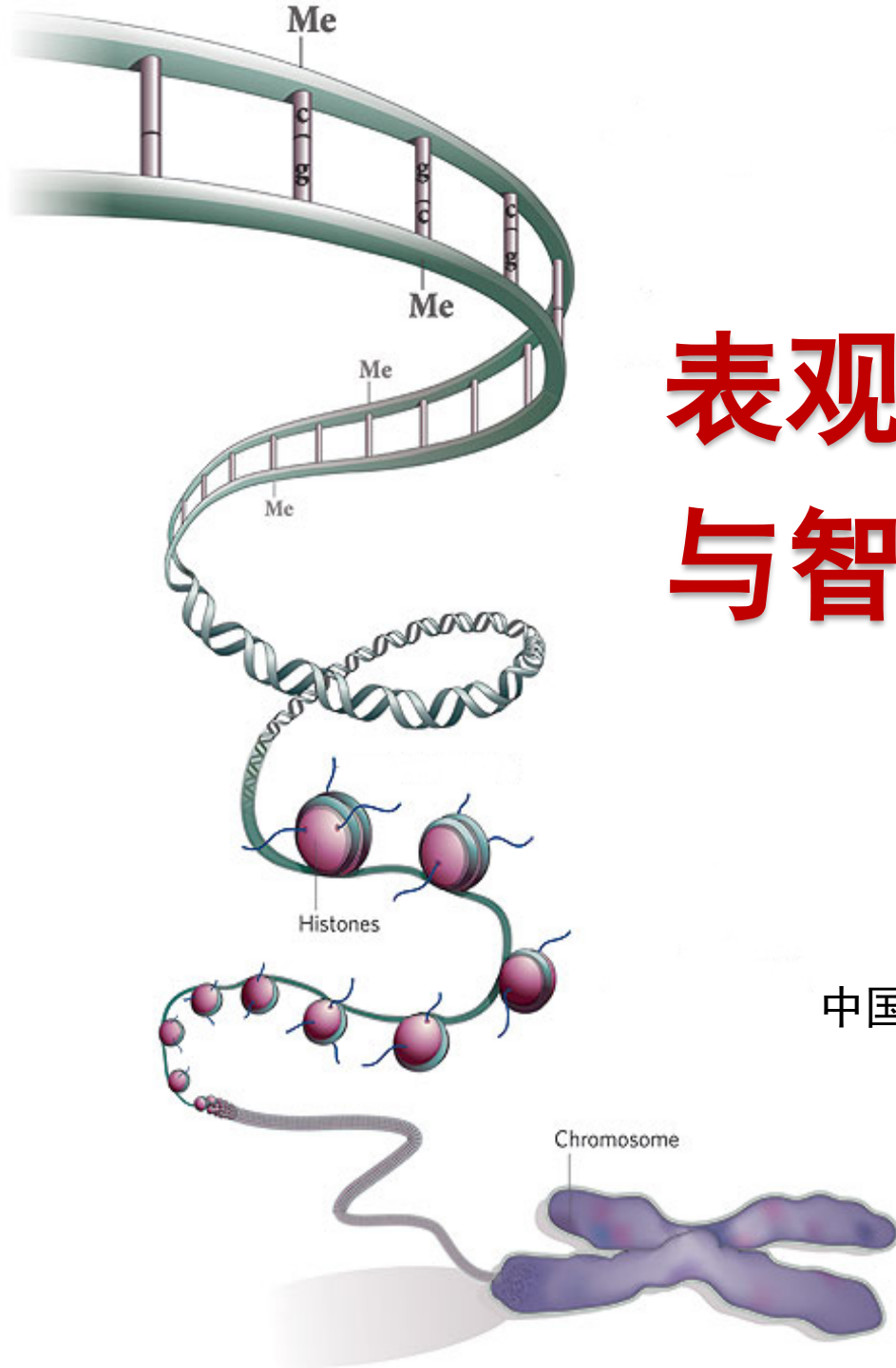




表观遗传学前沿 与智能设计育种

普 莉

中国农业科学院生物技术研究所

2020年3月24日

21世纪重大科学难题

国际学科趋势



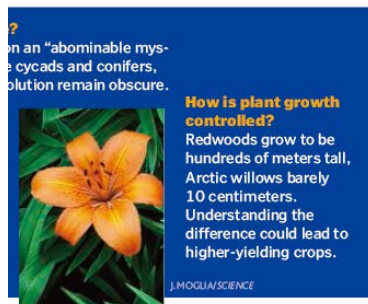
在逆境环境下,植物表型
变异的遗传基础是什么?

“我们需要能够更好适应干旱或寒冷等极端环境的作物,但是哪些基因参与其中还知之甚少”



植物生长发育的规律和分子调控
机制是什么?

“植物的大小、高矮和开花生长习性有很大不同,
阐明这些分子机制将有助于高产作物的设计”



什么决定了物种多样性?

“物种多样性的遗传基础、表观调控基础还知之甚少”



全球粮食安全和生态安全问题日趋突出



极端气候、灾害严重



耕地减少、质量退化

?

农业环境污染



农业资源短缺

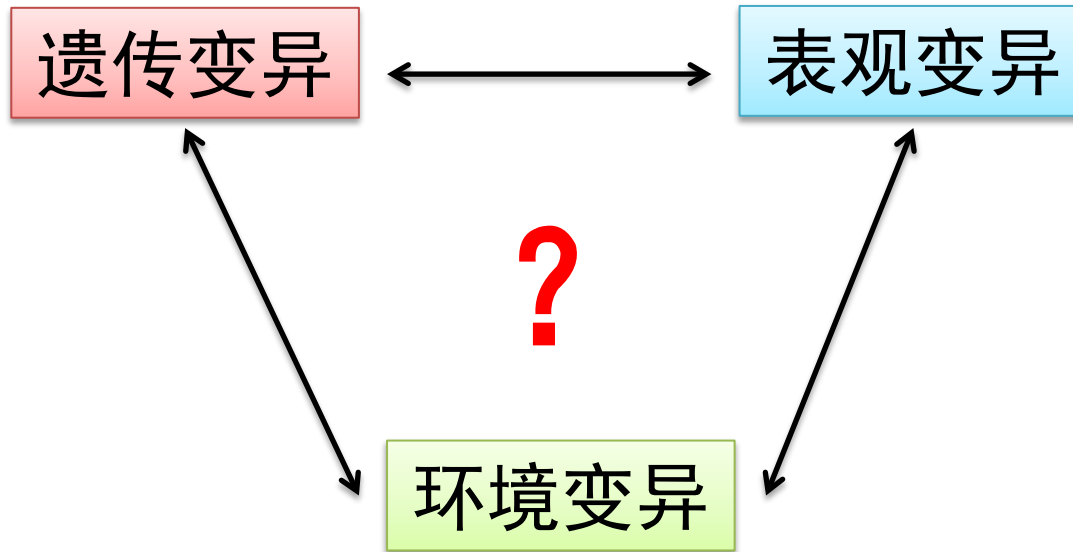


Why Your DNA Isn't Your Destiny | Jan. 18, 2010



表观遗传学特别强调生活的环境对人体表观遗传因素的影响

生物复杂性状形成的基础

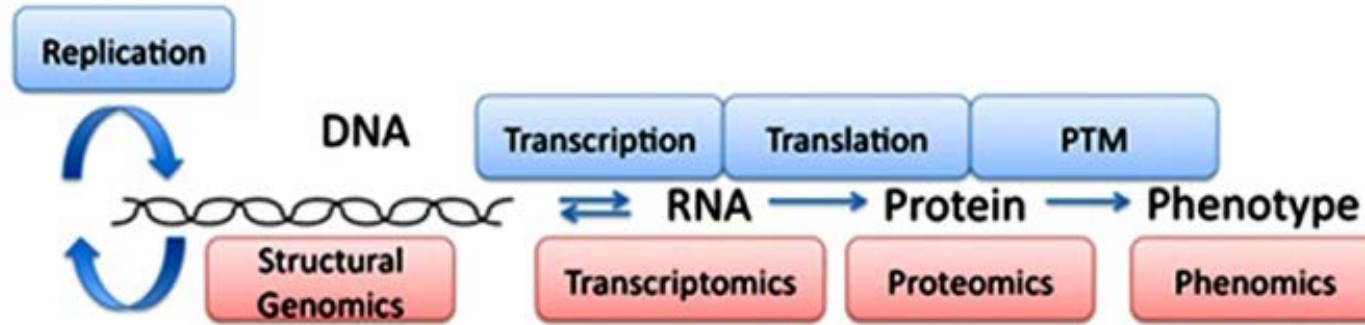


- 精准控制了复杂性状的形成
- 决定了物种的不同表型
- 造就了物种的多样性

- I. 表观遗传学概念以及发展历史
- II. 表观遗传学研究进展
- III. 表观遗传智能设计育种技术

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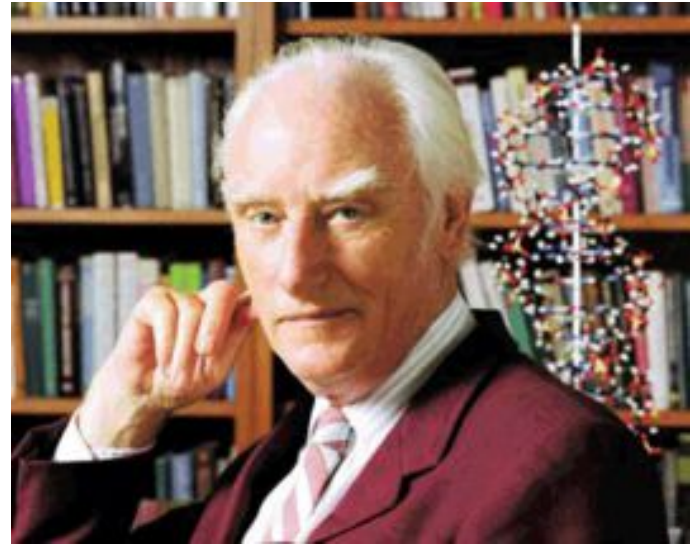
孟德尔遗传定律和中心法则



