



Botanical Garden Zürich

Epigenetic Gene Regulation: Genomic Imprinting in Plants

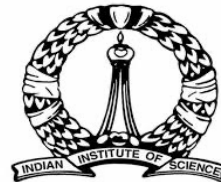
Ueli Grossniklaus



Universität
Zürich ^{UZH}






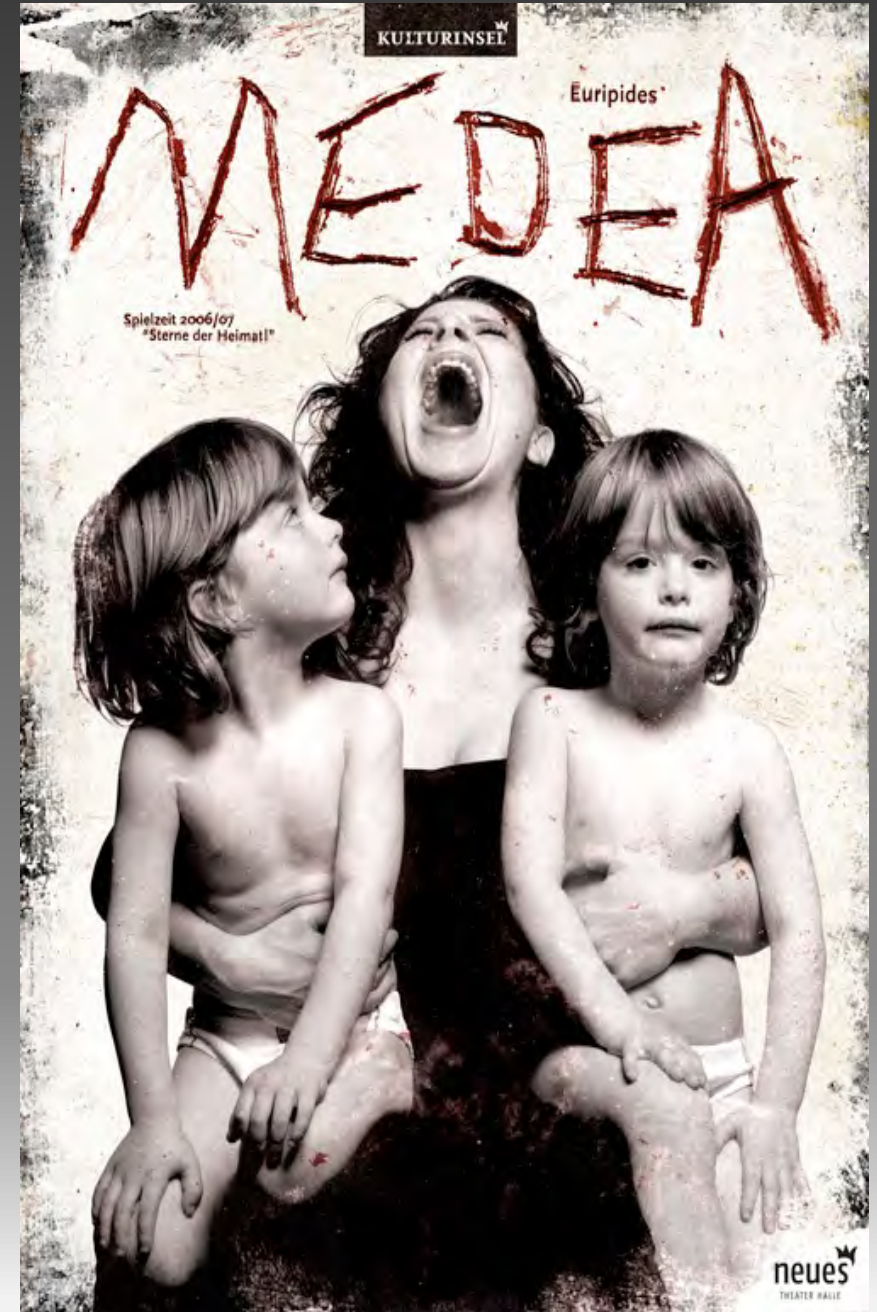
Zurich – Basel
Plant Science Center



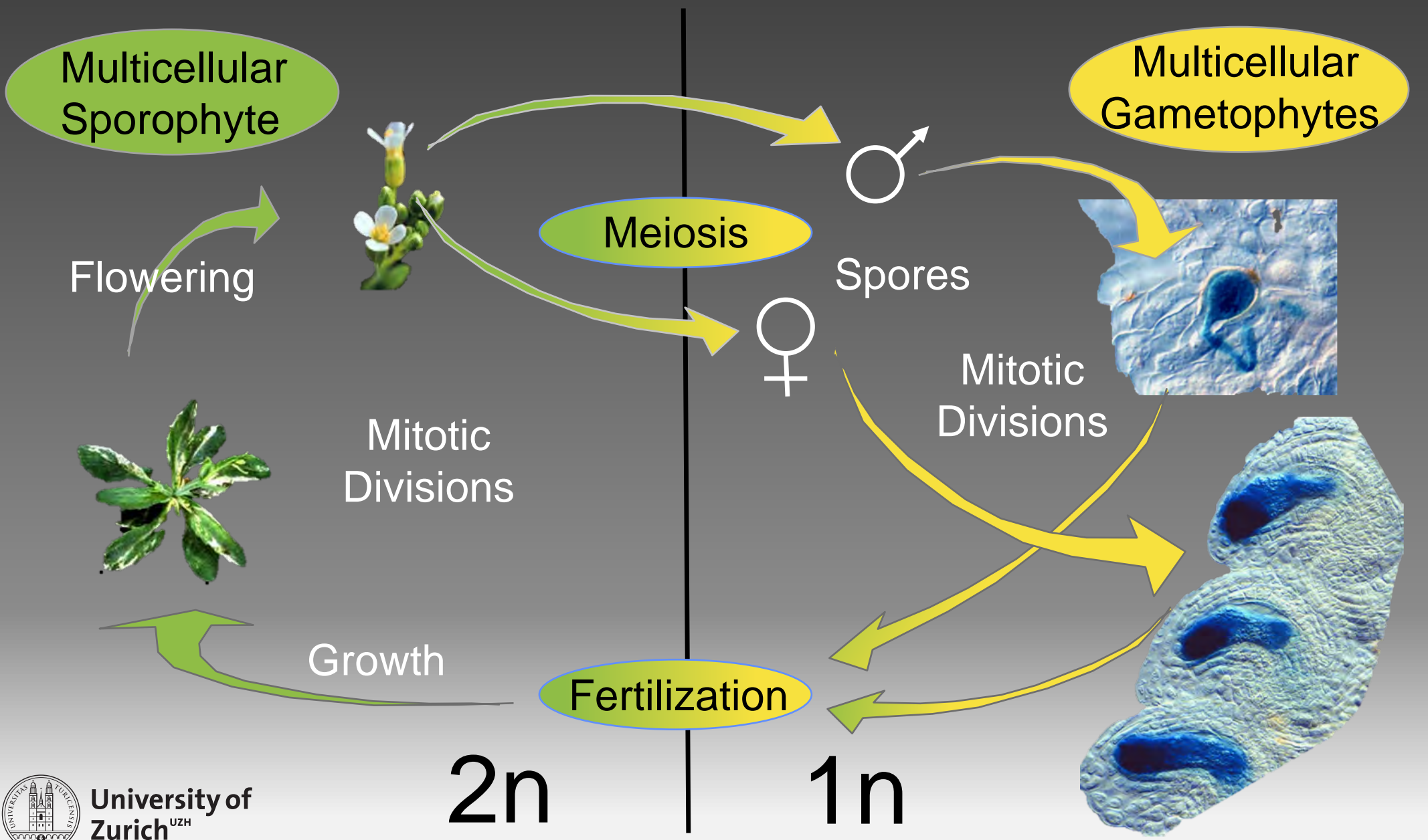
Molecular Diagnostics 2024, Zurich, March 7th to 8th, 2024

Overview

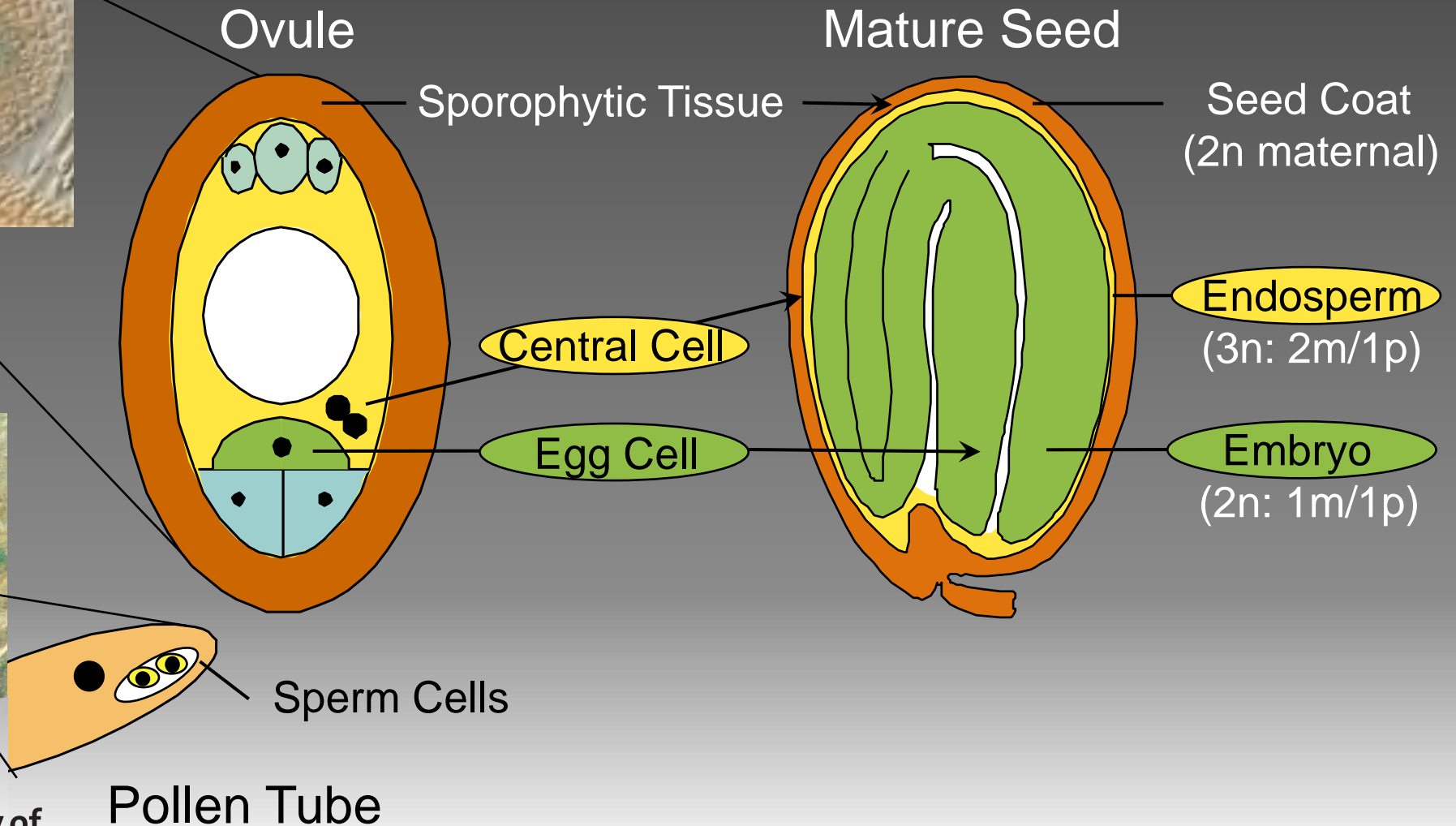
-  Introduction to plant reproduction and genomic imprinting
-  Evolution of genomic imprinting
-  Molecular mechanisms of genomic imprinting



