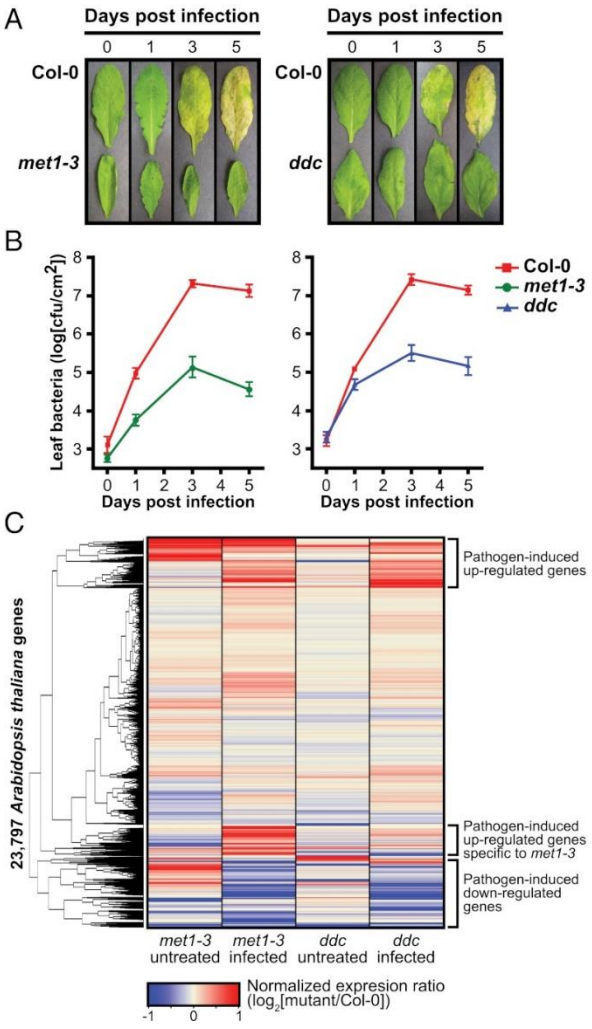
(Van Dam, Plant Biol 2009)

Epigenetic responses to stress: triple defense?

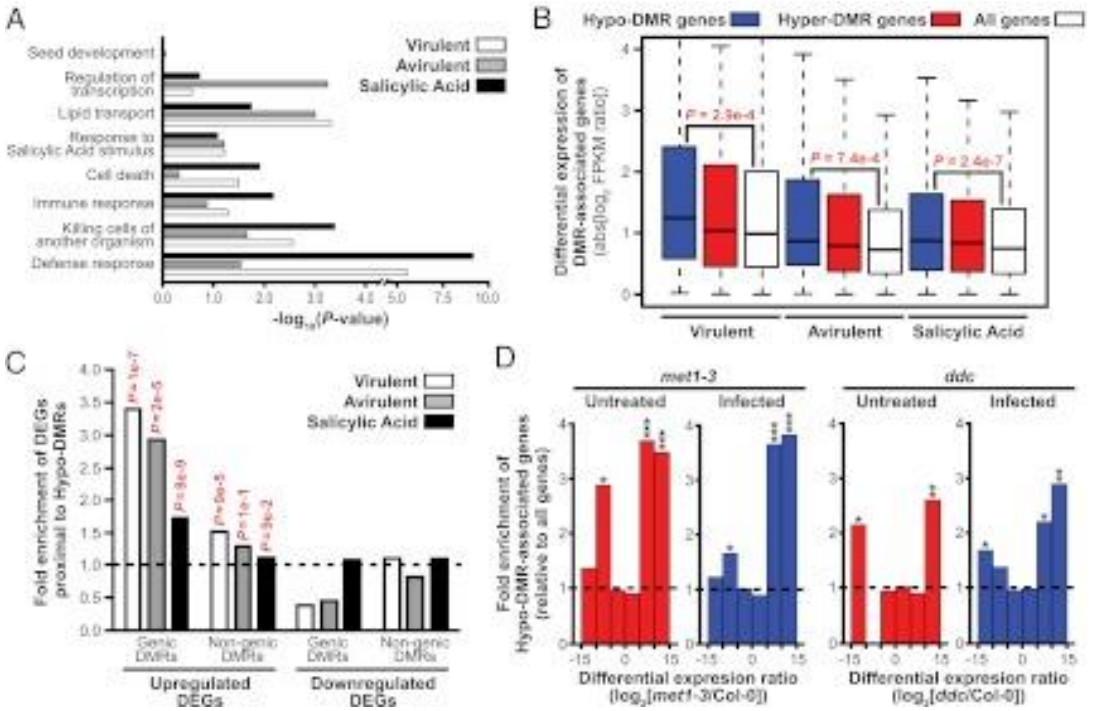


(Gutzat and Scheid, Curr Opin Plant Biol 2010)

Widespread dynamic DNA methylation in response to biotic stress



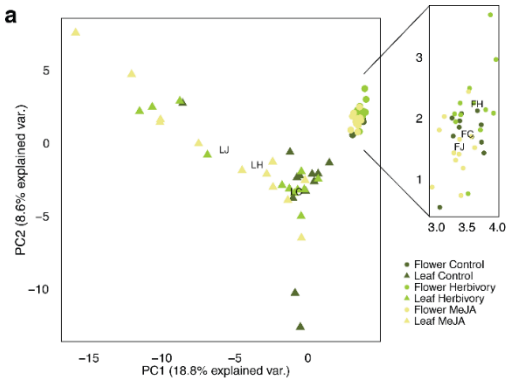
- ✓ Mutants defective in DNA methylation are resistant to pathogenic *P. syringae*.



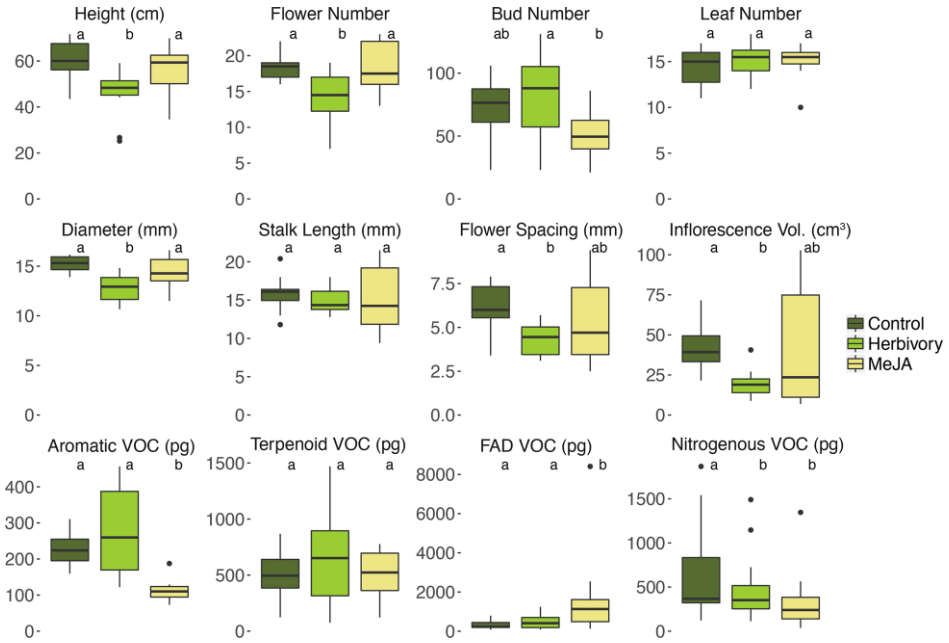
- ✓ DMR-associated genes in response to *Pst* or SA are enriched in genes that function in plant defense