Gregor Johann Mendel
7.20.1822 – 1.6.1884

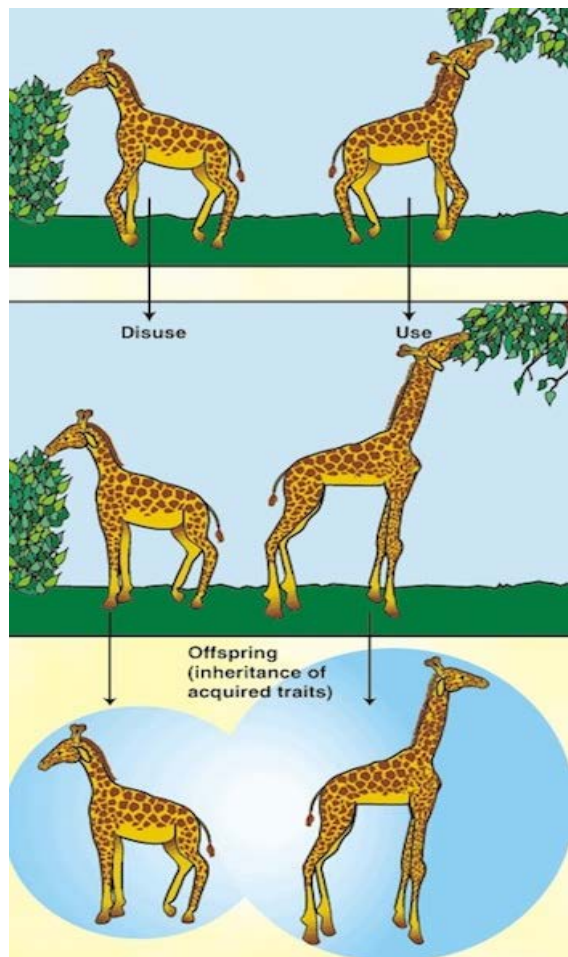


Thomas Hunt Morgan
9.25.1866 – 12.4.1945

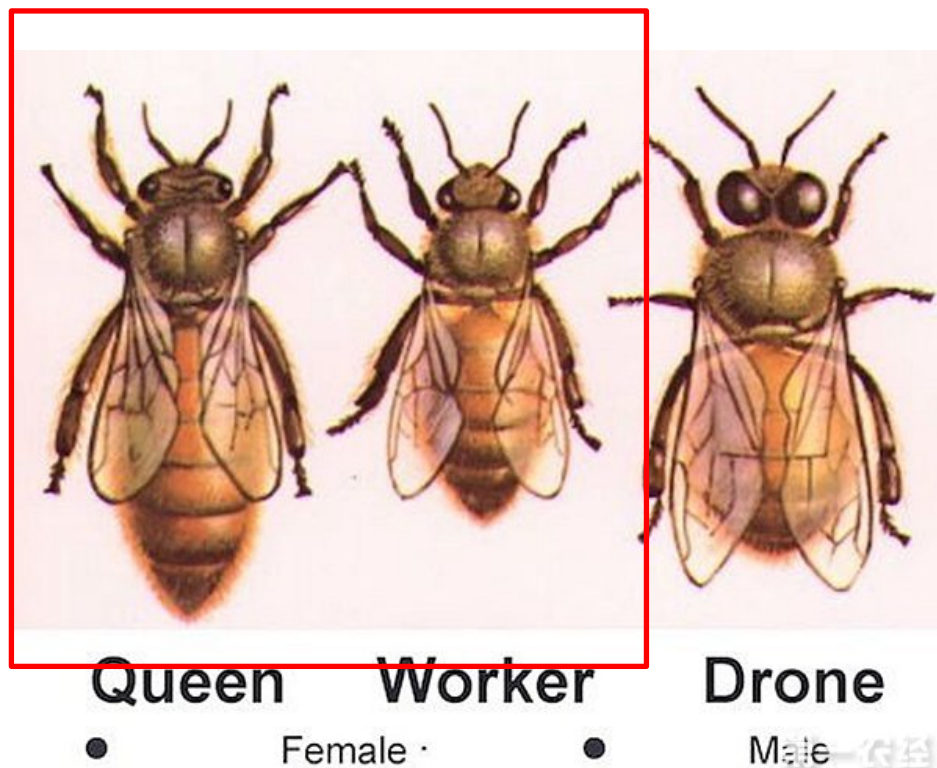


Francis Harry Compton Crick
6.8.1916 – 7.28.2004

非孟德尔遗传现象



获得性遗传



蜂后和工蜂

表观遗传学发展历史



- 最早1939年，生物学家 Waddington CH（1905-1975）首先在《现代遗传学导论》中提出了epigenetics这一术语。
- 1942年，由Waddington提出并确定这一说法，当时定义为“基因与环境互作导致的表型”。最初人们认为表观遗传只是一种表型，它不符合经典的孟德尔遗传规律，当时并没有引起很大重视。
- 1975年，Holliday对表观遗传学进行了较为准确的描述。他认为表观遗传学不借助于DNA序列的改变，也就是说表观遗传是非DNA序列差异的核遗传。

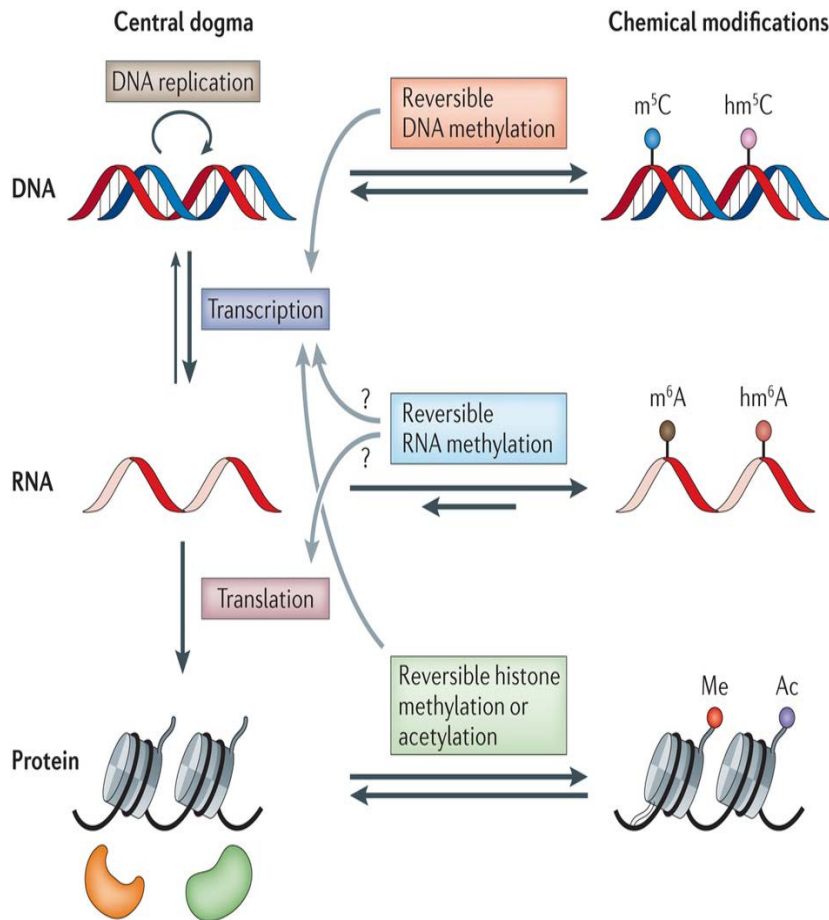
Barbara McClintock

(June 16, 1902 – September 2, 1992)



- 在二十世纪五十年代Barbara McClintock首次发现了转座子。而调控转座子活性的一个重要因素就是DNA甲基化。
- 在1993年，Martienssen和他的同事发现一个他们梦寐以求的突变体——真核生物中第一例DNA甲基化缺失的突变体——他们称之为*DNA methylation1 (DDM1)*。
- 之后，植物表观遗传学的研究才出现井喷式的发展。

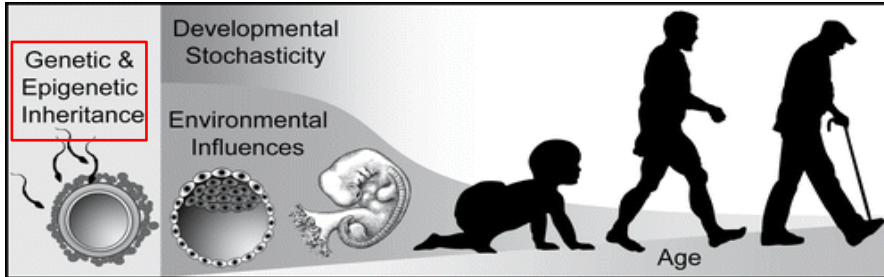
表观遗传调控



- DNA Methylation
- RNA Methylation
- Histone Modification
- nc RNA
- Chromo remodeling