Alternation of Generations



Double Fertilization and Seed Development



Double Fertilization and Seed Development



Ovule

Sporophytic Tissue

Mature Seed

Seed Coat
(2n maternal)

Central Cell

Endosperm
(3n: 2m/1p)

Egg Cell

Embryo
(2n: 1m/1p)

Sperm Cells



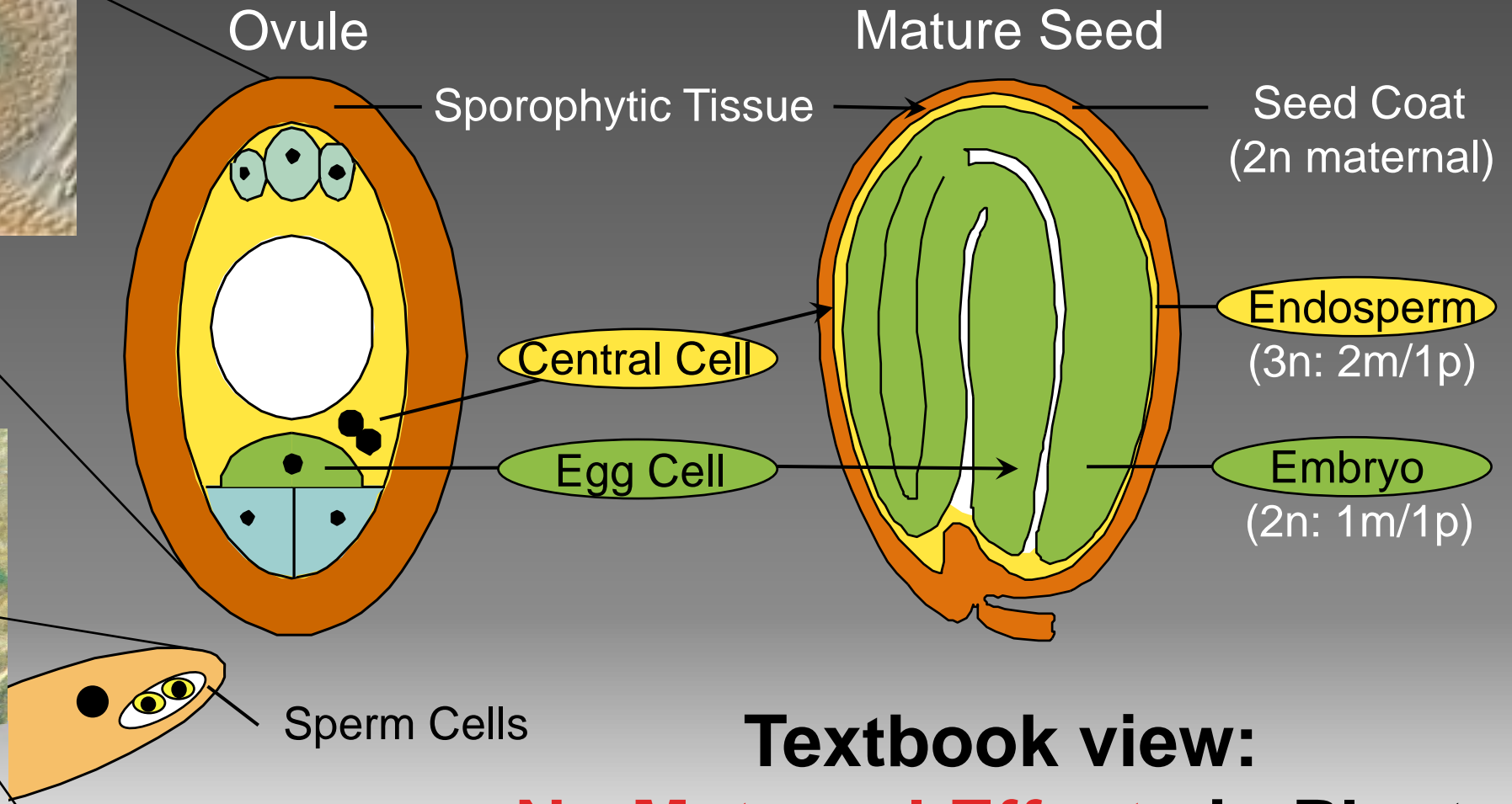
Sporophytic Maternal Effects



Gametophytic Maternal Effects

Pollen Tube

Double Fertilization and Seed Development



Textbook view:

No Maternal Effects in Plants

The *medea* Mutation Causes Parent-of-Origin-Dependent Seed Abortion

mea/MEA x wt

wt x *mea/MEA*



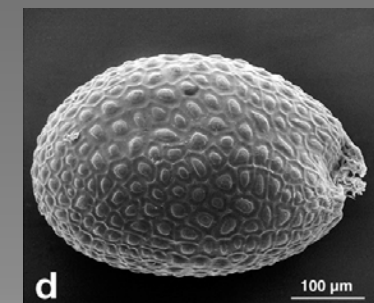
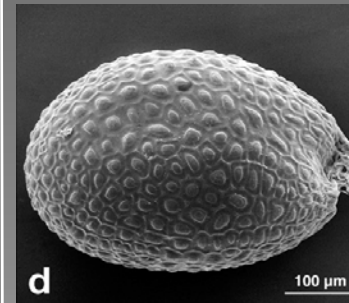
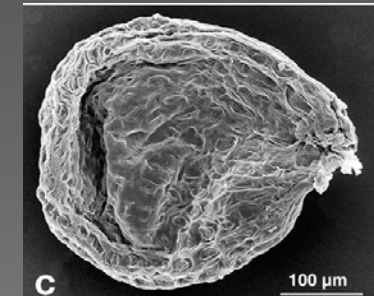
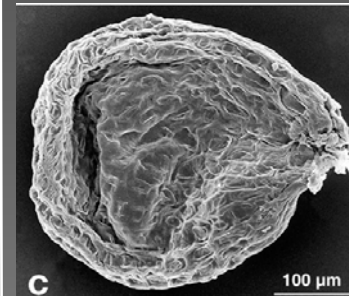
paternal

mea^p

MEA^p

maternal
mea^m

MEA^m



seeds from *mea* embryo sacs abort irrespective of paternal contribution



The *medea* Mutation Causes Parent-of-Origin-Dependent Seed Abortion

mea/MEA x wt

wt x *mea/MEA*



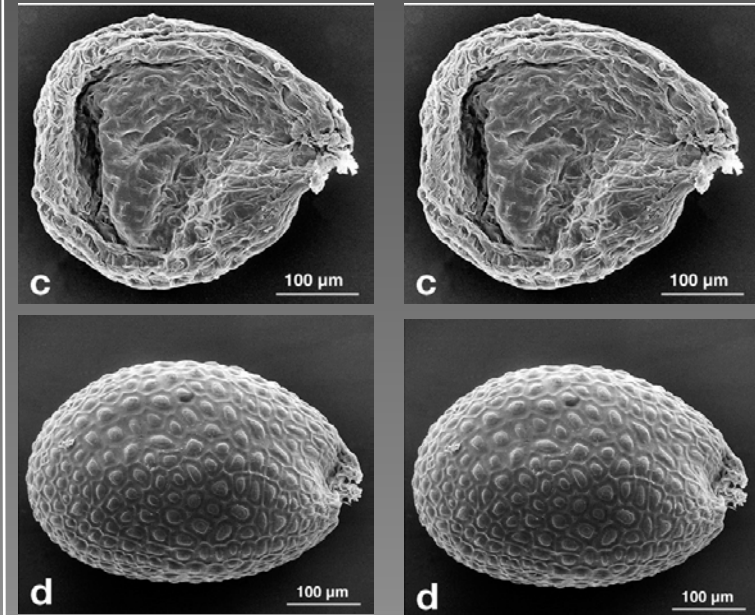
paternal

mea^p

MEA^p

maternal
mea^m

MEA^m



seeds from *mea* embryo sacs abort
irrespective of paternal contribution



University of
Zurich^{UZH}

Genomic Imprinting at the *R1* Locus in Maize



$R^m/R^m/r^p$



$r^m/r^m/R^p$



Jerry L. Kermicle

Genomic Imprinting at the *R1* Locus in Maize



$R^m/R^m/r^p$



$r^m/r^m/R^p$



caused by a dosage effect,
not a maternal factor



maternal effect of '**extra-chromosomal**' nature, i.e.,
cytoplasmically stored factors
like proteins, mRNA, sRNAs,
metabolites, organelles



'**chromosomally based**'
maternal effect (genomic
imprinting)



Jerry L. Kermicle

Genomic Imprinting at the *R1* Locus in Maize



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‘**chromosomally based**’
maternal effect (genomic
imprinting):

DEPENDENCE OF THE *R*-MOTTLED ALEURONE PHENOTYPE IN
MAIZE ON MODE OF SEXUAL TRANSMISSION¹

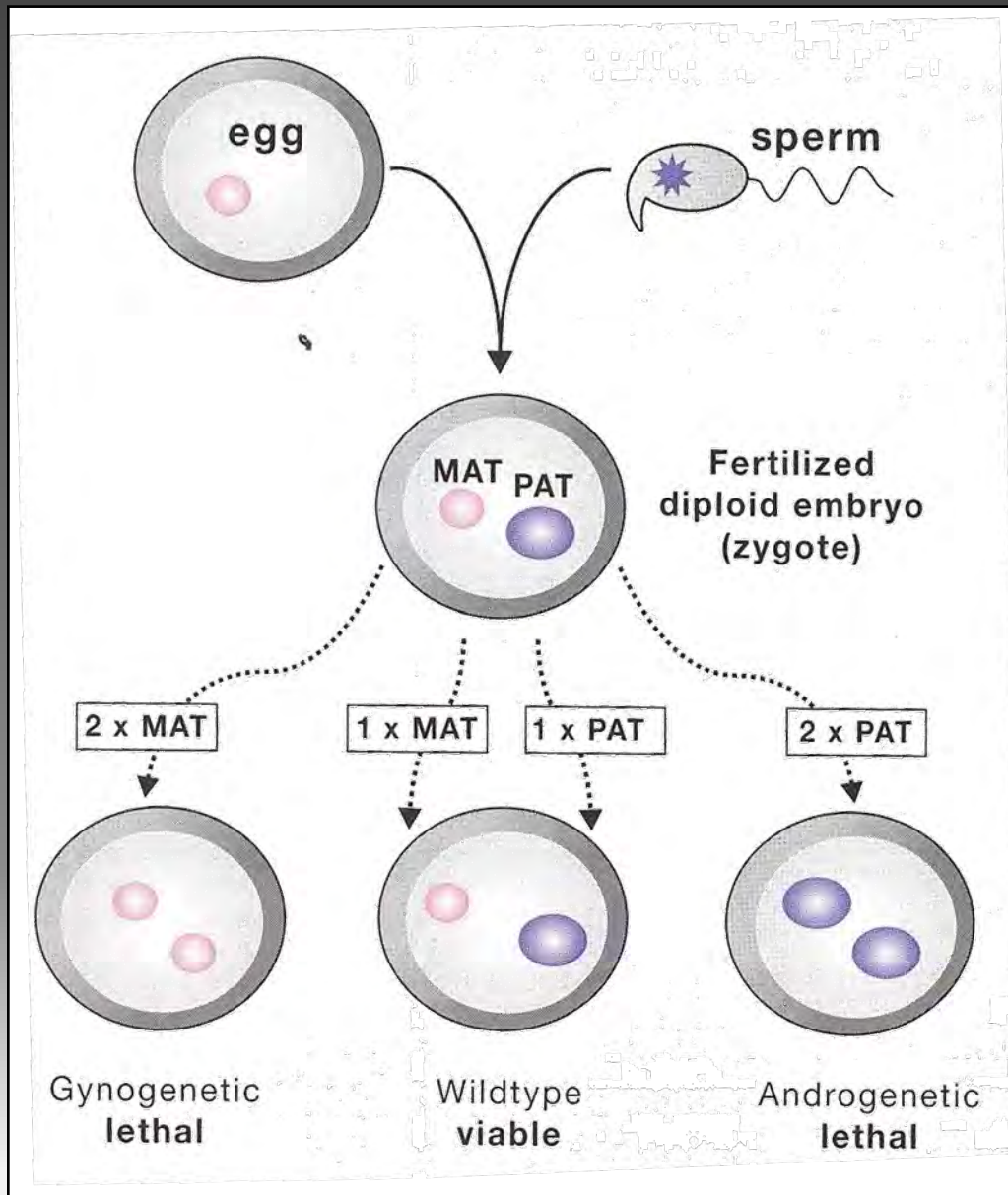
J. L. KERMICLE

Laboratory of Genetics, University of Wisconsin, Madison 53706

Received April 13, 1970

“ ... that the **differential expression of *R* according to sexual origin** is chromosomal.”