(Dowen et al., Proc Natl Acad Sci USA 2012)

Herbivore-Induced DNA Demethylation Changes Floral Signalling and Attractiveness to Pollinators in *Brassica rapa*



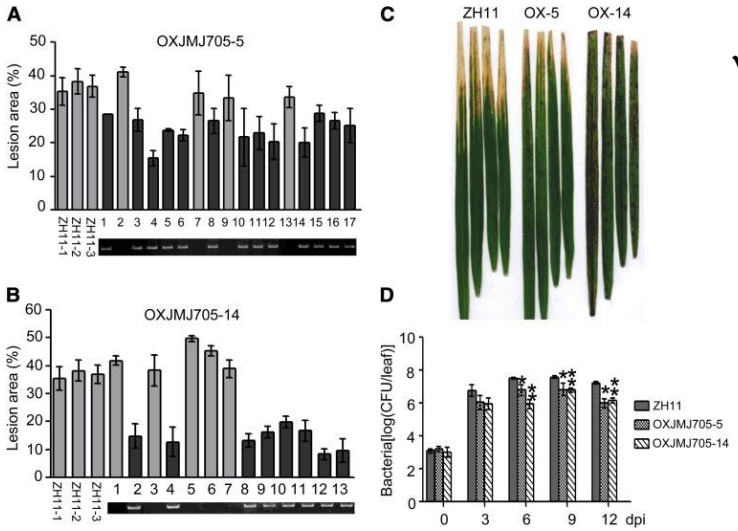
✓ **Foliar herbivory leads to genome-wide methylation changes not only in the leaves, but also in the undamaged flowers of *B. rapa*.**

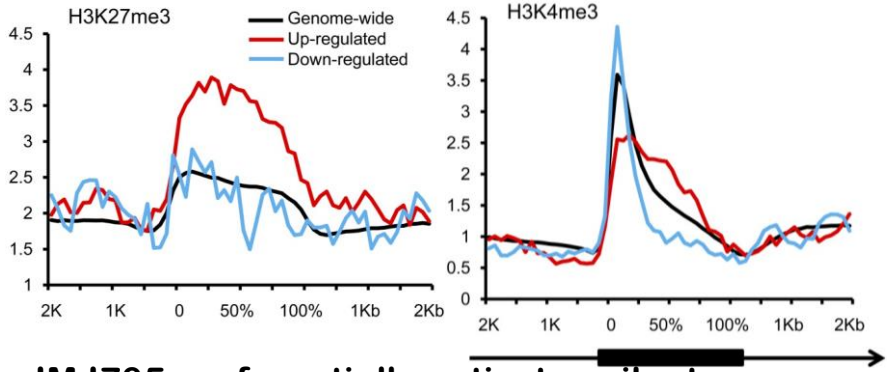


✓ **Methylation changes are associated with phenotypic effects including plant attractiveness.**

(Kellenberger et al., PLoS One 2016)

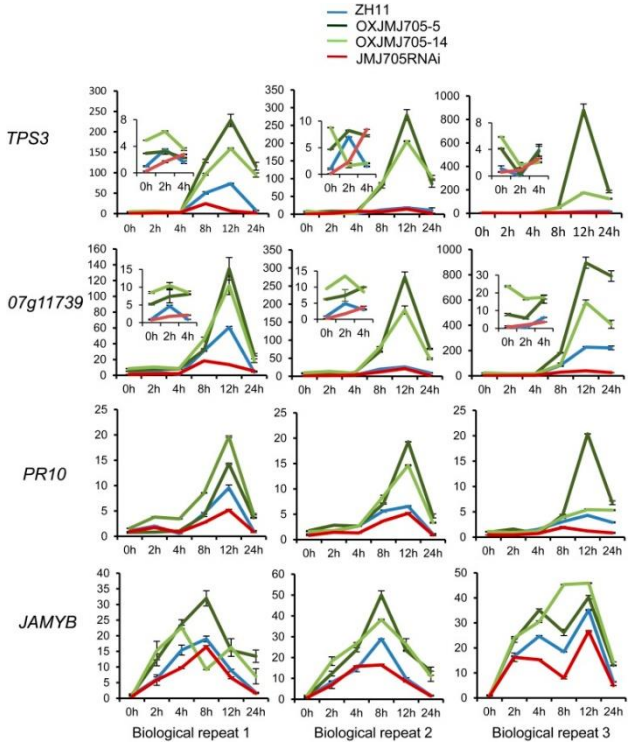
Jumonji C domain protein JMJ705-mediated removal of histone H3 lysine 27 trimethylation is involved in defense-related gene activation in rice





✓ JMJ705 preferentially activates silent or underexpressed genes that were marked by a relatively high level of H3K27me3 and a relatively low level of H3K4me3

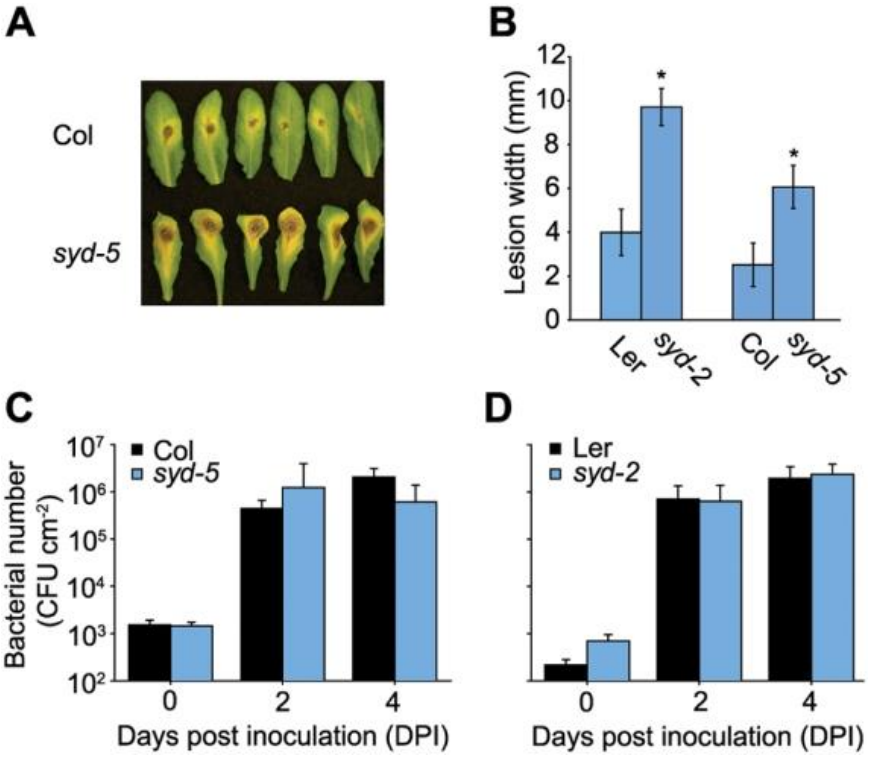
✓ JMJ705 Overexpression Enhances Rice Resistance to the Bacterial Pathogen *Xanthomonas oryzae* pathovar *oryzae*