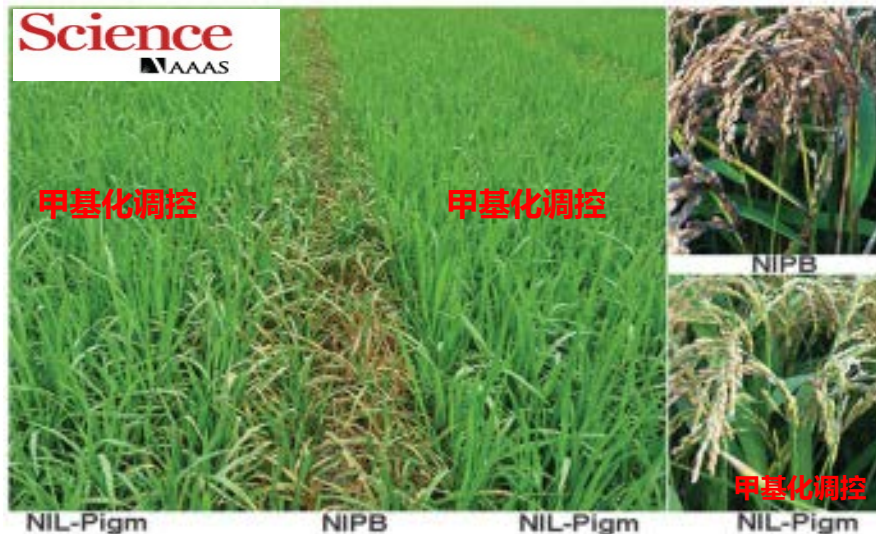
Fu et al., 2014, *Nat Rev Genet*

表观遗传调控生命发育



表观遗传参与生物发育的每一个阶段，起着关键的调控作用

 Waterland RA, Michels KB. 2007. Annu. Rev. Nutr. 27:363–88



DNA甲基化(胞嘧啶)调控水稻广谱抗病与产量平衡 (何祖华课题组)

Deng *et al.*, 2017 Science

DNA甲基化(胞嘧啶)调控水稻杂种优势与产量 (万建民课题组)

Zhang *et al.*, 2012 Plant Cell

小RNA调控水稻产量(李家洋、曹晓风课题组)

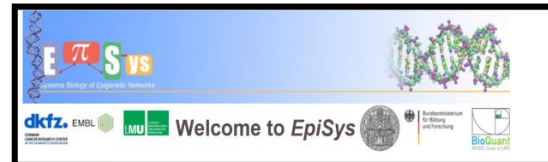
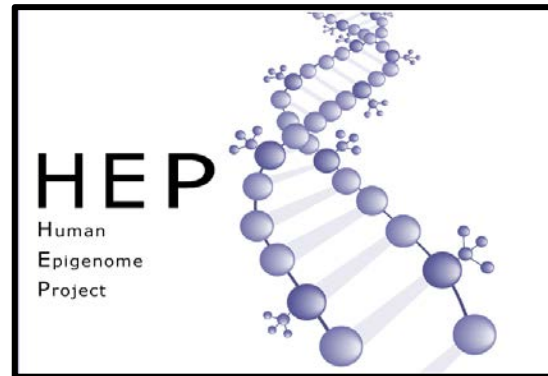
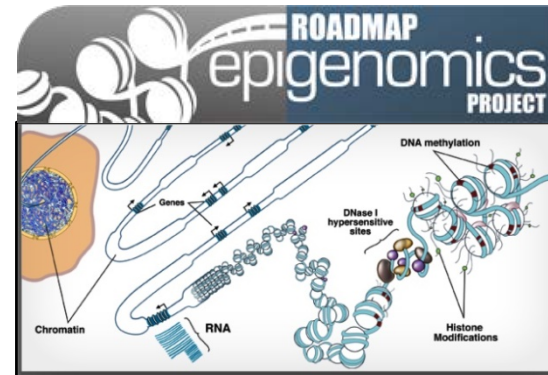
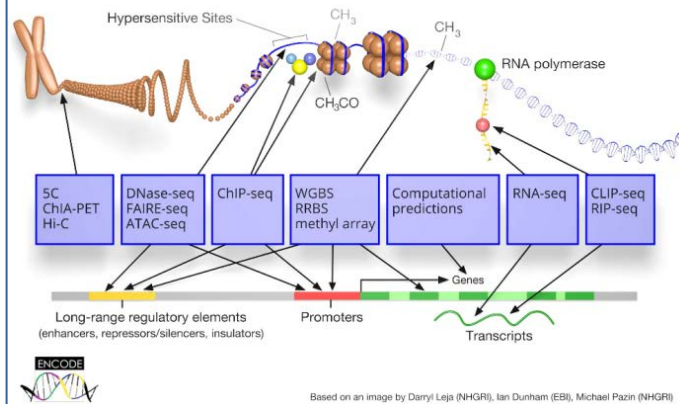
Wei *et al.*, 2014 PNAS

Jiao *et al.*, 2010 Nature Genetics

表观遗传学研究和育种是培育高产优质品种的新路径和方法



ENCODE: Encyclopedia of DNA Elements



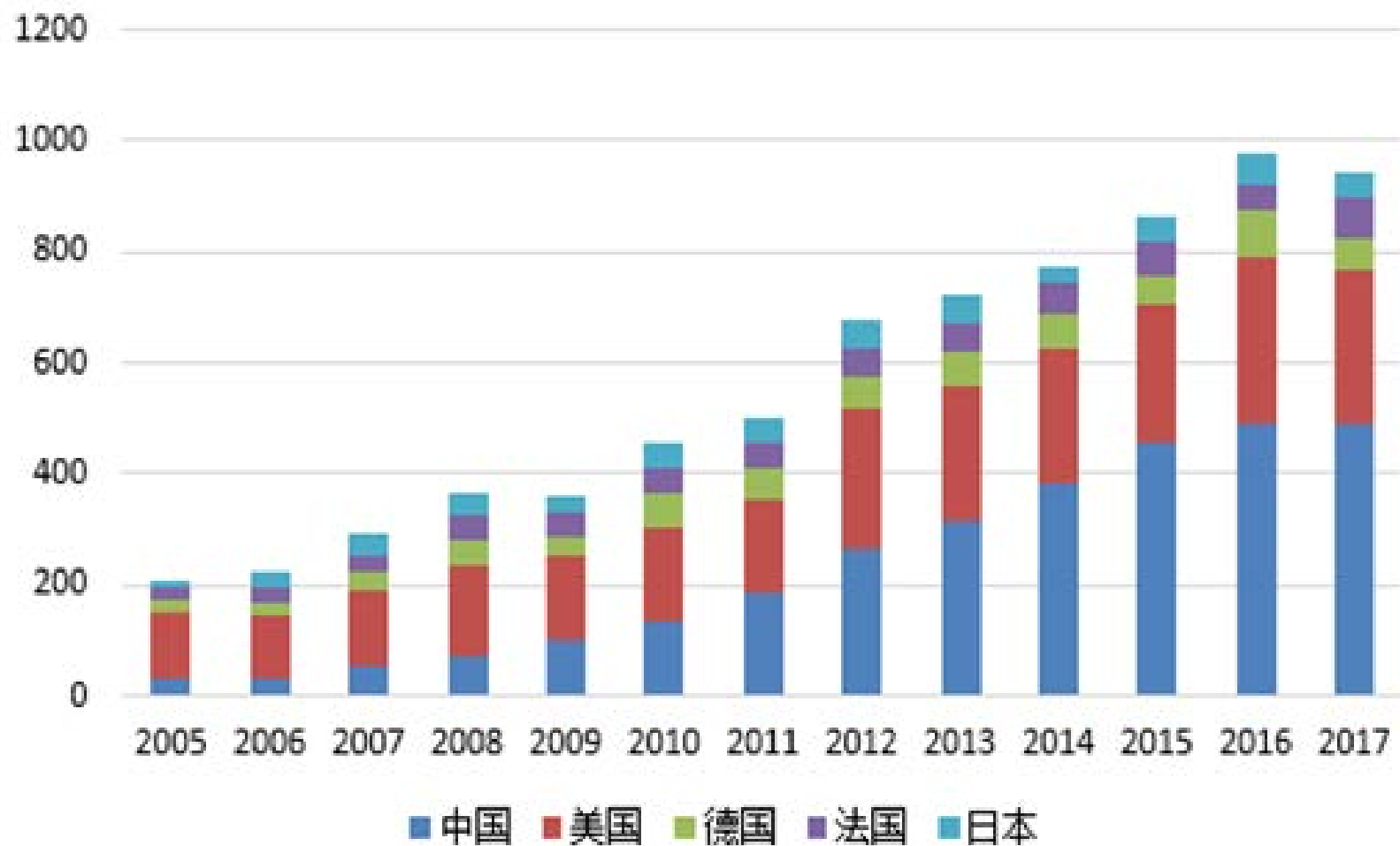
<https://www.4dnucleome.org/>

2005-2017年 国家/地区表观遗传领域发文量和被引情况

发文排序	国家/地区	发文量/ 篇	总被引		篇均被引	
			频次	排序	频次	排序
1	中国	2995	63327	2	21.14	15
2	美国	2600	141997	1	54.61	3
3	德国	661	33701	4	50.98	5
4	法国	588	28528	5	48.52	7
5	日本	524	20220	6	38.59	8
6	英国	452	45623	3	100.94	1
7	印度	411	6507	12	15.83	19
8	澳大利亚	339	12797	7	37.75	9
9	西班牙	313	9965	9	31.84	10
10	加拿大	282	8126	10	28.82	13
11	韩国	274	5478	15	19.99	16
12	意大利	220	6445	13	29.30	12
13	瑞士	206	12235	8	59.39	2
14	波兰	142	2302	18	16.21	18
15	荷兰	139	6802	11	48.94	6
16	巴西	127	1897	20	14.94	20
17	奥地利	116	6204	14	53.48	4
18	墨西哥	110	2958	17	26.89	14
19	比利时	106	3370	16	31.79	11
20	捷克共和国	101	1972	19	19.52	17