Genomic Imprinting at the *R1* Locus in Maize



Azim Surani

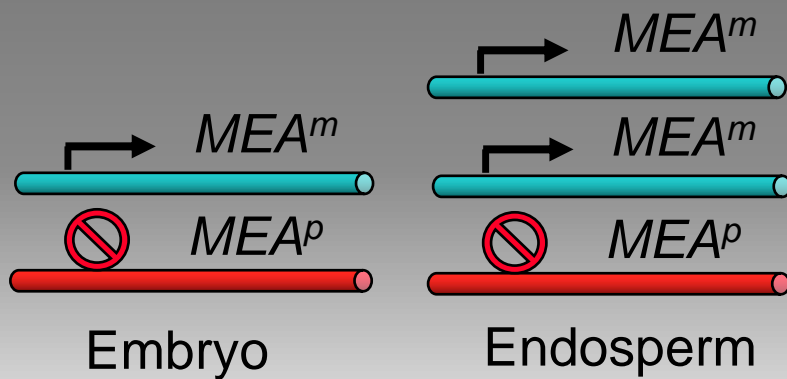
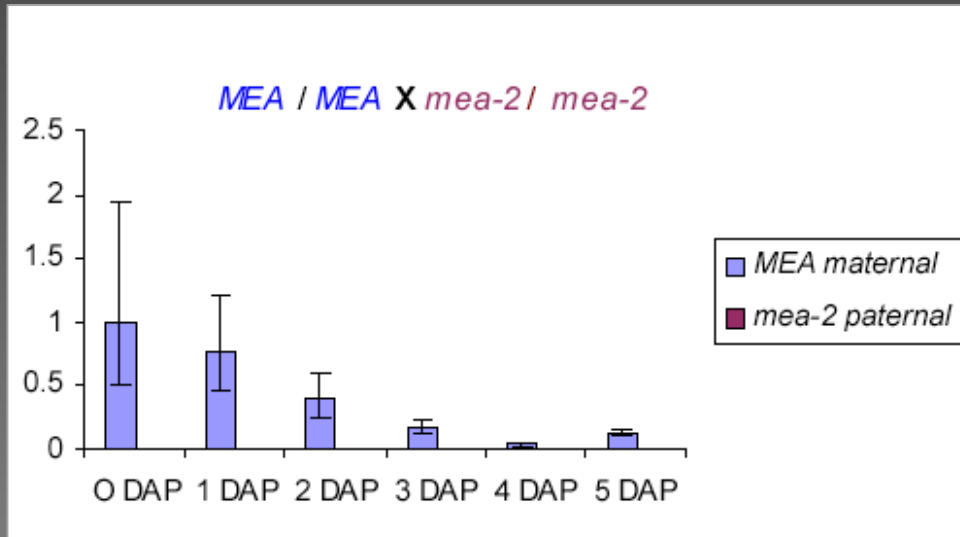


Davor Solter

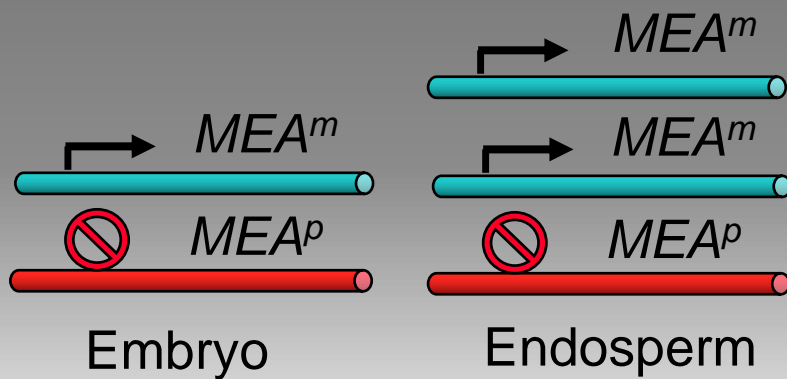
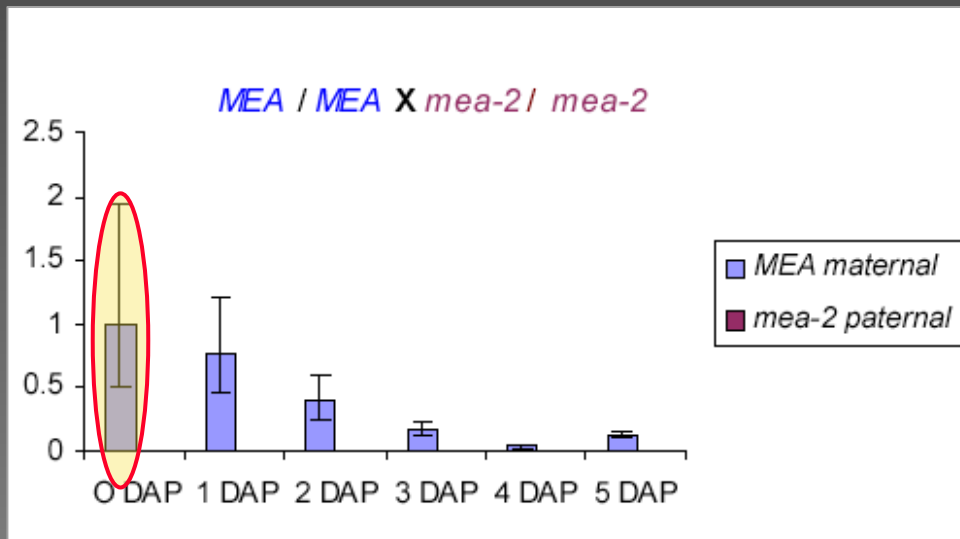
In 1984, imprinting was discovered in mice and studied extensively at the mechanistic level

McGrath & Solter (1984) *Cell* **37**, 170
Surani et al. (1984) *Nature* **308**, 548

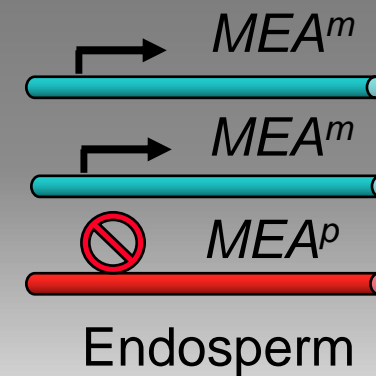
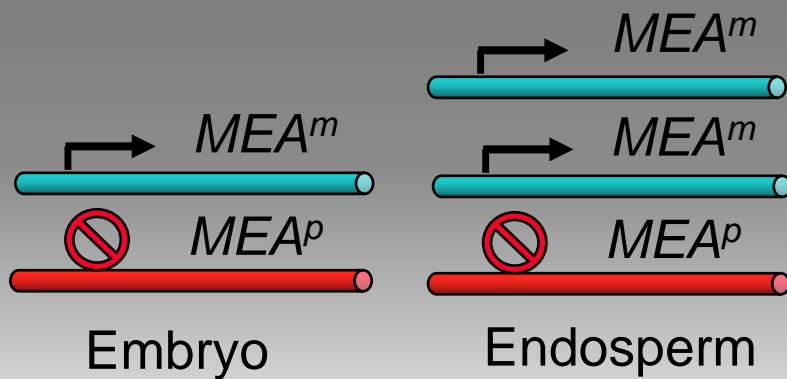
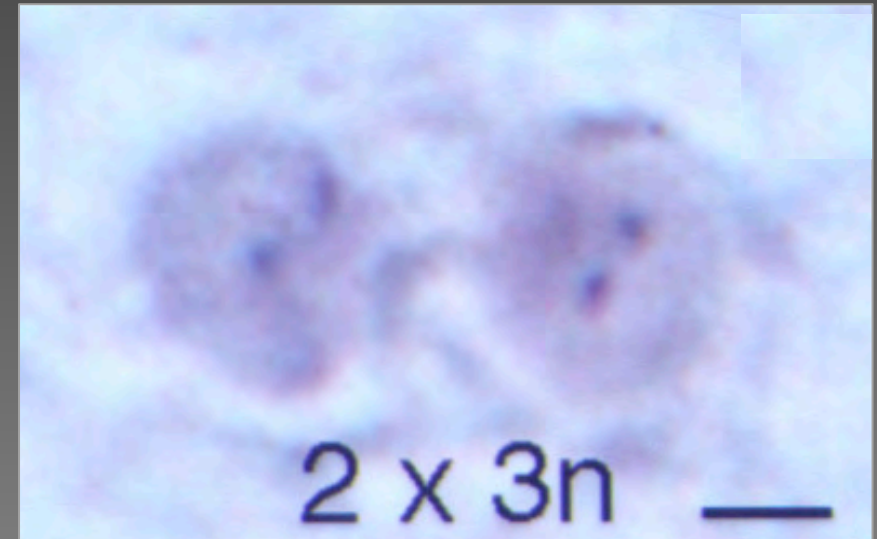
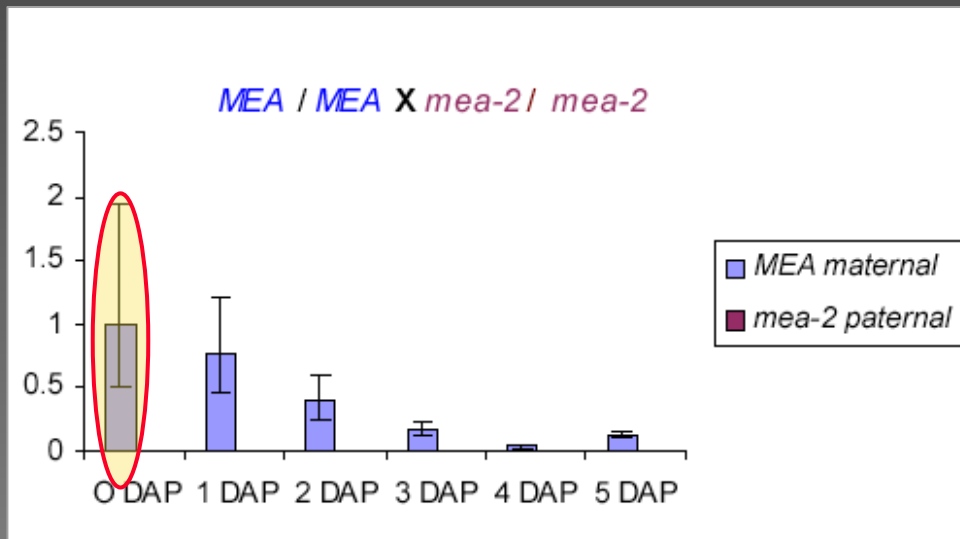
The *MEDEA* Locus Is Regulated by Genomic Imprinting