✓ JMJ705 Enhances JA Induction of Gene Expression

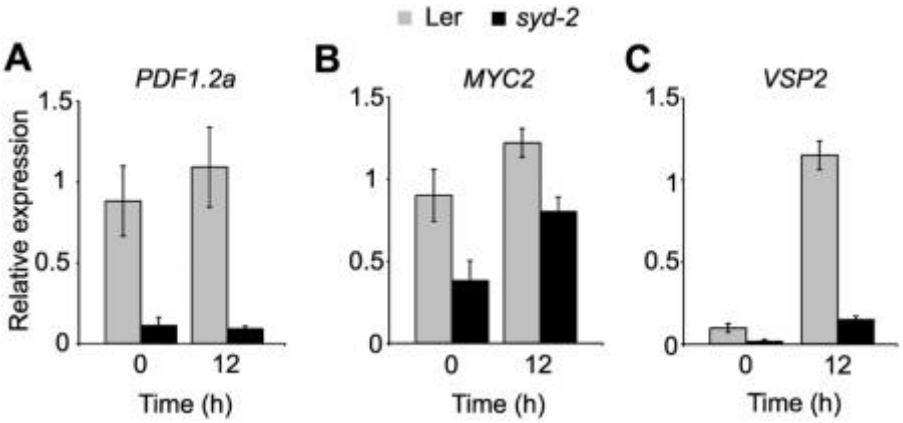
(Li et al., Plant Cell 2013)

The Chromatin Remodeler SPLAYED Regulates Specific Stress Signaling Pathways



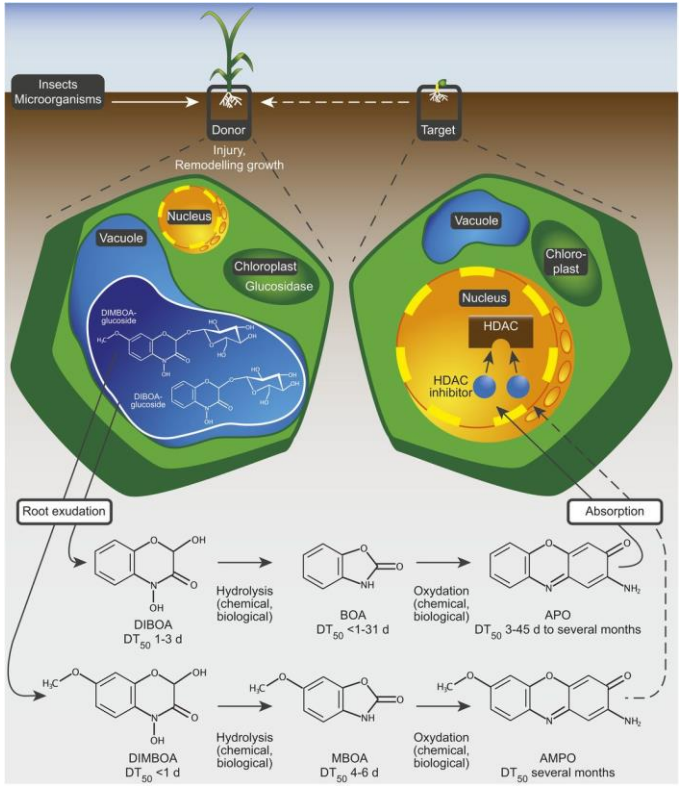
- ✓ The chromatin remodeling ATPase SYD is required for resistance to *B. cinerea* (A, B) but not *P. syringae* (C, D)

- ✓ SYD regulates expression of ET and JA responsive defense genes

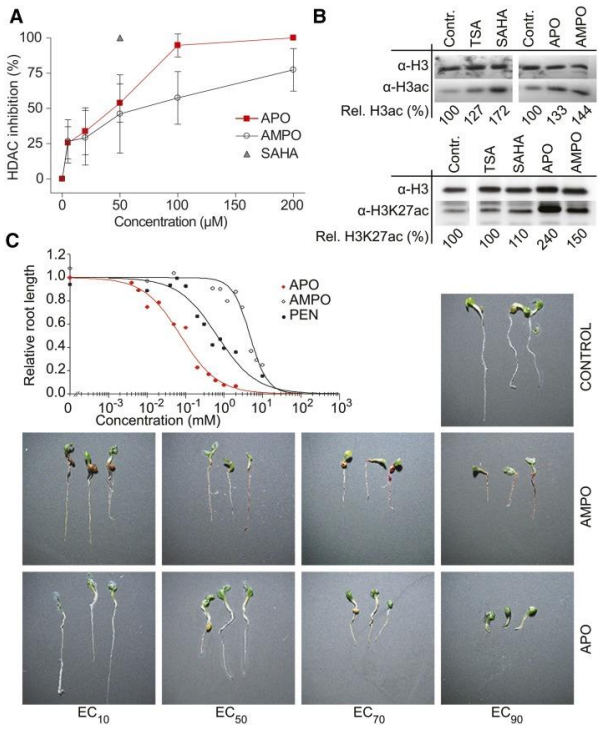


(Walley et al., PLoS Pathol 2008)

Plants Release Precursors of Histone Deacetylase Inhibitors to Suppress Growth of Competitors