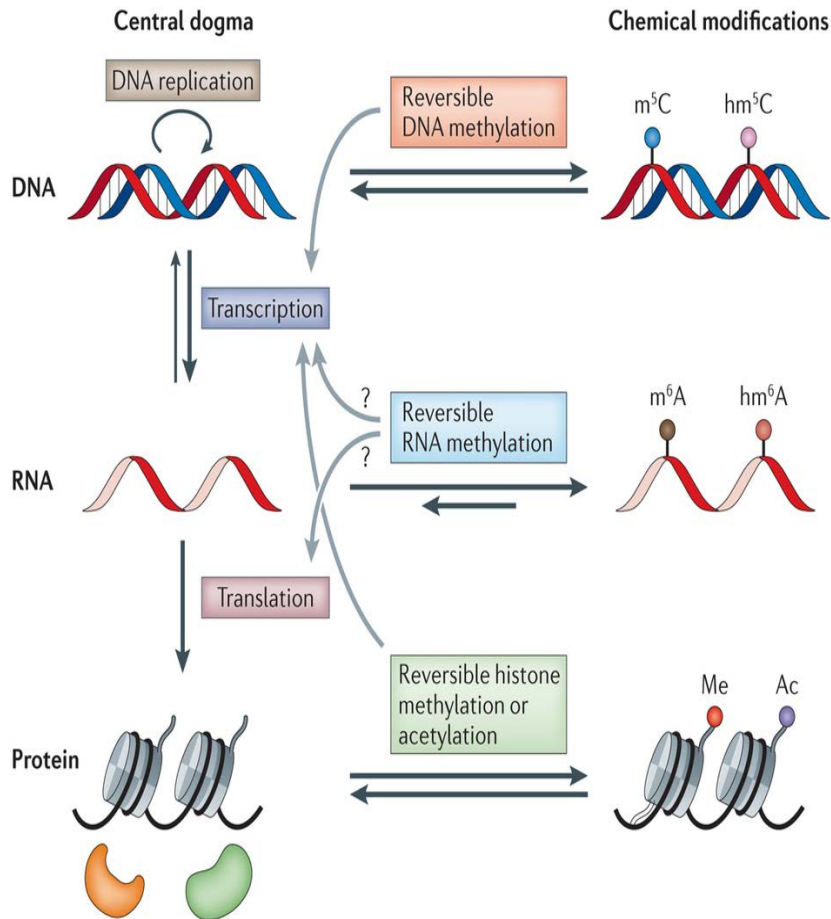
(Unpublished)

表观遗传领域发文量排名前5位国家各年发文量



(Unpublished)

- I. 表观遗传学概念以及发展历史
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- DNA Methylation
- RNA Methylation
- Histone Modification
- nc RNA
- Chromo remodeling

Fu et al., 2014, *Nat Rev Genet*

“组蛋白甲基化和小RNA调控植物生长发育和转座子活性的机制研究” 成果
荣获2019年度国家自然科学二等奖



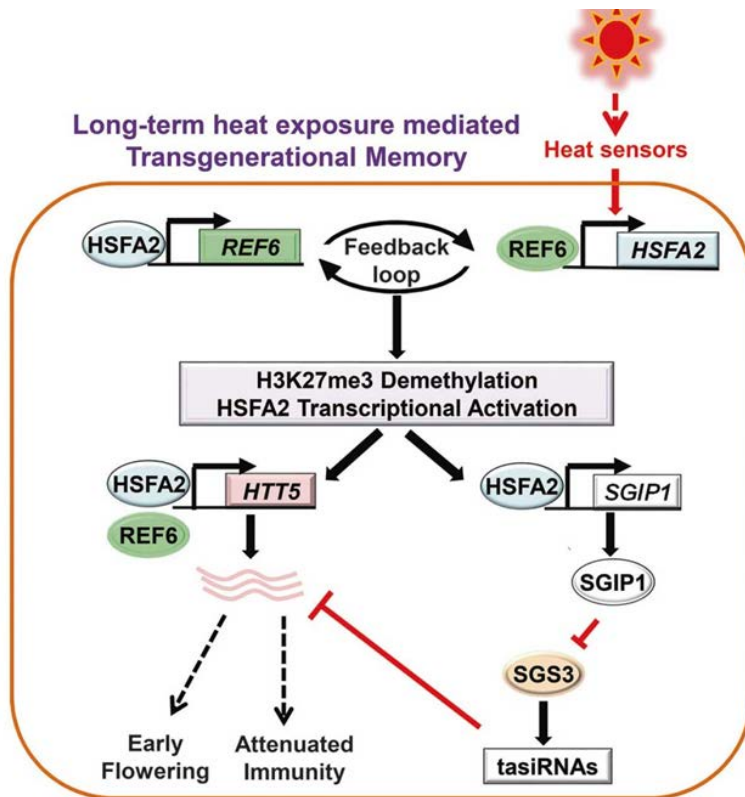
曹晓风院士团队历时11年：
率先开展了植物组蛋白去甲基化研究；
发现了植物组蛋白甲基化调控转座子沉默的新机制；
系统阐明了水稻小RNA合成途径及对生长发育的调控机制，首次在基因组水平上
证实了转座子是调控元件。

组蛋白甲基化调控植物对高温传代记忆的新机制

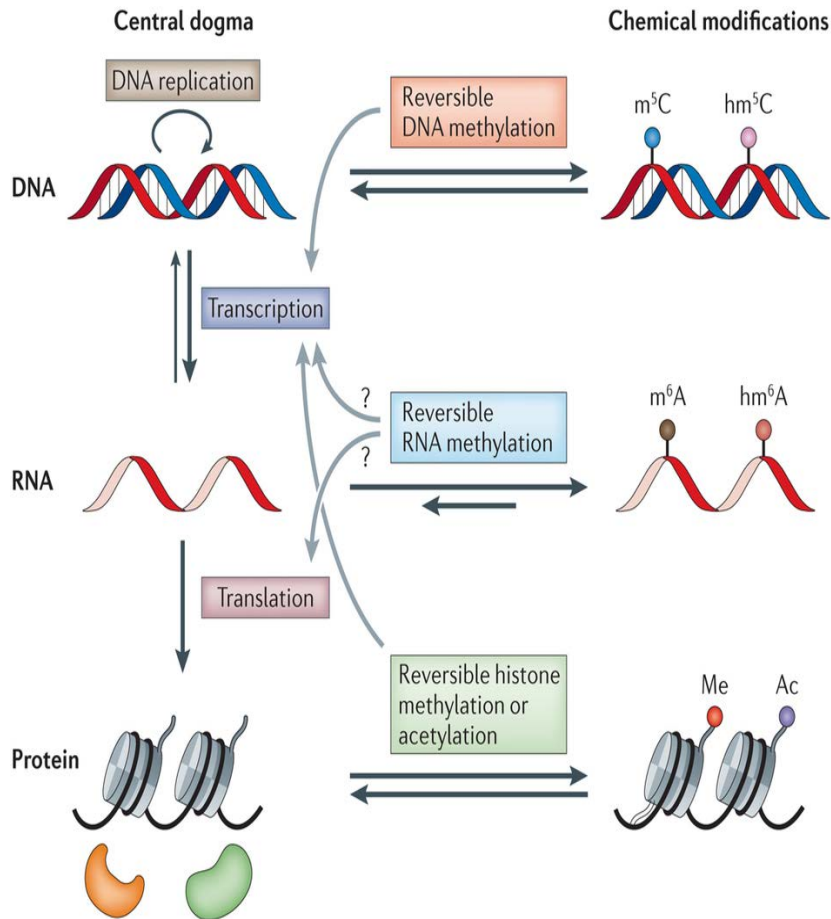
ARTICLE OPEN

An H3K27me3 demethylase-HSFA2 regulatory loop orchestrates transgenerational thermomemory in *Arabidopsis*

Junzhong Liu¹, Lili Feng^{1,2,3}, Xueting Gu^{1,2}, Xian Deng⁴, Qi Qiu^{2,4}, Qun Li¹, Yingying Zhang¹, Muyang Wang^{1,5}, Yiwen Deng¹, Ertao Wang¹, Yuke He¹, Isabel Bäurle⁶, Jianming Li^{5,7}, Xiaofeng Cao^{2,4,8} and Zuhua He^{1,3}



该研究揭示了一个由组蛋白去甲基化酶、染色质重塑因子、转录因子、泛素连接酶和小分子RNAs共同组成的复杂的表观调控网络参与植物对高温的传代记忆，促使植物提前开花（早结种子）同时以降低抗病性为代价来保证植物能顺利繁衍和适应高温逆境。



- DNA Methylation: C、
- RNA Methylation
- Histone Modification
- nc RNA
- Chromo remodeling

Fu et al., 2014, *Nat Rev Genet*

营养（蜂皇浆）对蜂后和工蜂造成DNA甲基化影响



Queen

Worker

Drone

●

Female

●

Male

OPEN ACCESS Freely available online

PLOS BIOLOGY

The Honey Bee Epigenomes: Differential Methylation of Brain DNA in Queens and Workers

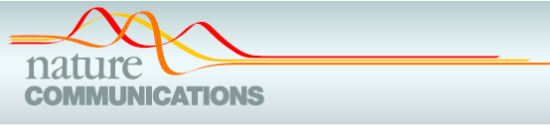
Frank Lyko¹, Sylvain Foret², Robert Kucharski³, Stephan Wolf⁴, Cassandra Falckenhayn¹, Ryszard Maleszka^{3*}

¹ Division of Epigenetics, DKFZ-ZMBH Alliance, German Cancer Research Center, Heidelberg, Germany, ² ARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, Australia, ³ Research School of Biology, the Australian National University, Canberra, Australia, ⁴ Genomics and Proteomics Core Facility, German Cancer Research Center, Heidelberg, Germany

Table 1. Cytosine DNA methylation in queens and workers in CG, CHG, and CHH genomic contexts (H = A, T, or C).