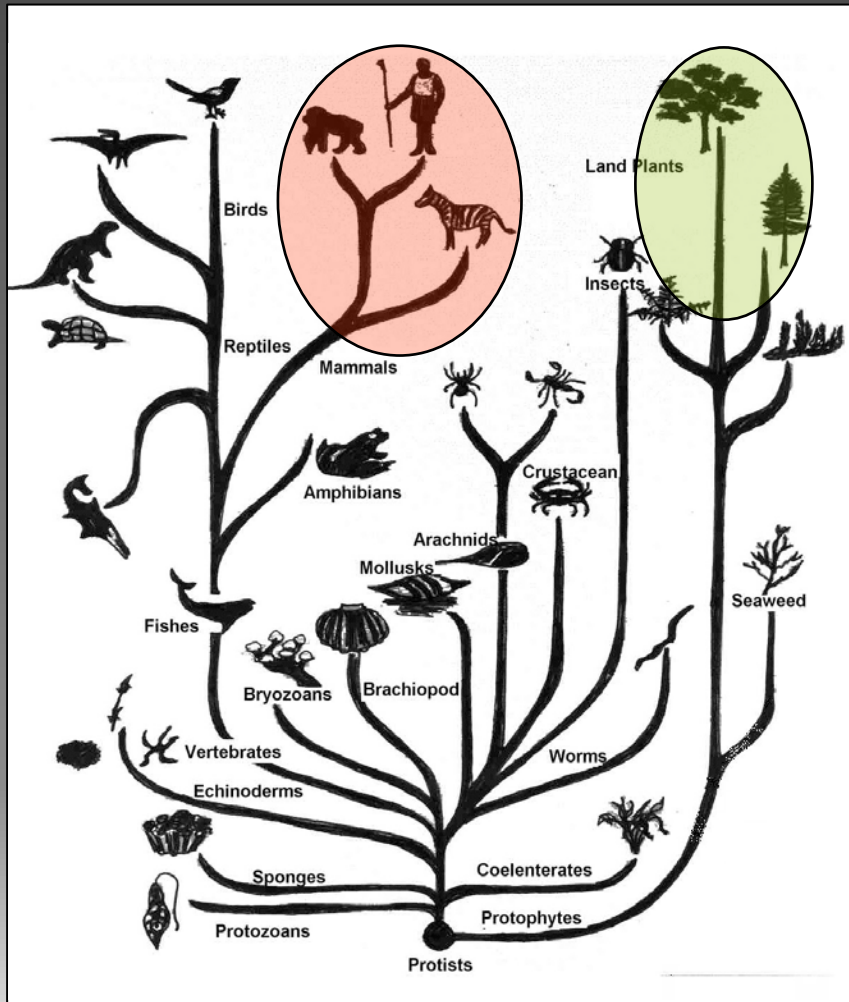
The *MEDEA* Locus Is Regulated by Genomic Imprinting



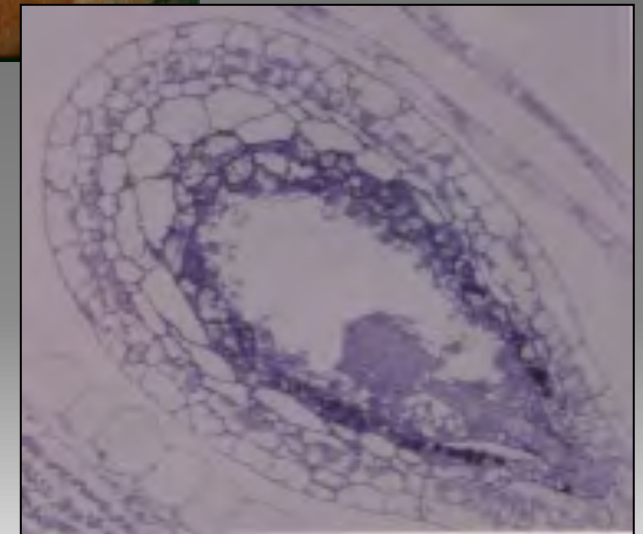
The *MEDEA* Locus Is Regulated by Genomic Imprinting



Mammals and Seed Plants Share a Placental Habit



The mother provides all nutrients for embryo or seed development



Parental Conflict Theory for the Evolution of Imprinting



David A. Haig



Hypothesis:

In polygamous organisms with a **placental habit** imprinting evolved as a consequence of a **conflict between maternal and paternal interests** over the allocation of nutrients from mother to offspring



Predictions:

- **Paternal expression** should tend to **increase offspring size**
- **Maternal expression** is expected to **restrict growth** of the embryo or seed



The *medea* Phenotype Is Consistent with the Parental Conflict Theory

MEA: maternally expressed
mutant: embryonic overgrowth

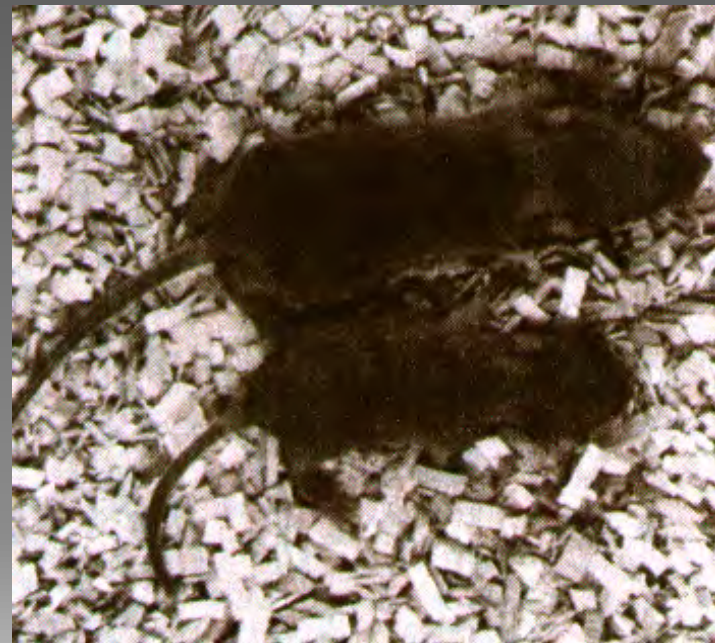
IGF-II: paternally expressed
mutant: small (40% less weight)



wild-type



mea^m/*MEA*^p



+/+

+/-

IGF-II^m/*Igf-II*^p

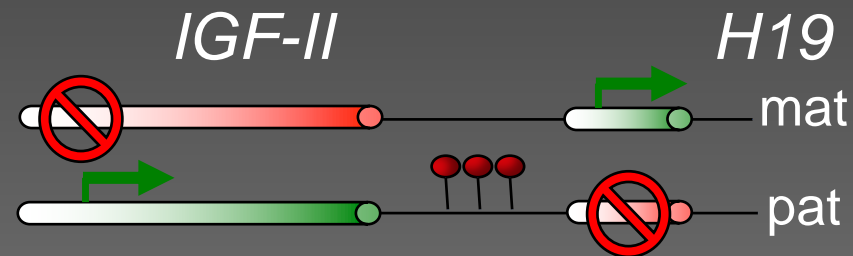


In Beckwith-Wiedemann (BWS) and Russell-Silver Syndromes (RSS) Imprinting Is Affected

BWS



5-10%

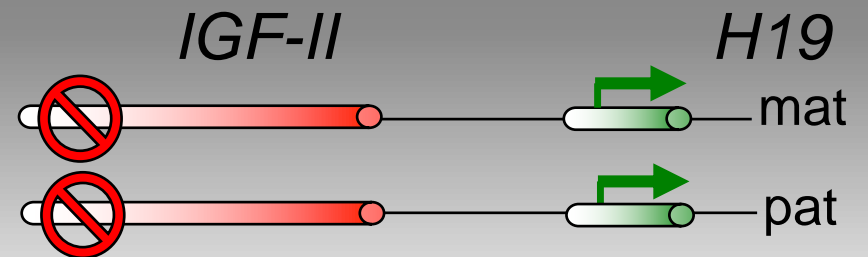
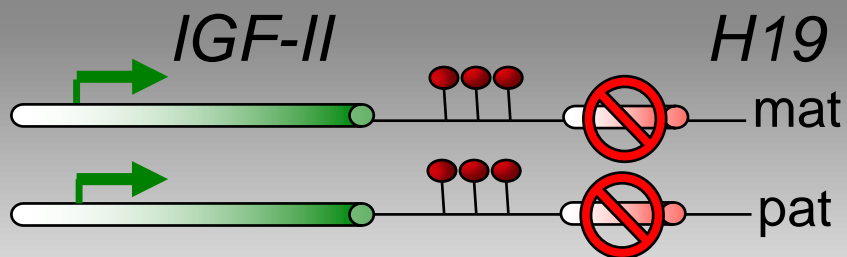