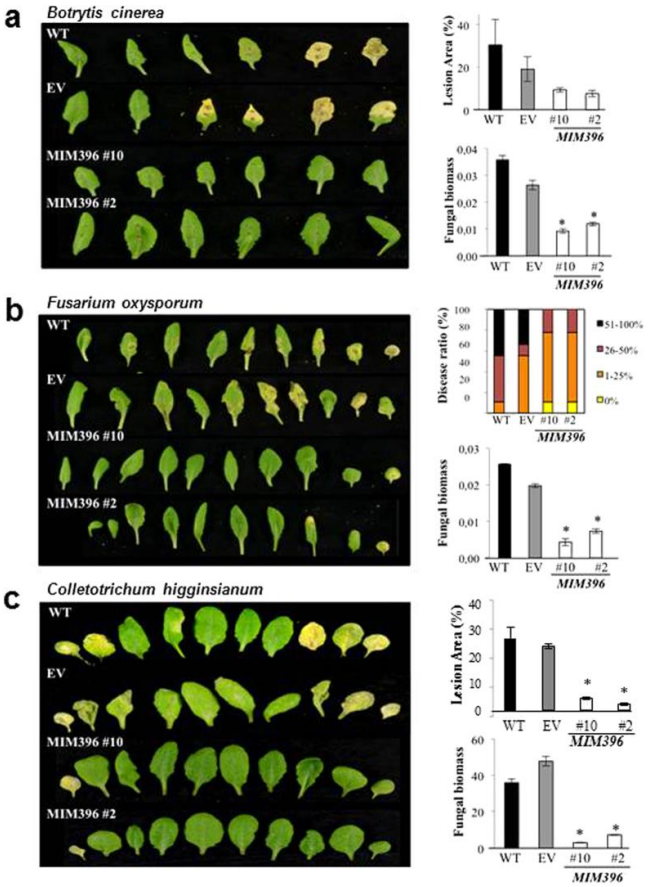
- ✓ The allelochemicals DIBOA and DIMBOA from root exudates are rapidly degraded in the soil to produce the highly phytotoxic APO and AMPO



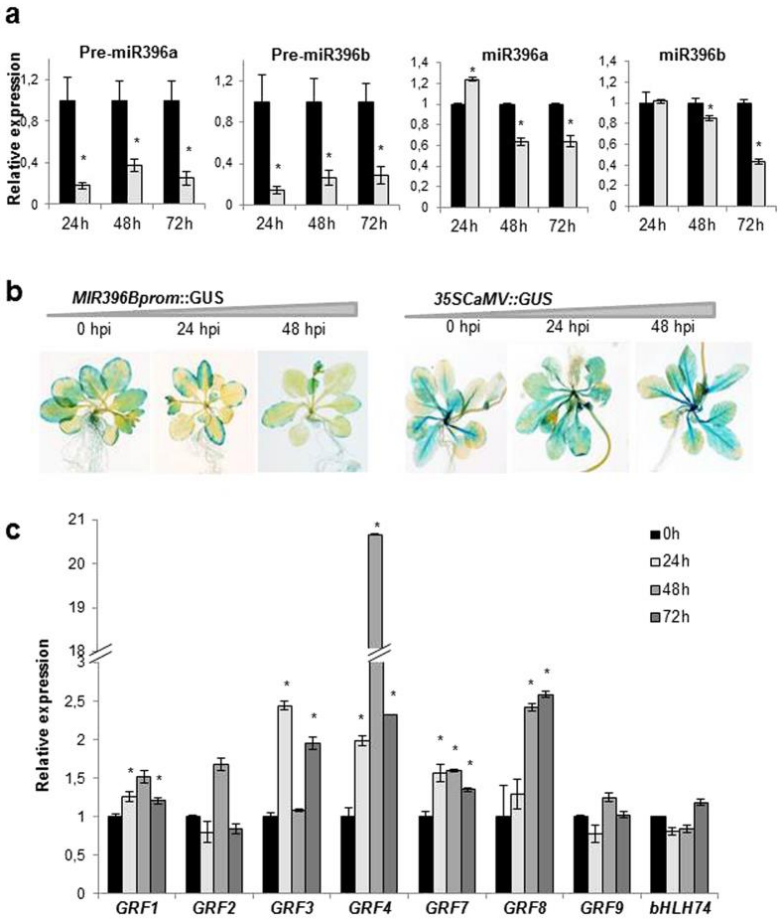
- ✓ APO and AMPO inhibit HDAC, impair H3 acetylation, deregulate gene expression and result in growth defects

(Venturelli et al., Plant Cell 2015)

The *Arabidopsis* miR396 mediates pathogen-associated molecular pattern-triggered immune responses against fungal pathogens



✓ Impairment of miR396 activity enhances resistance to infection by fungal pathogens with different lifestyles



✓ Fungal infection leads to transcriptional repression of miR386, and subsequent increased expression of its targets

(Soto-Suarez et al., Sci Rep 2017)