	Total	Methylated in Queens	Methylated in Workers	Methylated in Both Castes
CG	10,030,209	69,064	68,222	54,312
CHG	8,673,113	14	130	0
CHH	45,072,611	561	3,019 ^a	0

单个基因位点甲基化程度控制蚂蚁大小



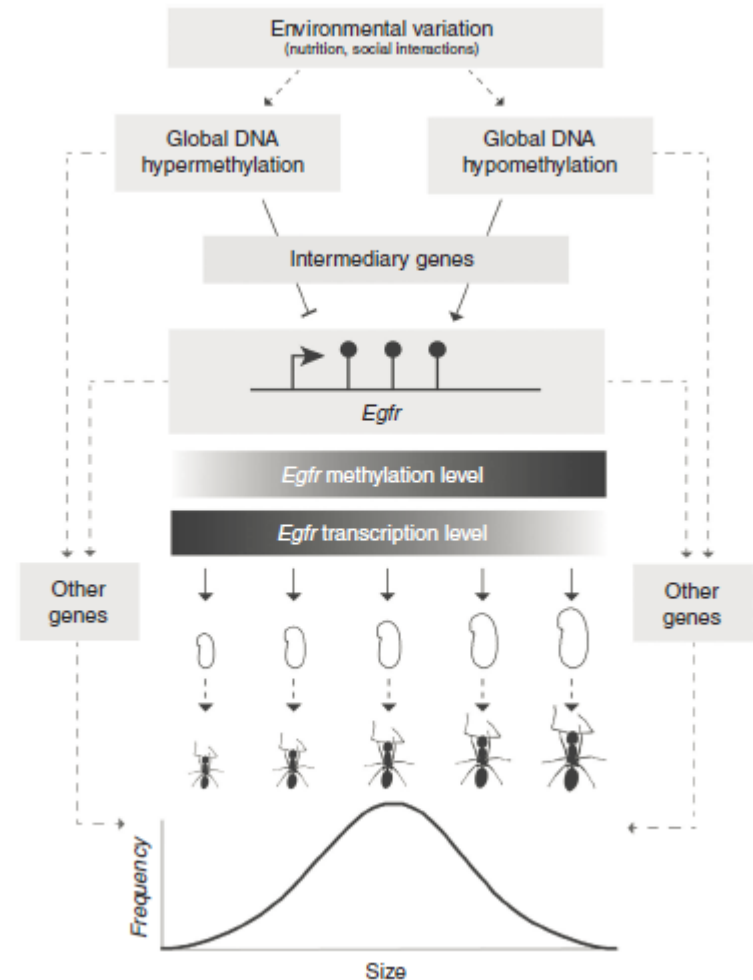
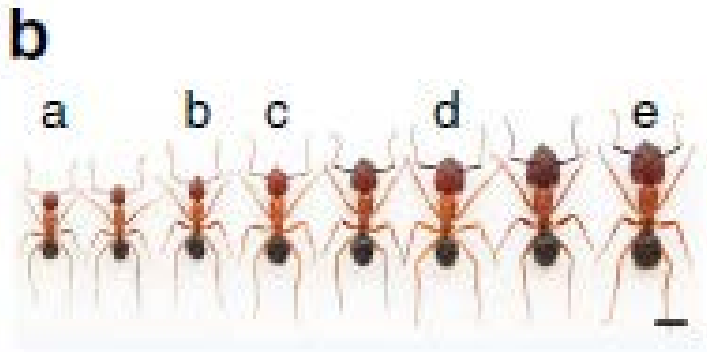
ARTICLE

Received 15 Jul 2014 | Accepted 5 Feb 2015 | Published 11 Mar 2015

DOI: 10.1038/ncomms7513

Epigenetic variation in the *Egfr* gene generates quantitative variation in a complex trait in ants

“Epigenetic processes, such as DNA methylation, can mediate gene-by-environment interactions during development to generate discrete **phenotypic variation**”.

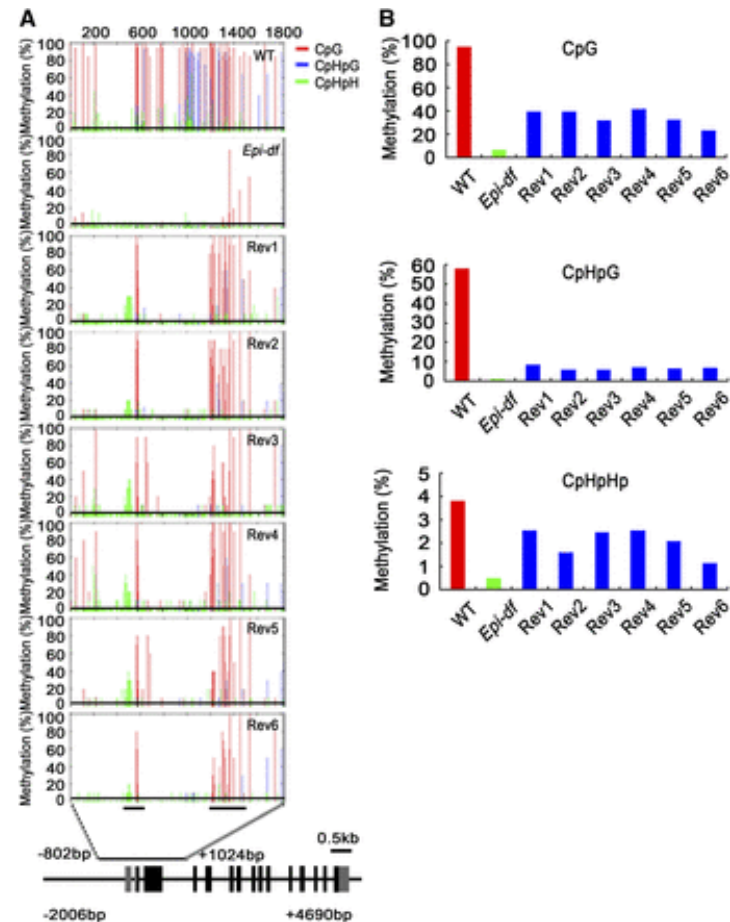
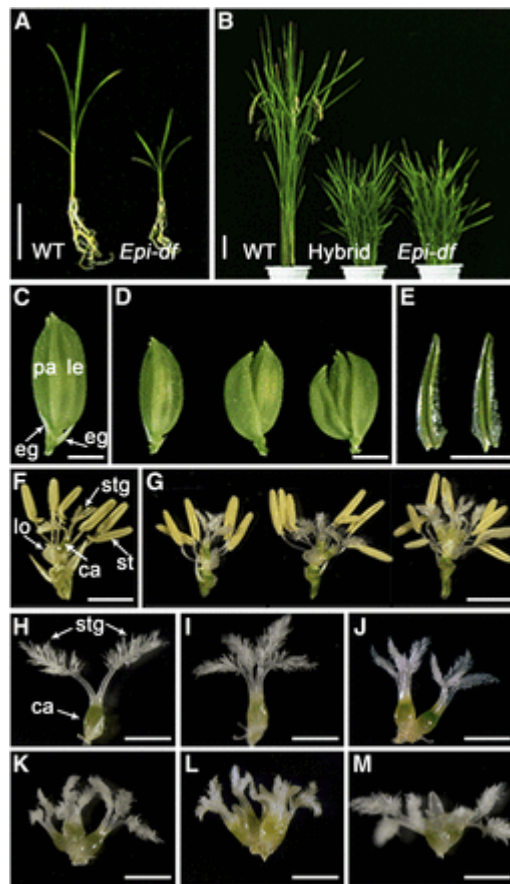


Model for the generation of a continuous distribution of worker size through quantitative DNA methylation of *Egfr*