Chromosome 11p15.5

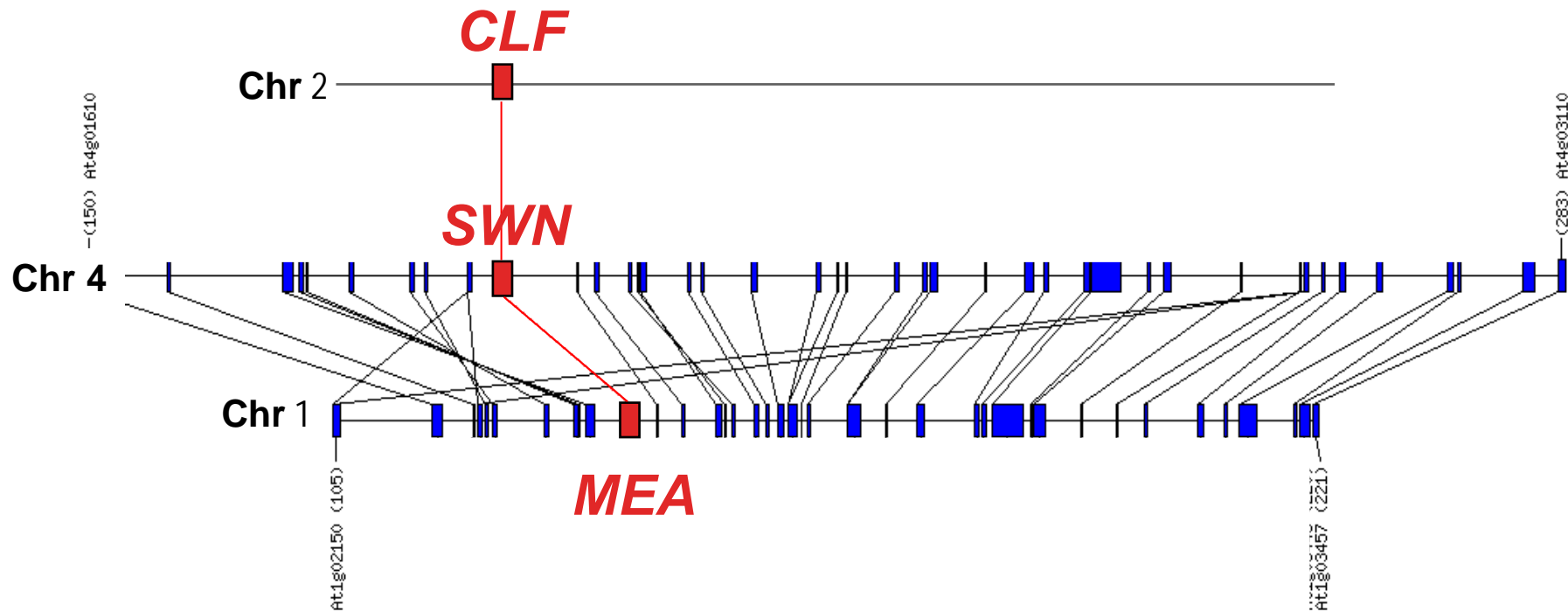
RSS



37-63%



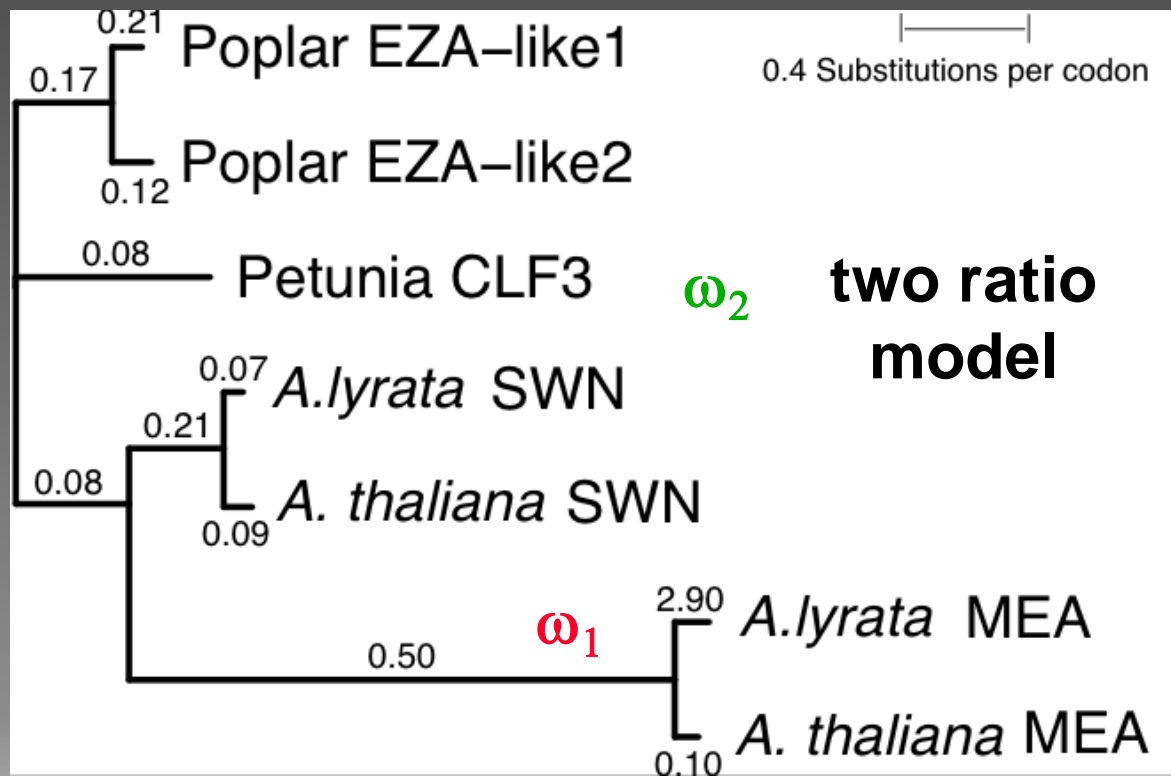
MEDEA Is A Paralog of *SWINGER* (*SWN*) that Arose 35-85 mya



Arabidopsis MEA & *SWN* are paralogs that arose by an ancestral segmental duplication which occurred ~35-85 Mya (Blanc *et al.* (2003) *Genome Res* 13, 137)



Branch Models (PAML) Provide Support for Positive Darwinian Selection at *MEDEA*



Tree topology was obtained with protml, and branch lengths were calculated with codeml using Model M0. The numbers above branches indicate ω -ratios, which were calculated with the free-ratio model.



MEA evolved more rapidly than SWN in the branch before *A. lyrata* and *A. thaliana* split



This could be due to neofunctionalization and/or genomic conflict



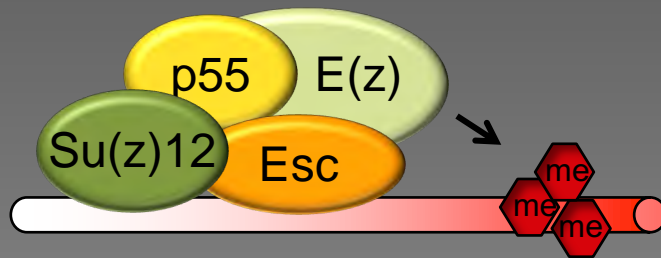
Within *A. thaliana*, SWN and *MEA* evolve similarly



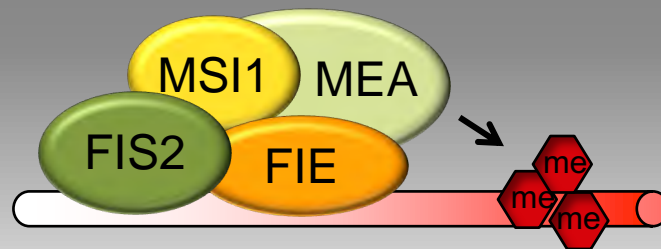
MEDEA Encodes the Methyltransferase of Plant *Polycomb* Repressive Complex 2 (PRC2)

PRC2 silences its target genes
by H3K27me₃

Drosophila PRC2



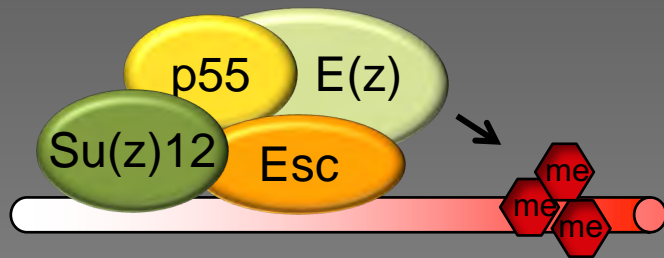
Arabidopsis FIS-PRC2



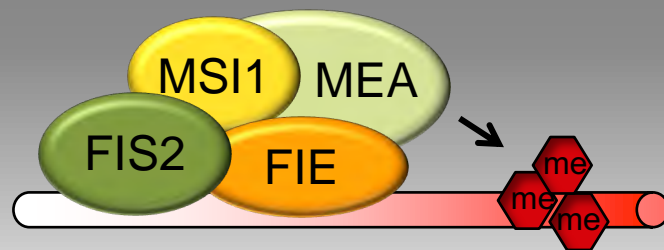
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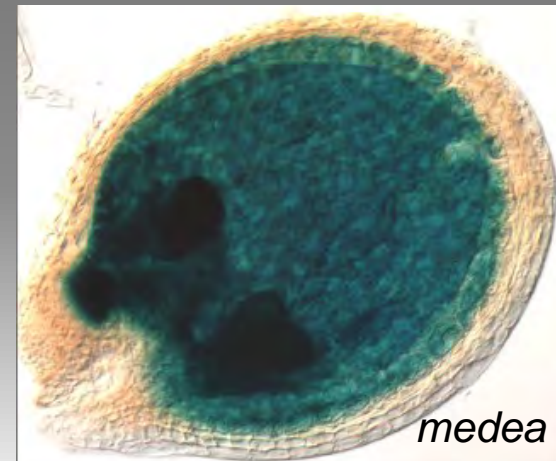
Drosophila PRC2