Many other examples

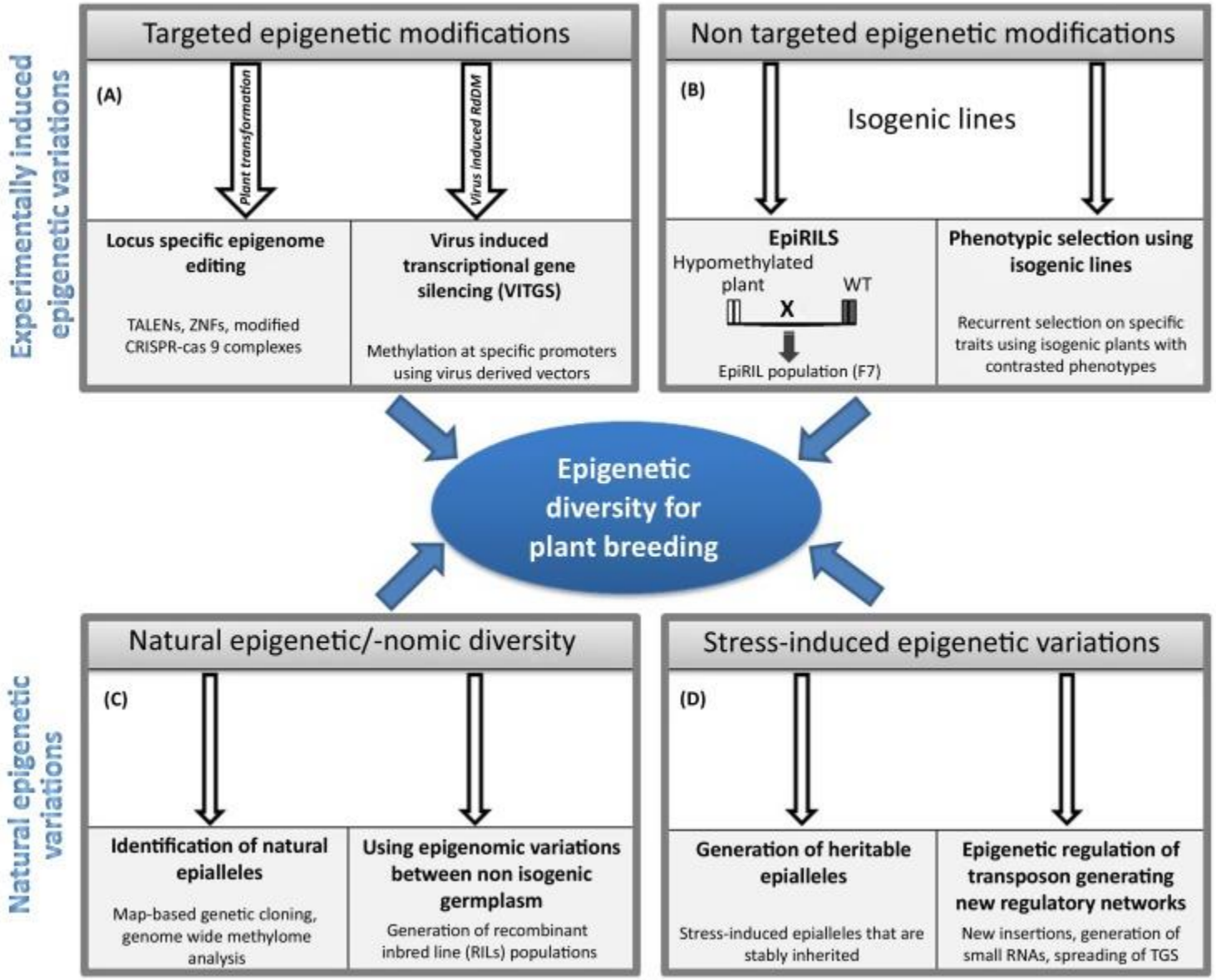
- ✓ Histone H3K9 and H3K27 methylation regulates fungal alkaloid biosynthesis in a fungal endophyte-plant symbiosis
- ✓ Chromatin assembly factor CAF-1 represses priming of plant defence response genes
- ✓ The role of DNA (de)methylation in immune responsiveness of *Arabidopsis*
- ✓ Regulation of disease-responsive genes mediated by epigenetic factors: Interaction of *Arabidopsis-Pseudomonas*
- ✓ Autoimmunity in *Arabidopsis acd11* Is Mediated by Epigenetic Regulation of an Immune Receptor
- ✓ Regulation of Transcription of Nucleotide-Binding Leucine-Rich Repeat-Encoding Genes SNC1 and RPP4 via H3K4 Trimethylation
- ✓ Functional analysis of a Wheat Homeodomain protein, TaR1, reveals that host chromatin remodelling influences the dynamics of the switch to necrotrophic growth in the phytopathogenic fungus *Zymoseptoria tritici*
- ✓ Monoubiquitination of histone 2B at the disease resistance gene locus regulates its expression and impacts immune responses in *Arabidopsis*

Epigenetic modifications play a role in plant biotic interactions

So what?

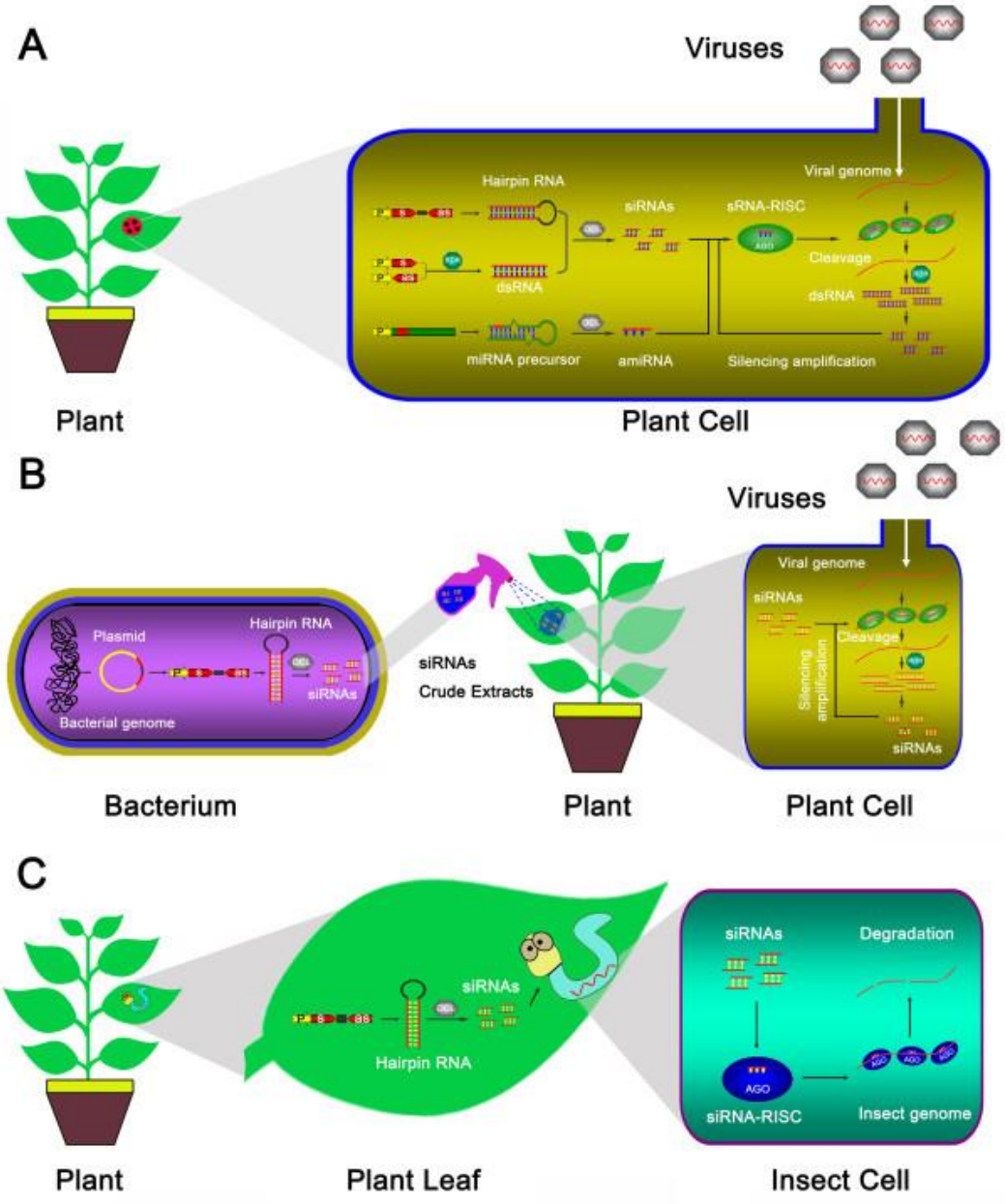
How to use epigenetics in plant breeding?