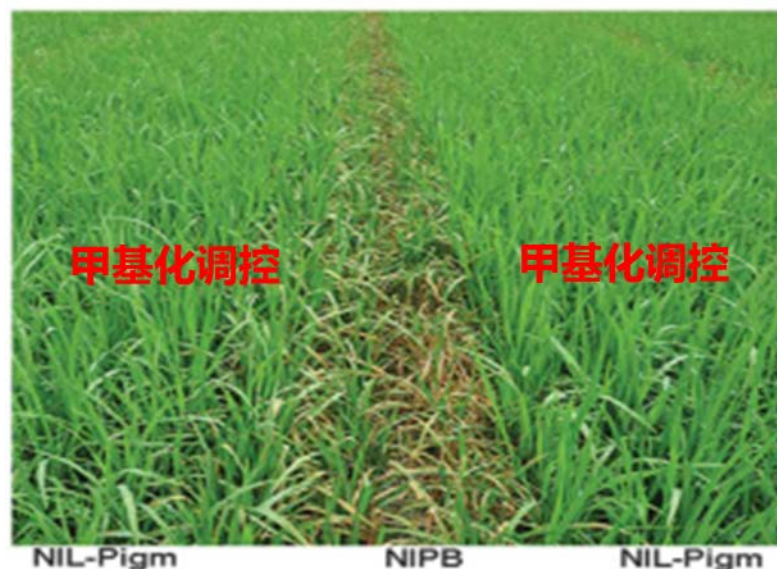
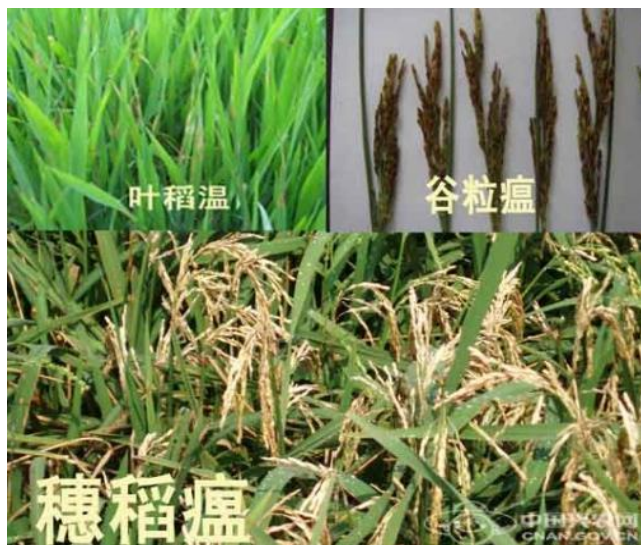
水稻DNA甲基化和组蛋白修饰协同调控株形和育性

Identification and Characterization of an Epi-Allele of *FIE1* Reveals a Regulatory Linkage between Two Epigenetic Marks in Rice

Liguo Zhang, Zhijun Cheng, Ruizhen Qin, Yang Qiu, Jiu-Lin Wang, Xiekui Cui, Lianfeng Gu, Xin Zhang, Xiuping Guo, Dan Wang, Ling Jiang, Chuan-yin Wu, Haiyang Wang, Xiaofeng Cao, Jianmin Wan



植物抗病性的表观遗传调控机制



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Epigenetic regulation of antagonistic receptors confers rice blast resistance with yield balance

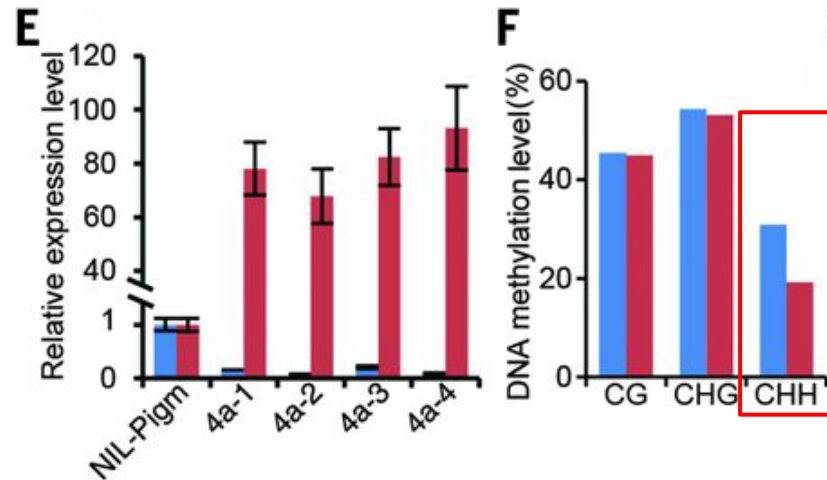
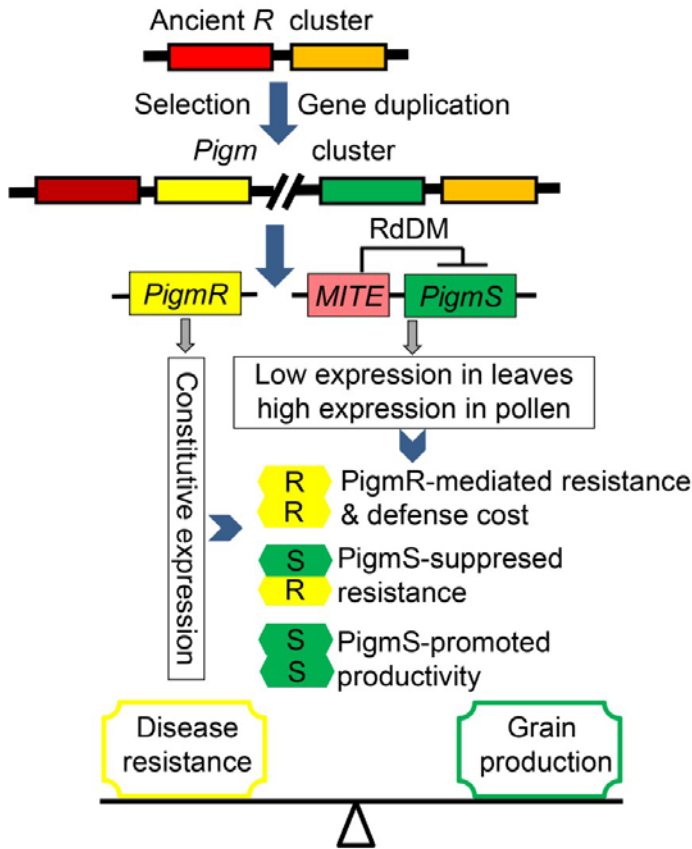
Yiwen Deng¹, Keran Zhai^{1,2}, Zhen Xie³, Dongyong Yang^{1,2}, Xudong Zhu⁴, Junzhong Liu¹, Xin Wang¹, Peng Qin⁵, Yuanzhu Yang⁵...

+ See all authors and affiliations

水稻抗病基因甲基化调控影响产量和抗病性

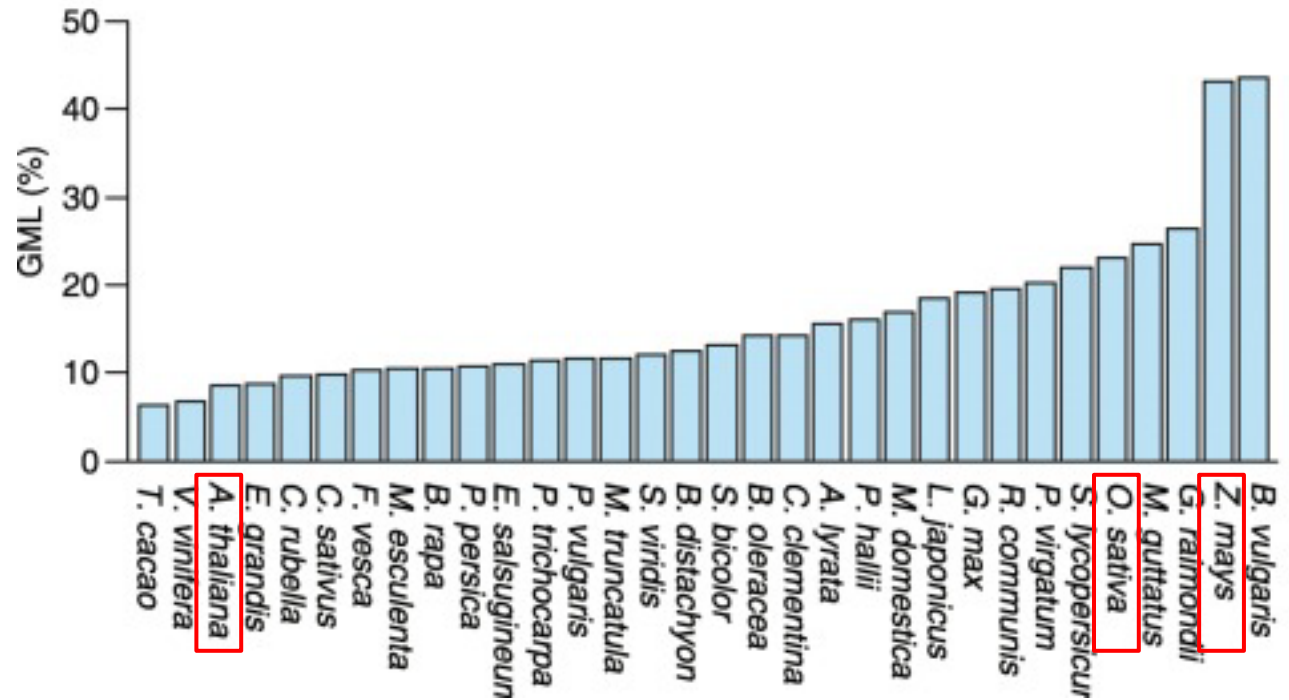
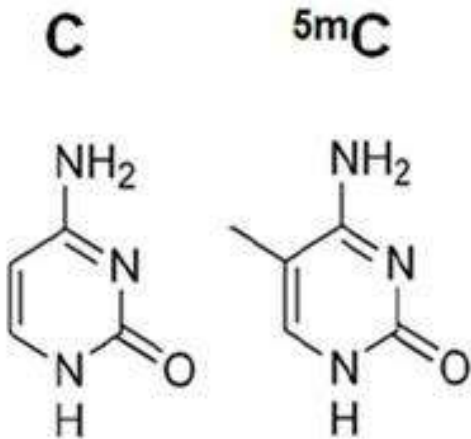
*Pigm*是一个包含多个NBS-LRR类抗病基因的基因簇。其中只有2个具有功能的蛋白PigmR和PigmS:

- PigmR发挥广谱抗病功能，但PigmR导致水稻千粒重降低，产量下降
- PigmS受到表观遗传的调控，可以提高水稻的结实率，抵消PigmR对产量的影响。

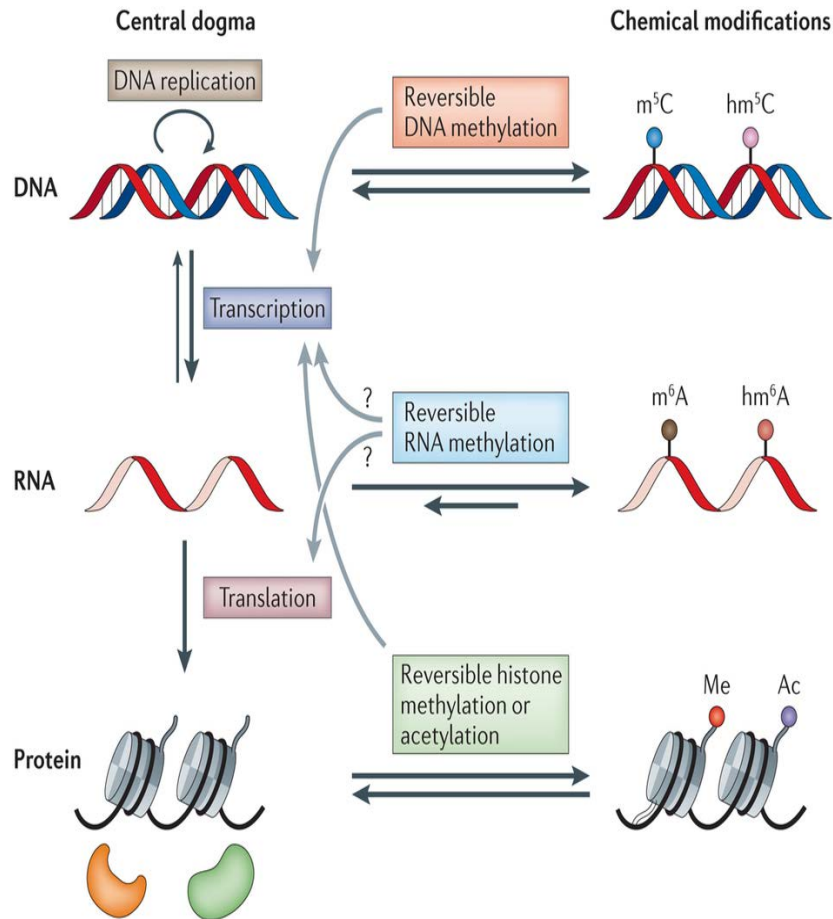


基础研究不仅在理论上扩展了植物免疫与抗病性机制的认识，也为作物抗病育种提供了有效的新工具！利用Pigm改良选育的品种既有广谱持久抗病性又不影响最终的产量。这个基因已经被国内30多家种子公司和育种单位应用于水稻抗病分子育种，已经有新品种参加区试和品种审定。

DNA 甲基化



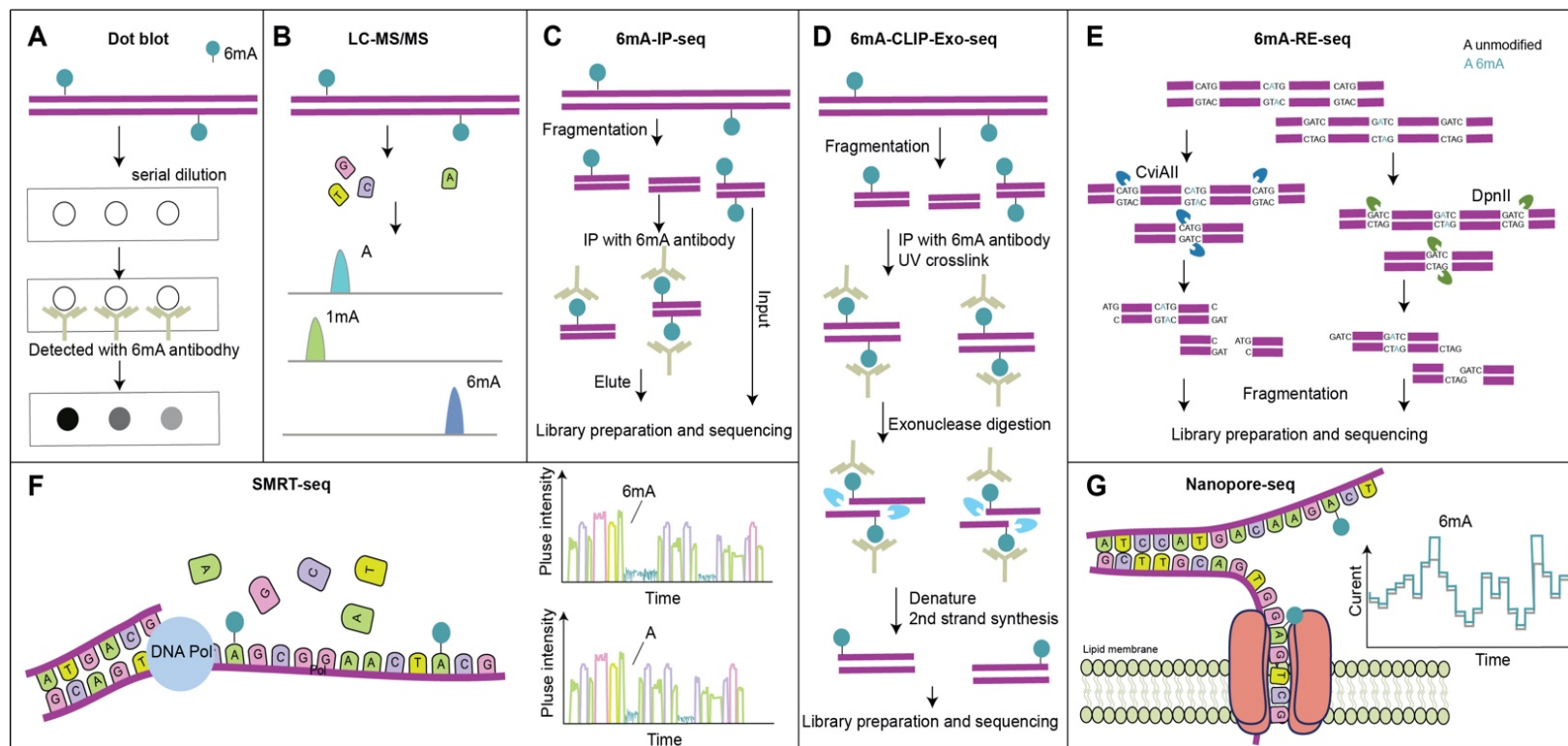
Genome-wide Methylation Levels (GMLs)



- DNA Methylation: C、A
- RNA Methylation
- Histone Modification
- nc RNA
- Chromo remodeling

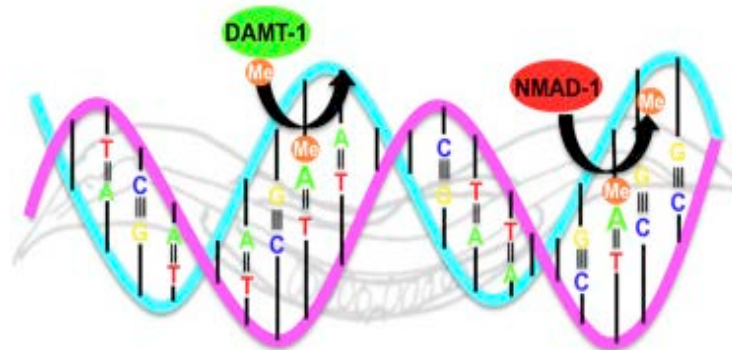
Fu et al., 2014, *Nat Rev Genet*

表观遗传研究体系和平台

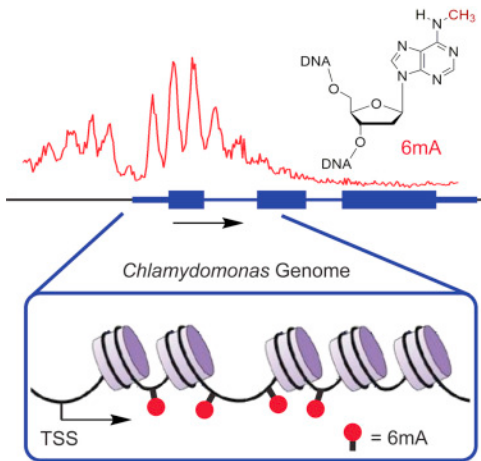


- 新核酸修饰检测和分析;
- 新核酸修饰全基因组鉴定和应用;