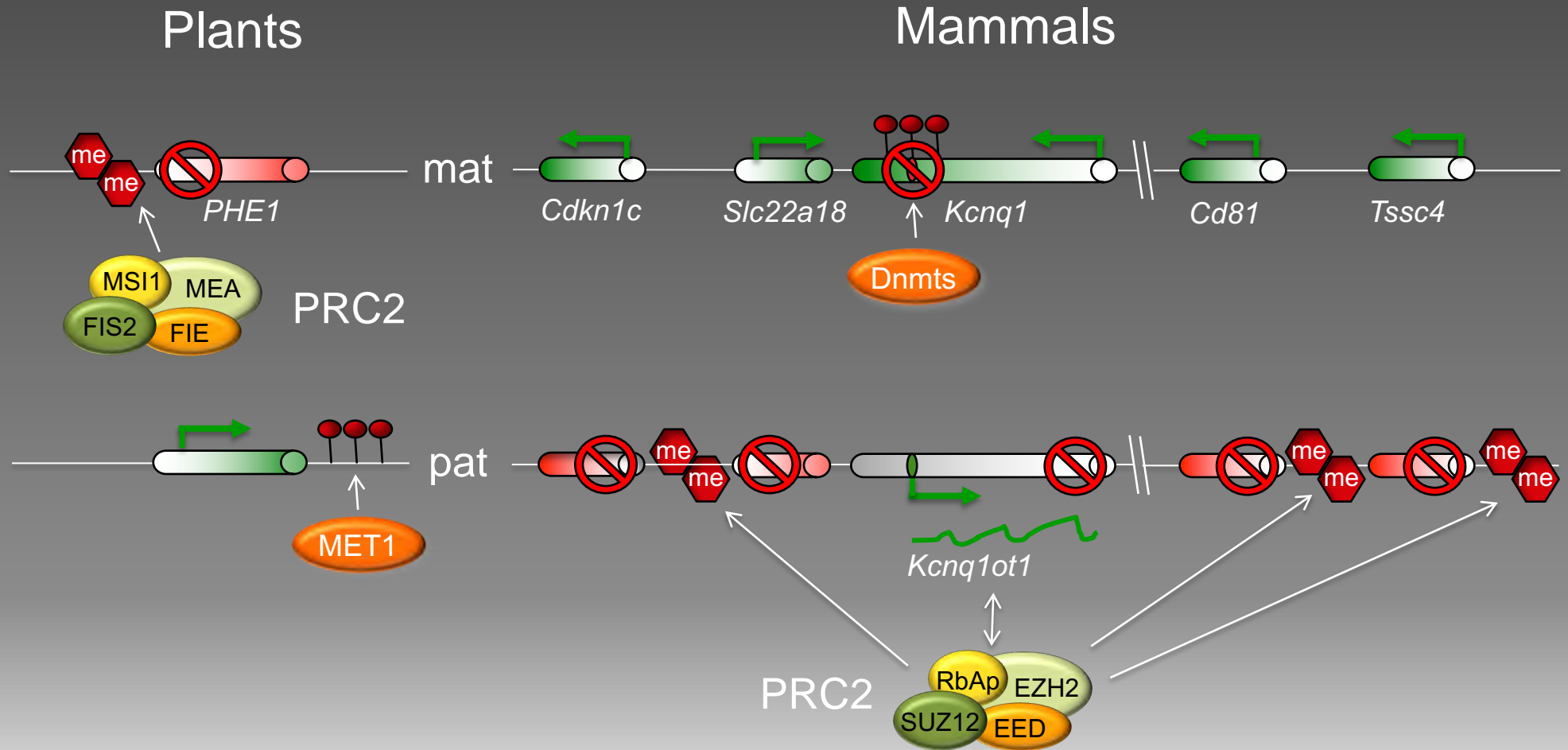
Arabidopsis FIS-PRC2



PHERES1 is a MEA target

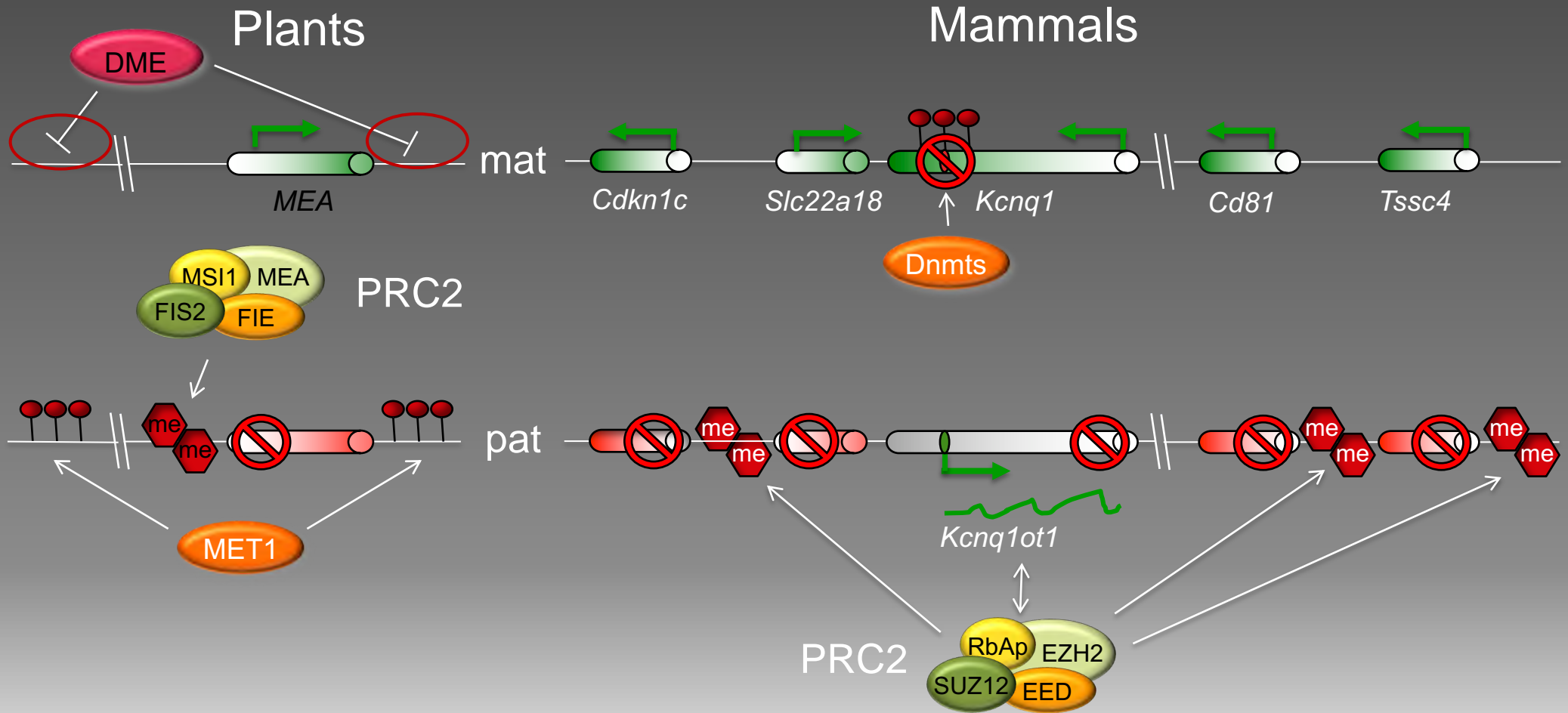


DNA Methylation and PRC2 Contribute to Imprinting in Mammals and Plants



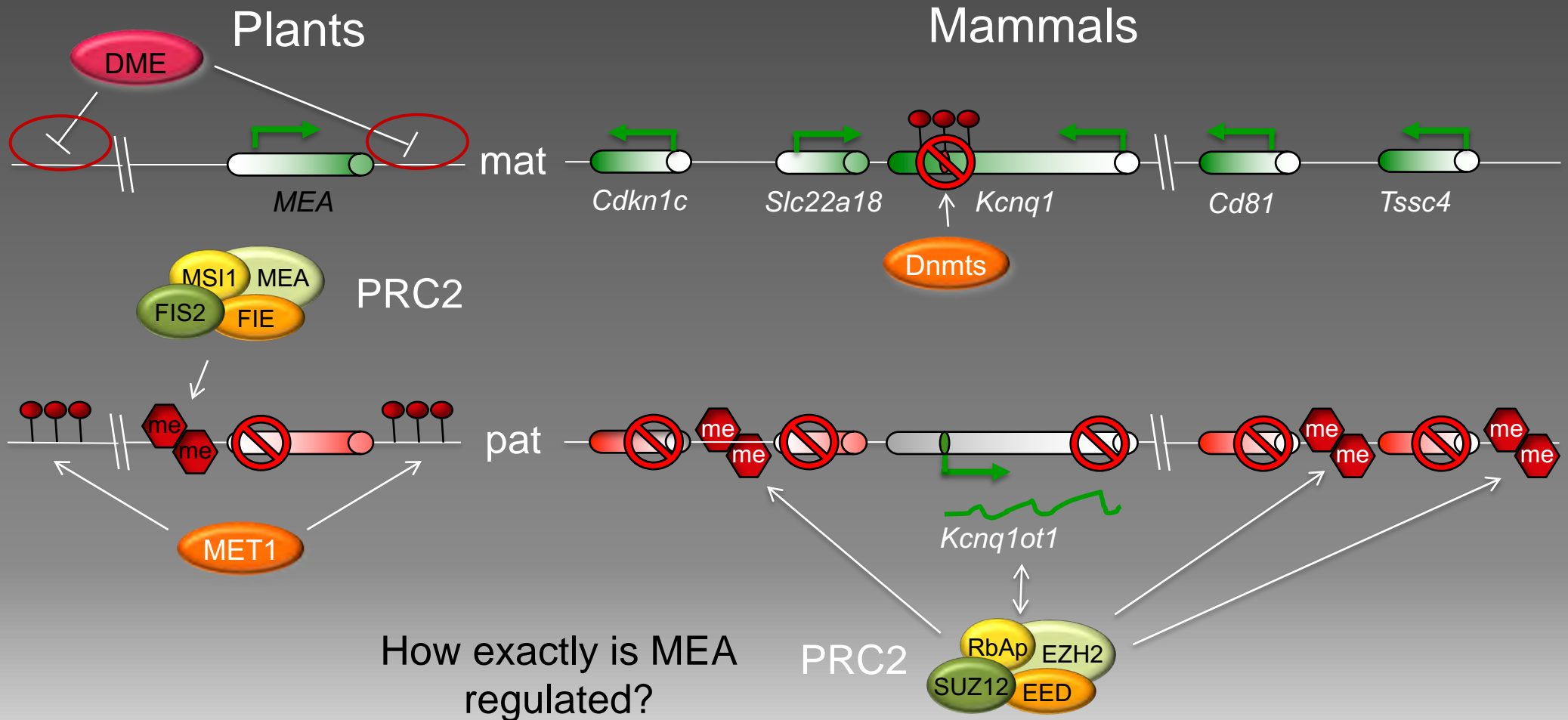
Köhler *et al. Genes Dev* (2003), Köhler *et al. Nat Genet* (2005), Makarevich *et al. J Cell Sci* (2008), Gehring *et al. Cell* (2006) Jullien *et al. Curr Biol* (2006); Baroux *et al. Genes Dev* (2006); Umlauf *et al. Nat Genet* (2004), Terranova *et al. Dev Cell* (2008)

DNA Methylation and PRC2 Contribute to Imprinting in Mammals and Plants



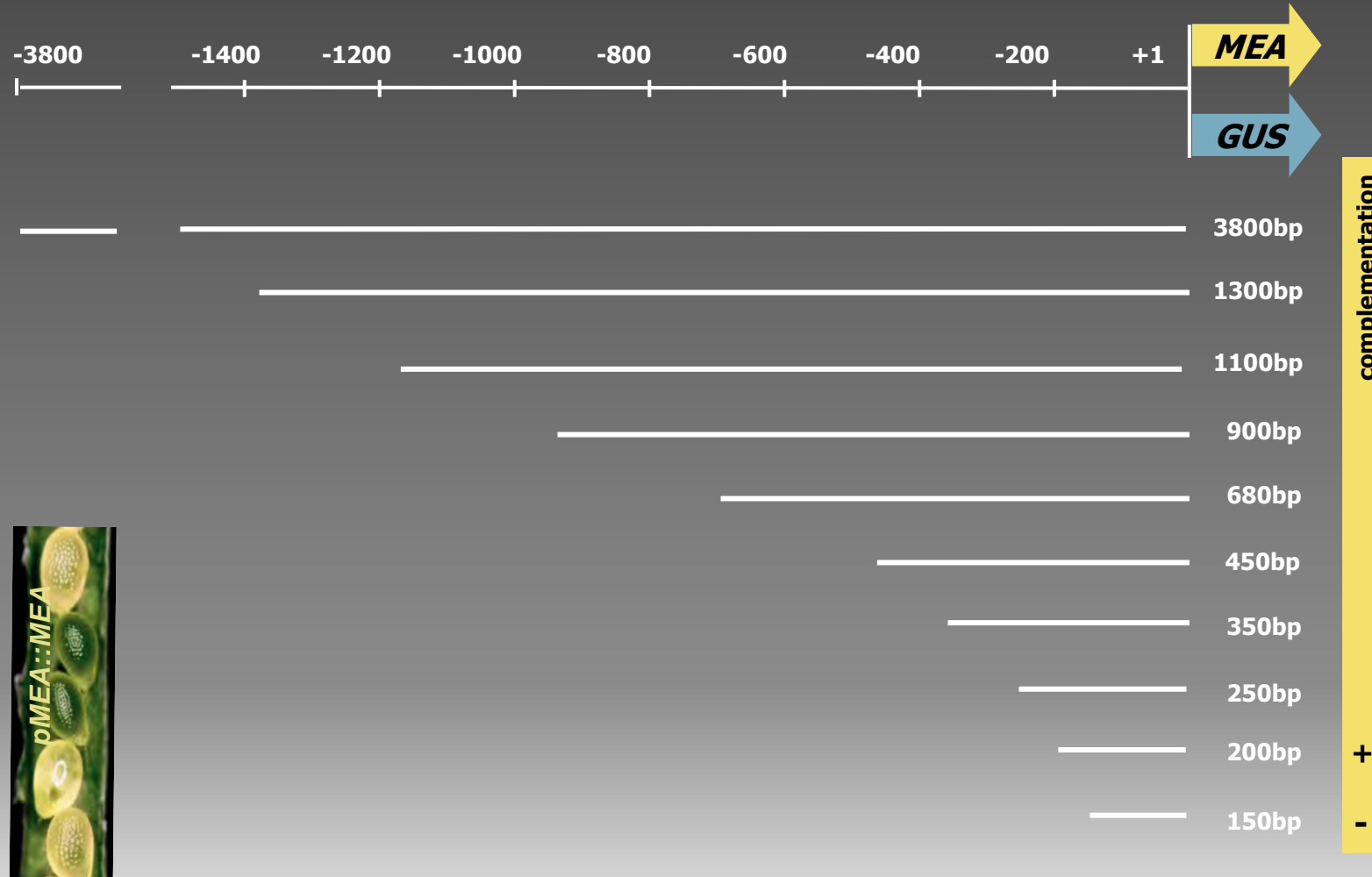
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DNA Methylation and PRC2 Contribute to Imprinting in Mammals and Plants