Epigenetics for Plant Improvement: Current Knowledge and Modeling Avenues



(Gallusci et al., Trends Plant Sci 2017)

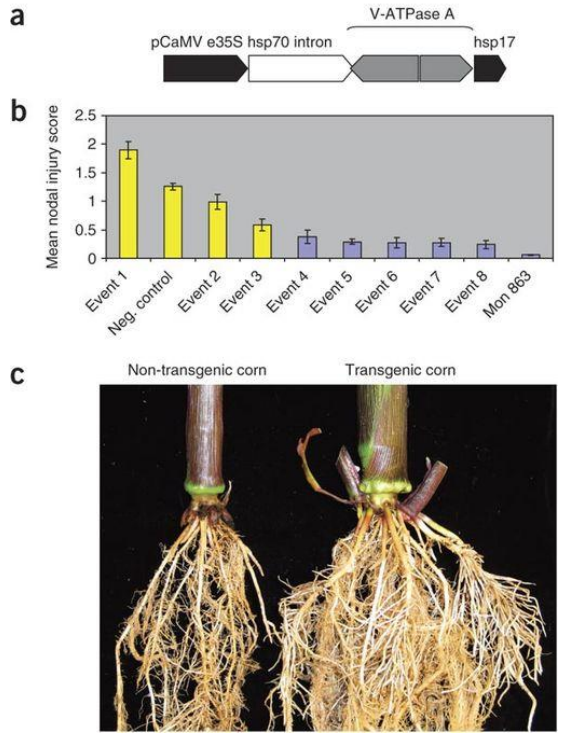
Application of RNA silencing to plant disease resistance



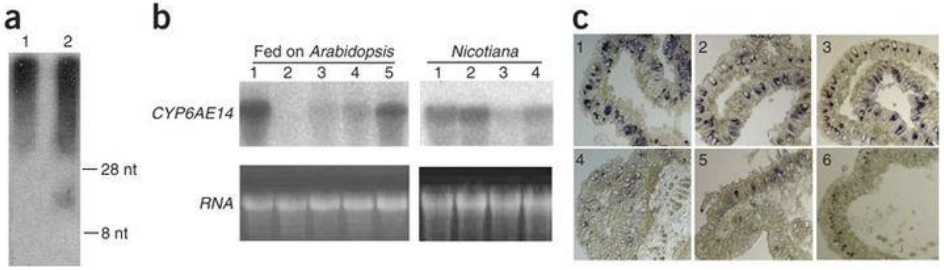
- ✓ Expression of viral small RNA in host plants triggers antiviral silencing
- ✓ Sprayed bacterium-processed siRNAs confers resistance against virus
- ✓ Feeding on transgenic plants that carry RNAi constructs confers resistance against insect

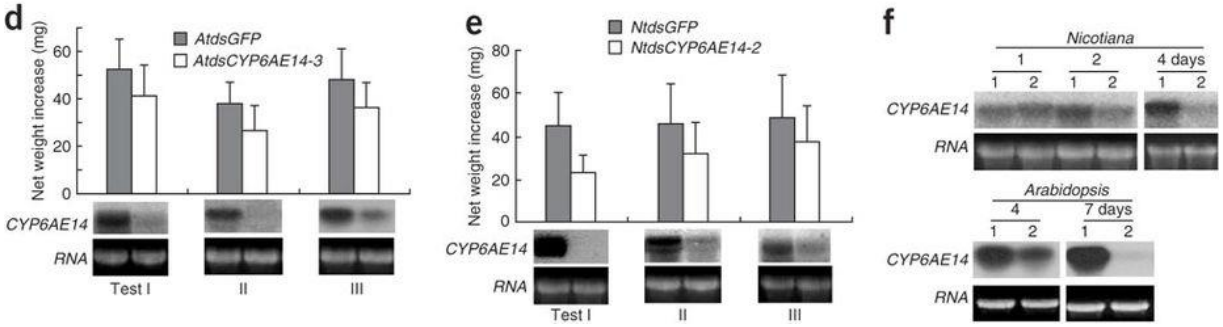
(Duan et al., Silence 2012)

RNAi for insect-proof plants



✓ **Transgenic corn plants engineered to express western corn rootworm dsRNAs targeting putative genes encoding vacuolar ATPase (V-ATPase) subunits show a significant reduction in WCR feeding damage**

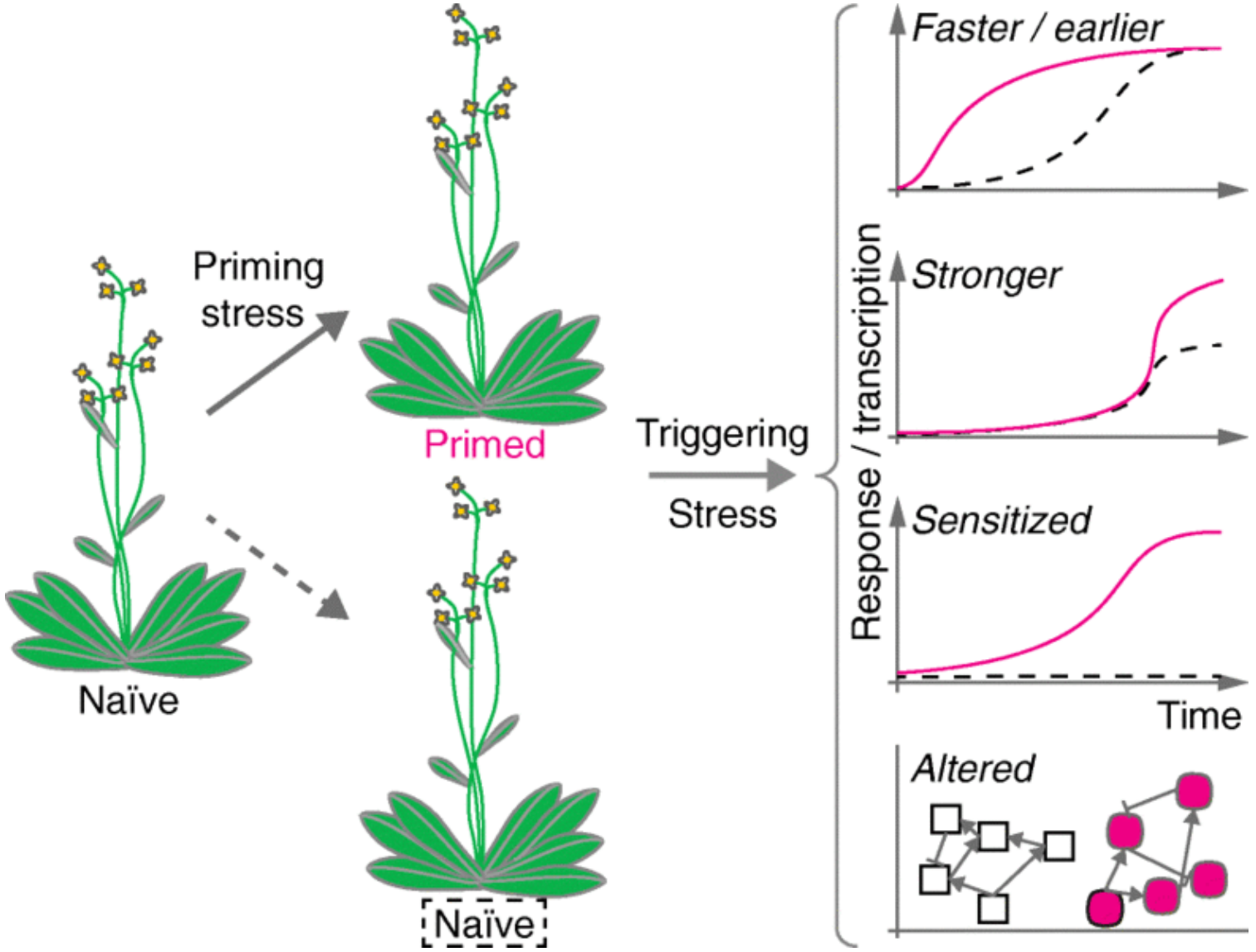




✓ **Silencing a cotton bollworm P450 monooxygenase gene by plant-mediated RNAi impairs larval tolerance to gossypol**

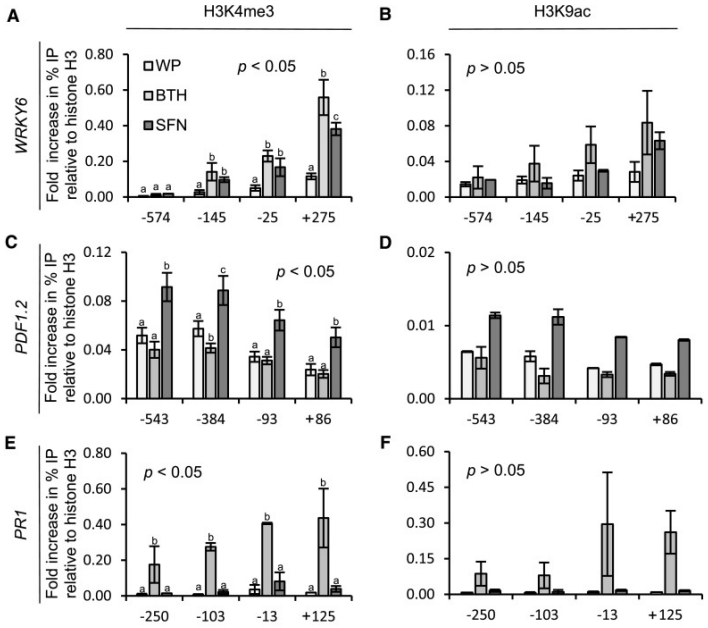
(Baum et al., Nature Biotech 2007; Mao et al., Nature Biotech 2007)

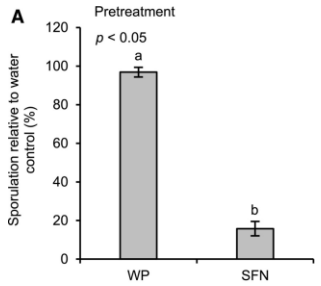
Epigenetic and chromatin-based mechanisms in environmental stress adaptation and stress memory in plants

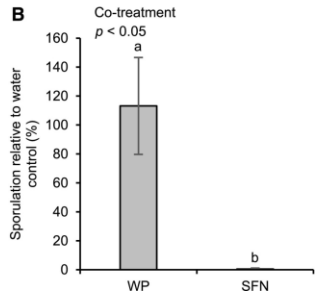


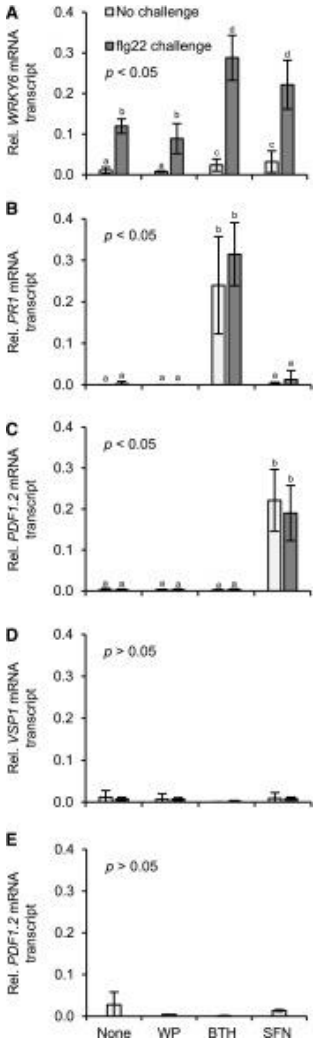
(Lämke and Bäurle, Genome Biol 2017)