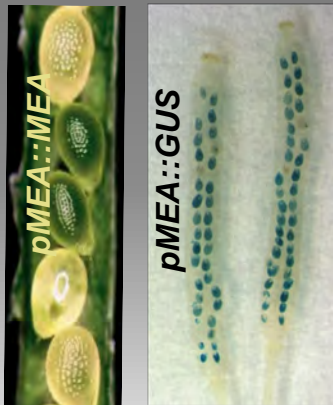
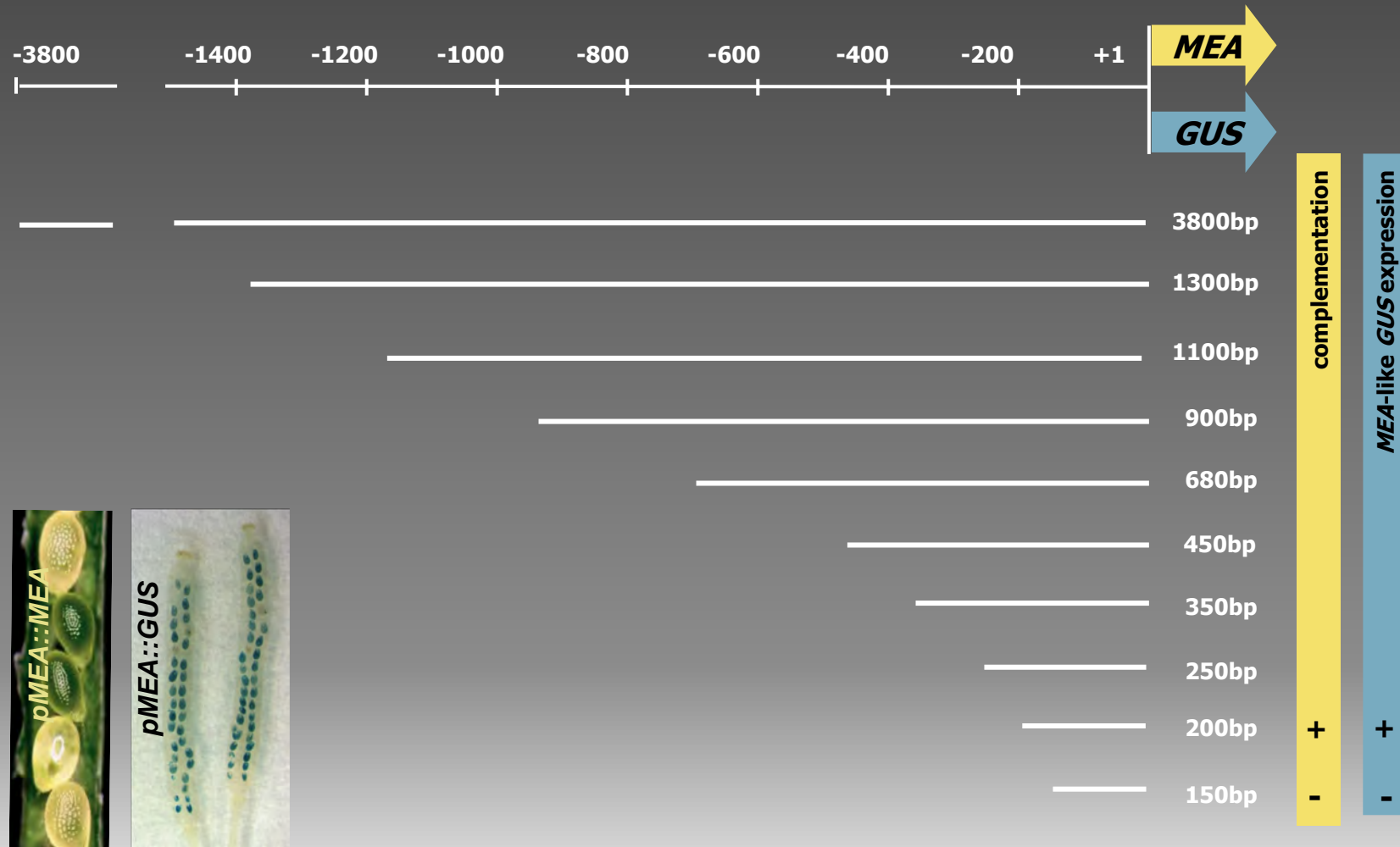


Köhler *et al. Genes Dev* (2003), Köhler *et al. Nat Genet* (2005), Makarevich *et al. J Cell Sci* (2008), Gehring *et al. Cell* (2006) Jullien *et al. Curr Biol* (2006); Baroux *et al. Genes Dev* (2006); Umlauf *et al. Nat Genet* (2004), Terranova *et al. Dev Cell* (2008)

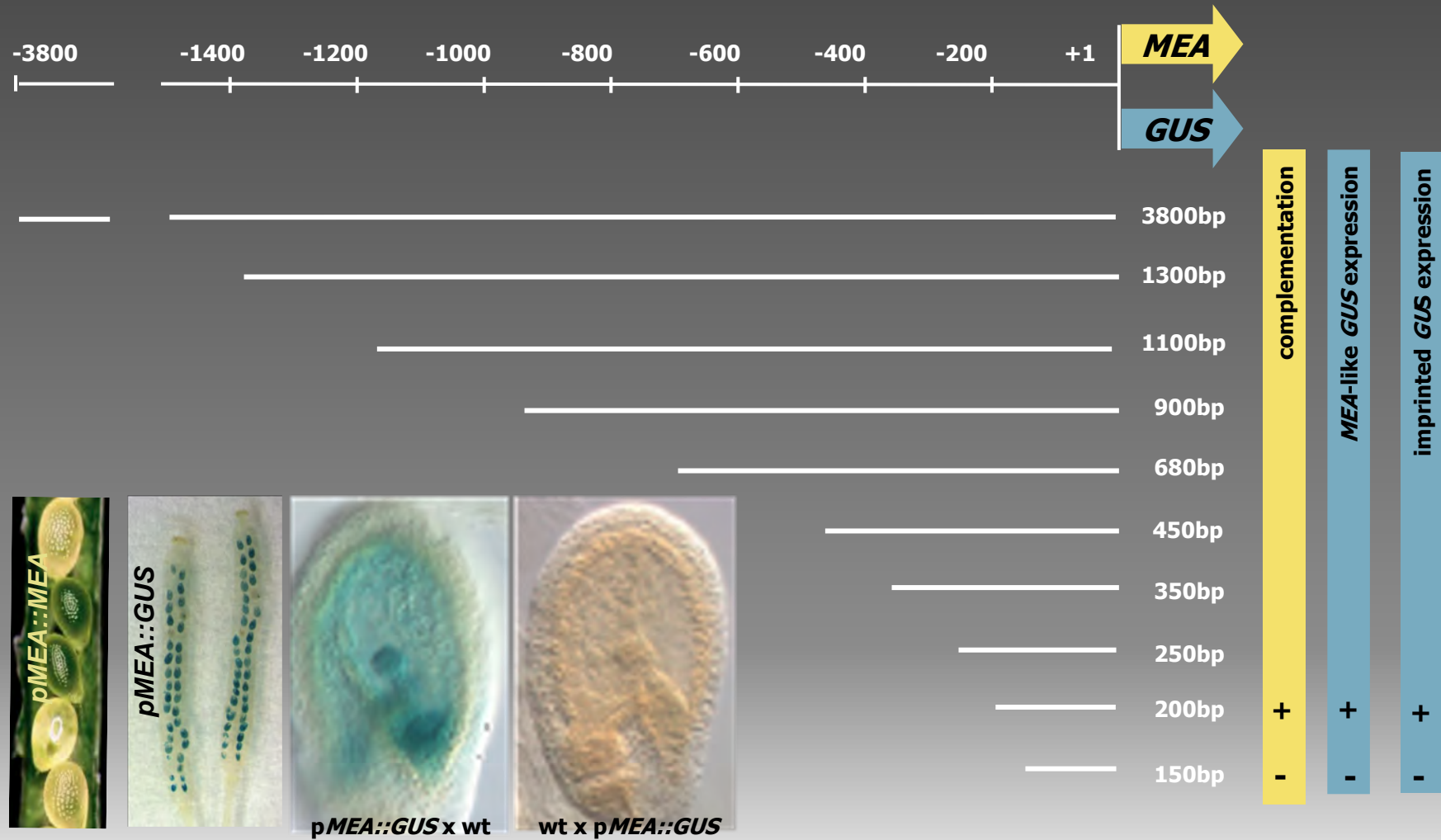
A 200 bp Region in the Promoter Is Required for *MEDEA* Expression and Function



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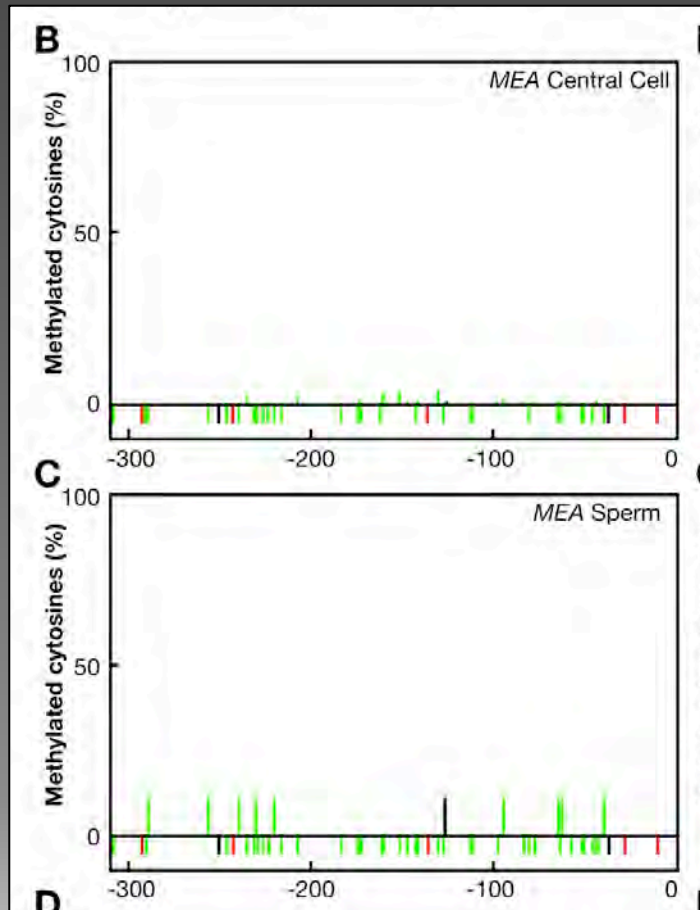