Sulforaphane Modifies Histone H3, Unpacks Chromatin, and Primes Defense





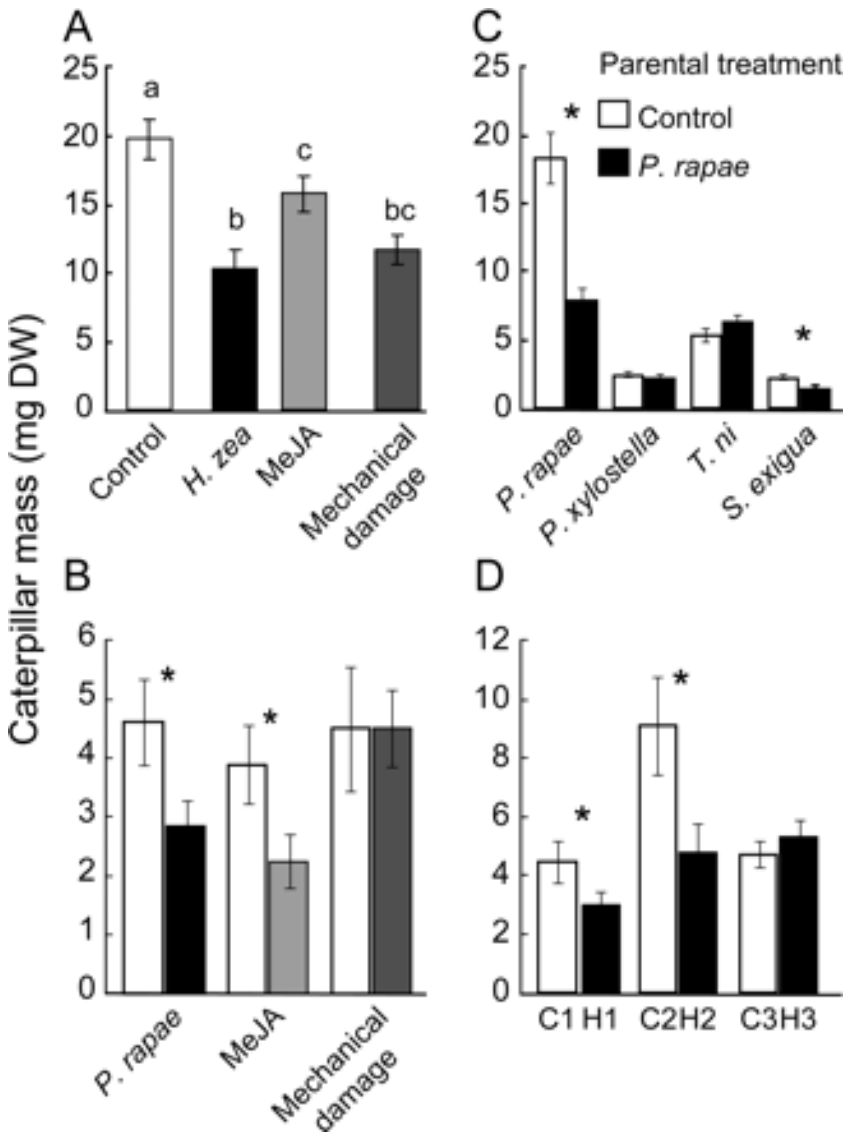




- ✓ SFN induces histone H3 modifications in some defense-related genes (top left panel)
- ✓ SFN stimulates ET signaling (right panel)
- ✓ SFN directly inhibits *H. arabidopsidis* and other plant pathogens (bottom left panel)

(Schillheim et al., Plant Physiol 2017)

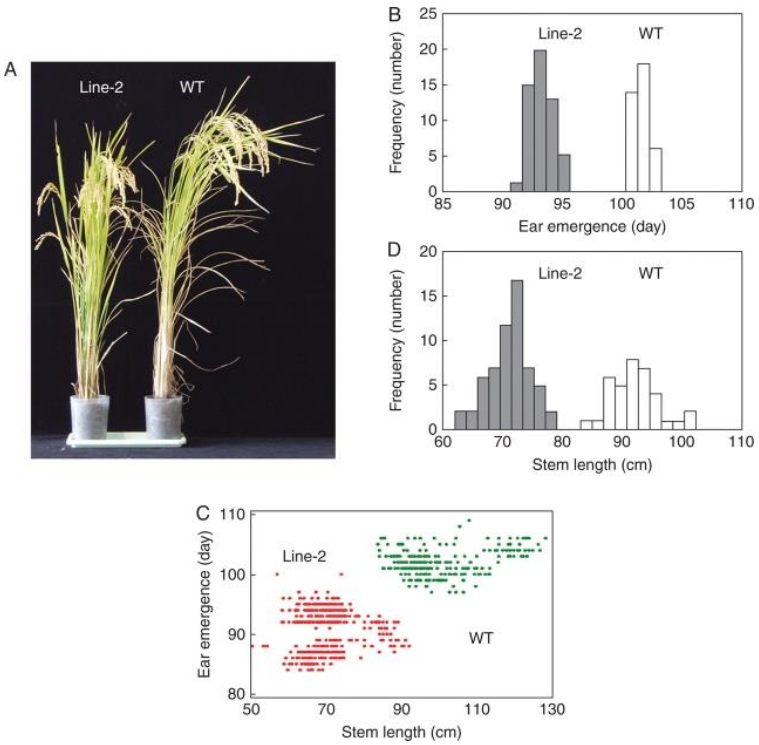
Herbivory in the Previous Generation Primes Plants for Enhanced Insect Resistance



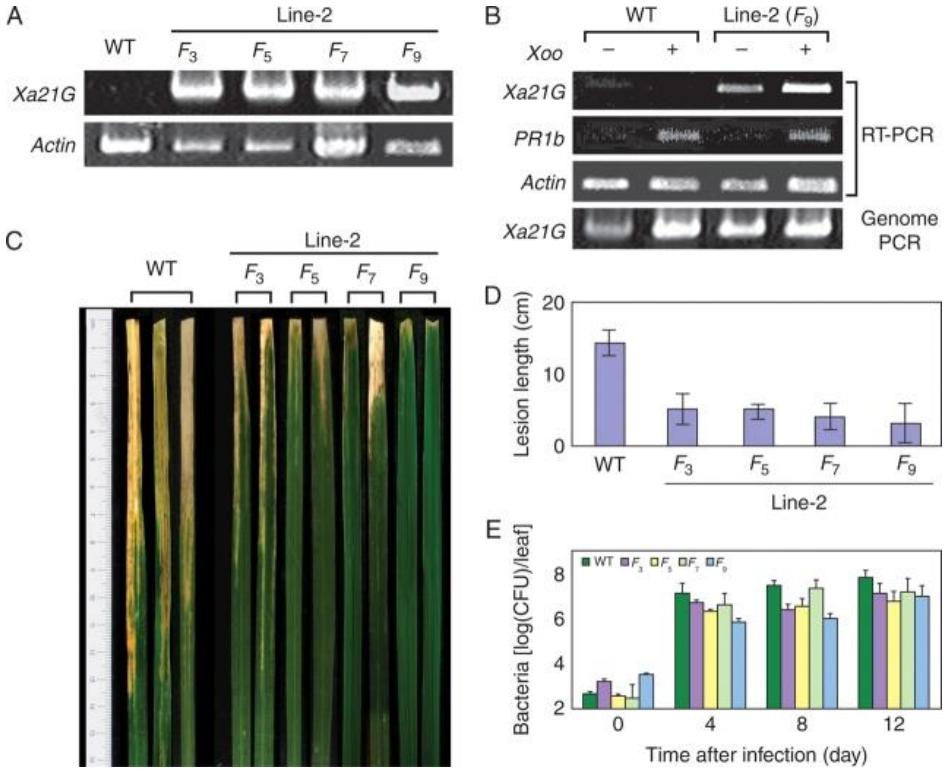
- ✓ Caterpillar feeding, MeJA exposure, and/or mechanical damage decreased the growth of herbivory on progeny of treated tomato and *Arabidopsis* plants (A, B)
- ✓ The transgenerational resistance is specific to the lepidopteran herbivore (C)
- ✓ Transgenerational resistance to *P. rapae* persisted in the H2 generation but not in the H3 generation (D)
- ✓ *Arabidopsis* mutants that are deficient in the biogenesis of small interfering RNA do not exhibit inherited resistance (not shown)

(Rasmann et al., Plant Physiol 2012)

Epigenetic Inheritance in Rice Plants



- ✓ azadC-treated hypomethylated rice plants display a wide range of phenotypic changes



- ✓ One line acquired resistance to *X. oryzae* pv. *oryzae* due to the deregulation of the *Xa21* gene.

(Akimoto et al., Ann Bot 2007)