DNA Methylation is NOT the Primary Imprint

MEA-ICR



First ICR without a DNA methylation mark in gametes



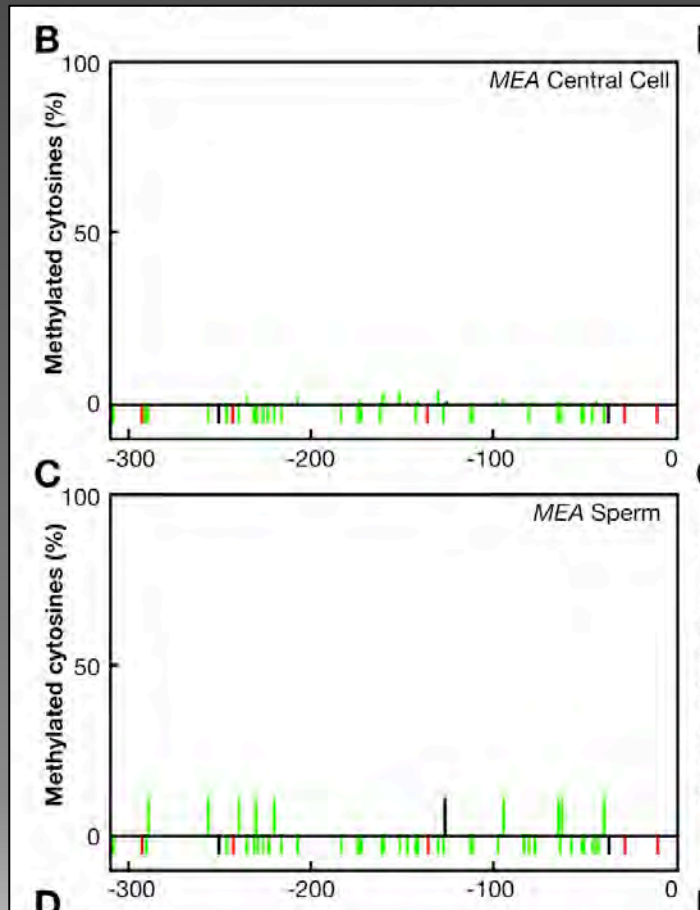
Wendelin Wehrle, Anja Schmidt
Julia Arand, Sascha Tierling, Jörn Walter



University of
Zurich^{UZH}

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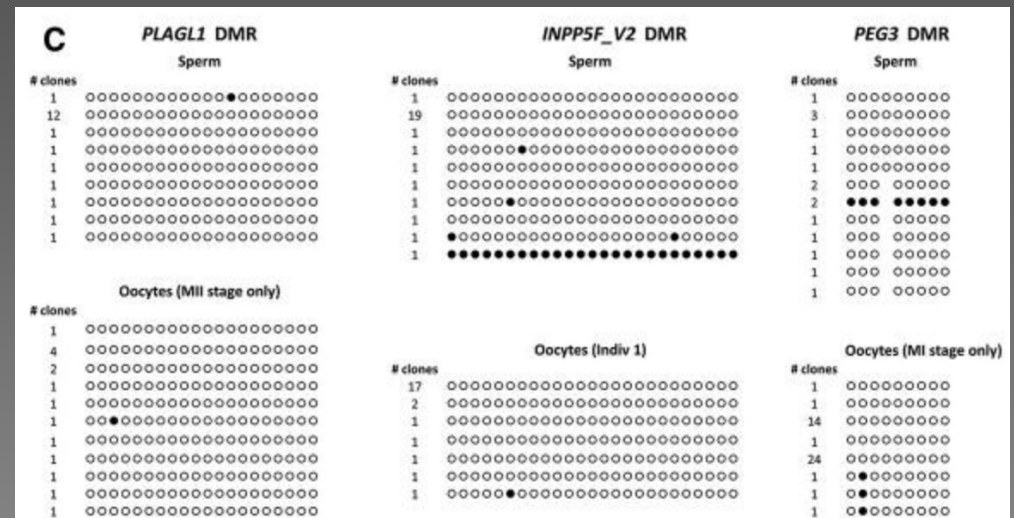
MEA-ICR



Wendelin Wehrle, Anja Schmidt
 Julia Arand, Sascha Tierling, Jörn Walter



First ICR without a DNA methylation mark in gametes



ICR w/o DNA methylation also exist in mice (Cheong et al. (2015) *Genome Res* 25, 611)



Maternal H3K27me3 controls DNA methylation-independent imprinting

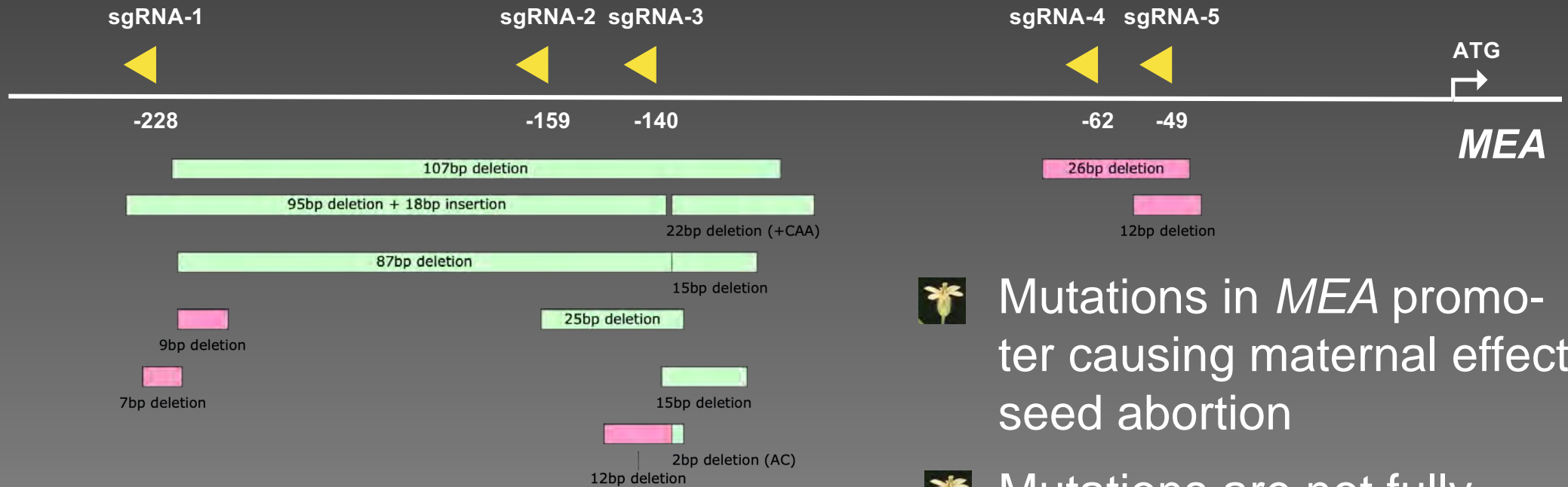
Azusa Inoue^{1,2,3*}, Lan Jiang^{1,2,3*}, Falong Lu^{1,2,3,4*}, Tsukasa Suzuki^{1,2,3} & Yi Zhang^{1,2,3,4,5}



University of Zurich ^{UZH}

Wöhrmann et al. (2012) *Genes Dev* 26, 1837

cis-Regulatory Mutagenesis by CRISPR/Cas9



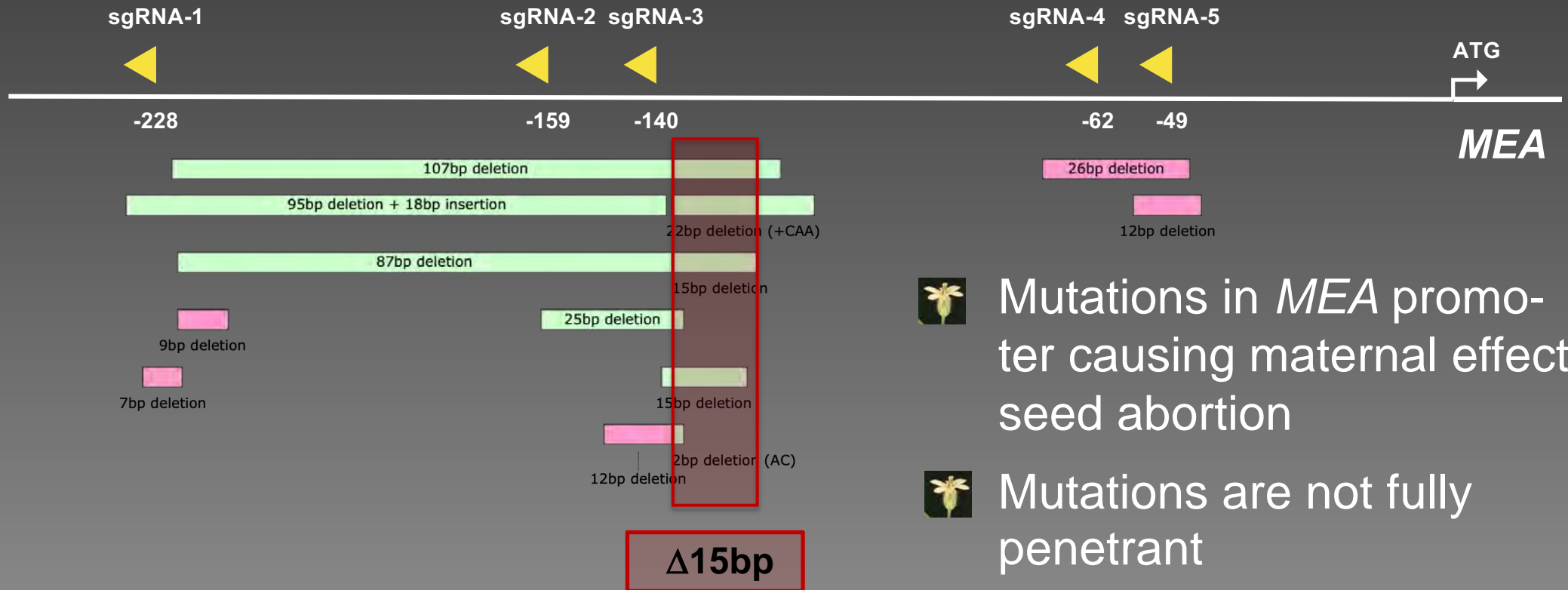
Mutations in *MEA* promoter causing maternal effect seed abortion







Mutations are not fully penetrant



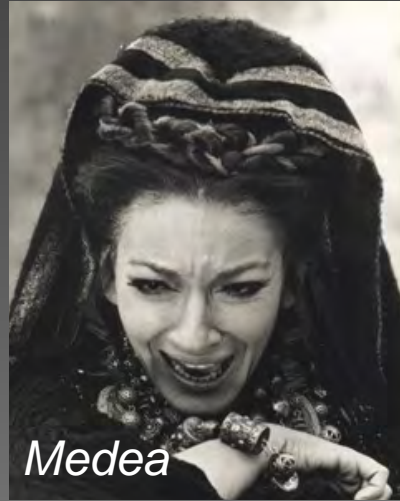
cis-Regulatory Mutagenesis by CRISPR/Cas9



Summary

-  *MEDEA* is regulated by **genomic imprinting** which likely evolved due to a parental conflict similar to the situation in mammals (convergent evolution)
-  For some imprinted loci in both mammals and plants, **DNA methylation** and **PRC2 repression** are key regulators, but for many imprinted plant genes, they are not
-  The molecular nature of the primary imprint at *MEDEA* is unknown; **DNA-methylation is NOT the primary imprint**
-  A **15bp cis-element** is required for imprinting; deletions lead to seed abortion due to loss of imprinting
→ Imprinting Control Region (ICR)

Acknowledgements: Imprinting



Medea

Former:

Sara Simonini
Marcel Brassler
Anja Schmidt
Marian Bemer
Nuno Pires
Michi Raissig

Heike Wöhrmann
Wendelin Wehrle
Célia Baroux
Claudia Köhler
Charlie Spillane
JP Vielle-Calzada



Current:

Wei Wei Chong
Valeria Gagliardini
Dorothee Stöckle



Collaborators: (Saarbrücken)

Jörn Walter
Julia Arand
Sascha Tierling



Thank you for your Attention!