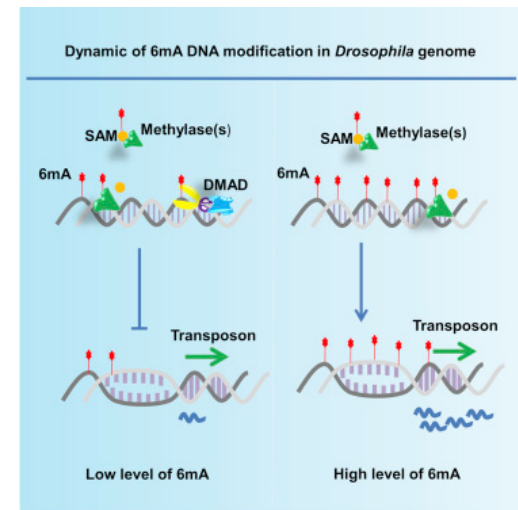
Multi-cellular 6mA



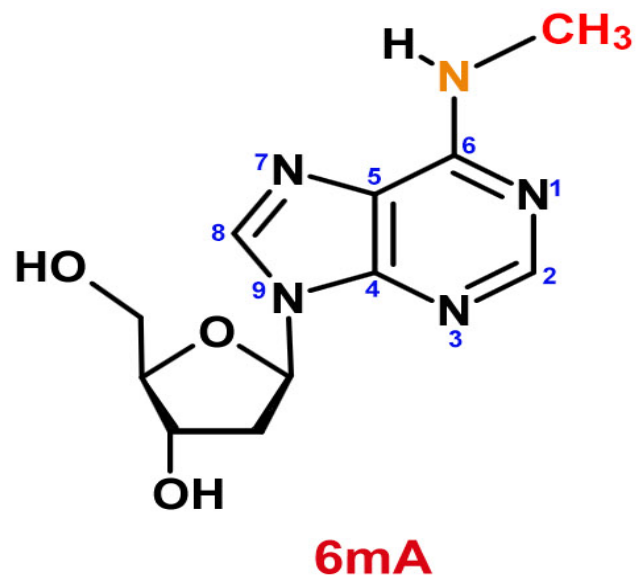
DNA Methylation on N⁶-Adenine in *C. elegans* **2015 Cell**



N⁶-Methyldeoxyadenosine Marks Active Transcription Start Sites in *Chlamydomonas* **2015 Cell**



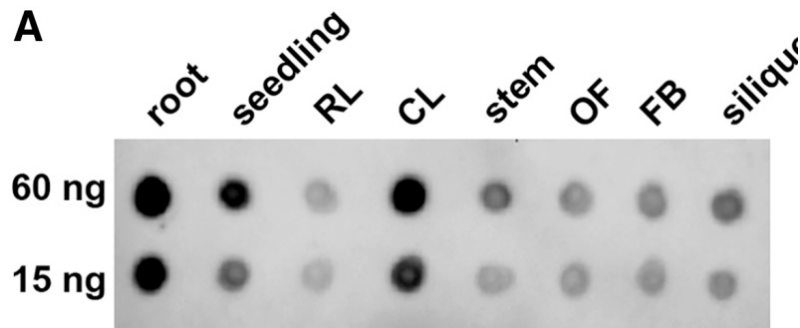
N⁶-Methyladenine DNA Modification in *Drosophila* **2015 Cell**



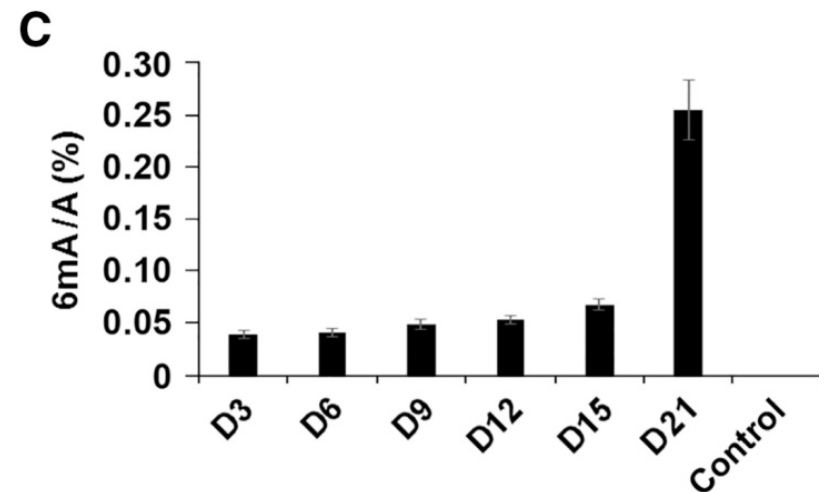
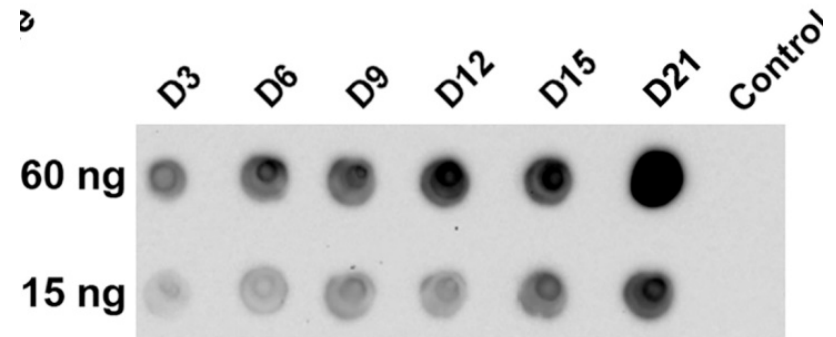
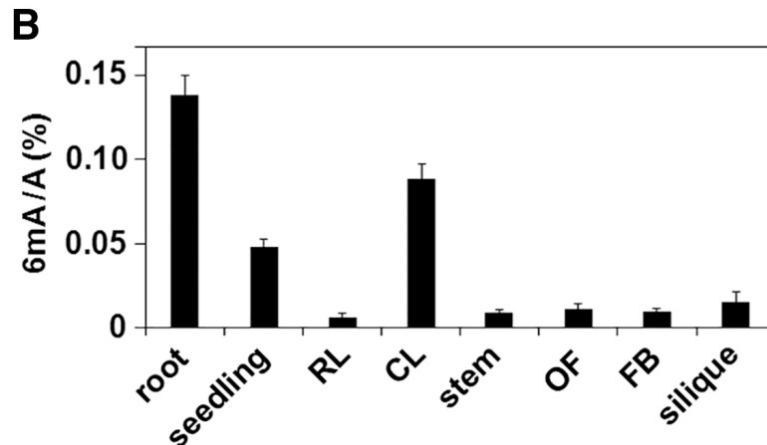
?

6mA modification in *Arabidopsis* Genome

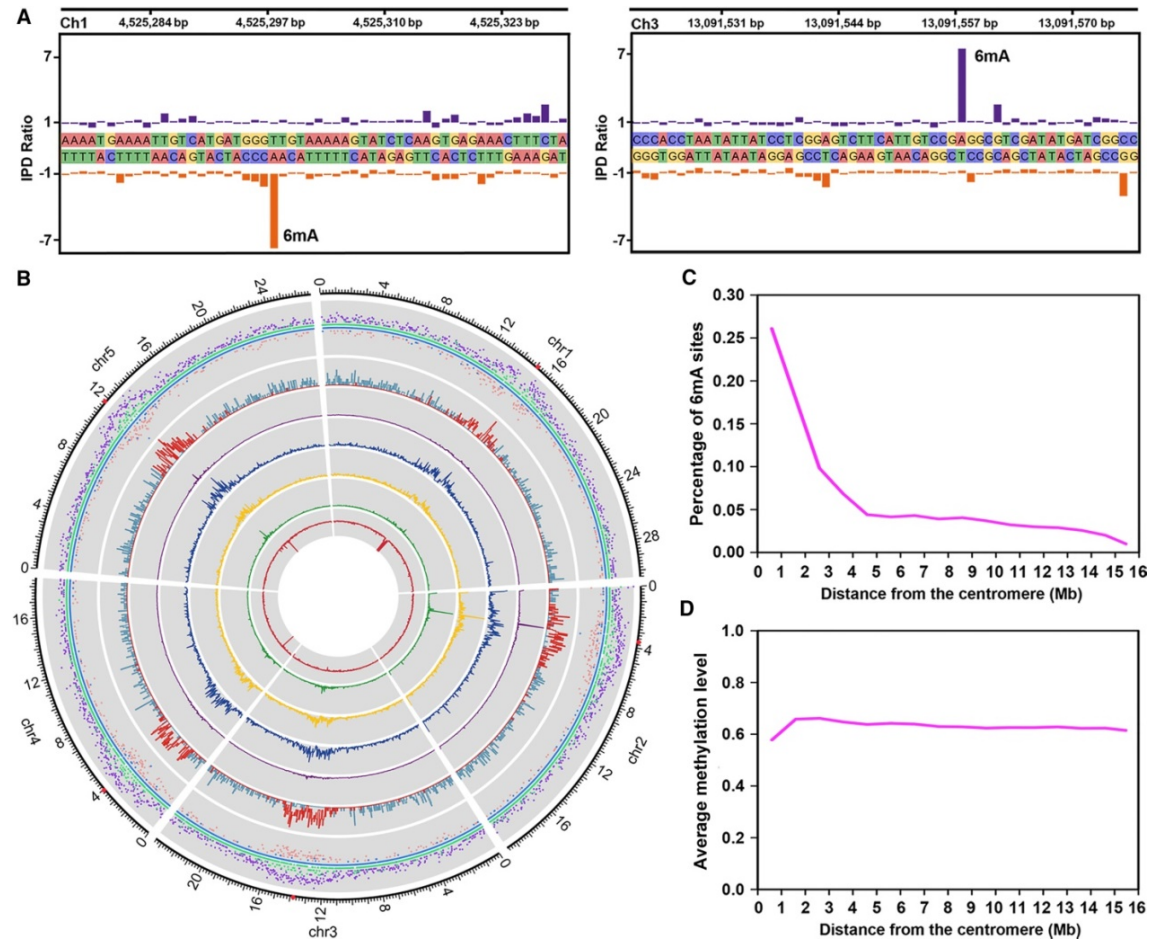
Dot-Blot



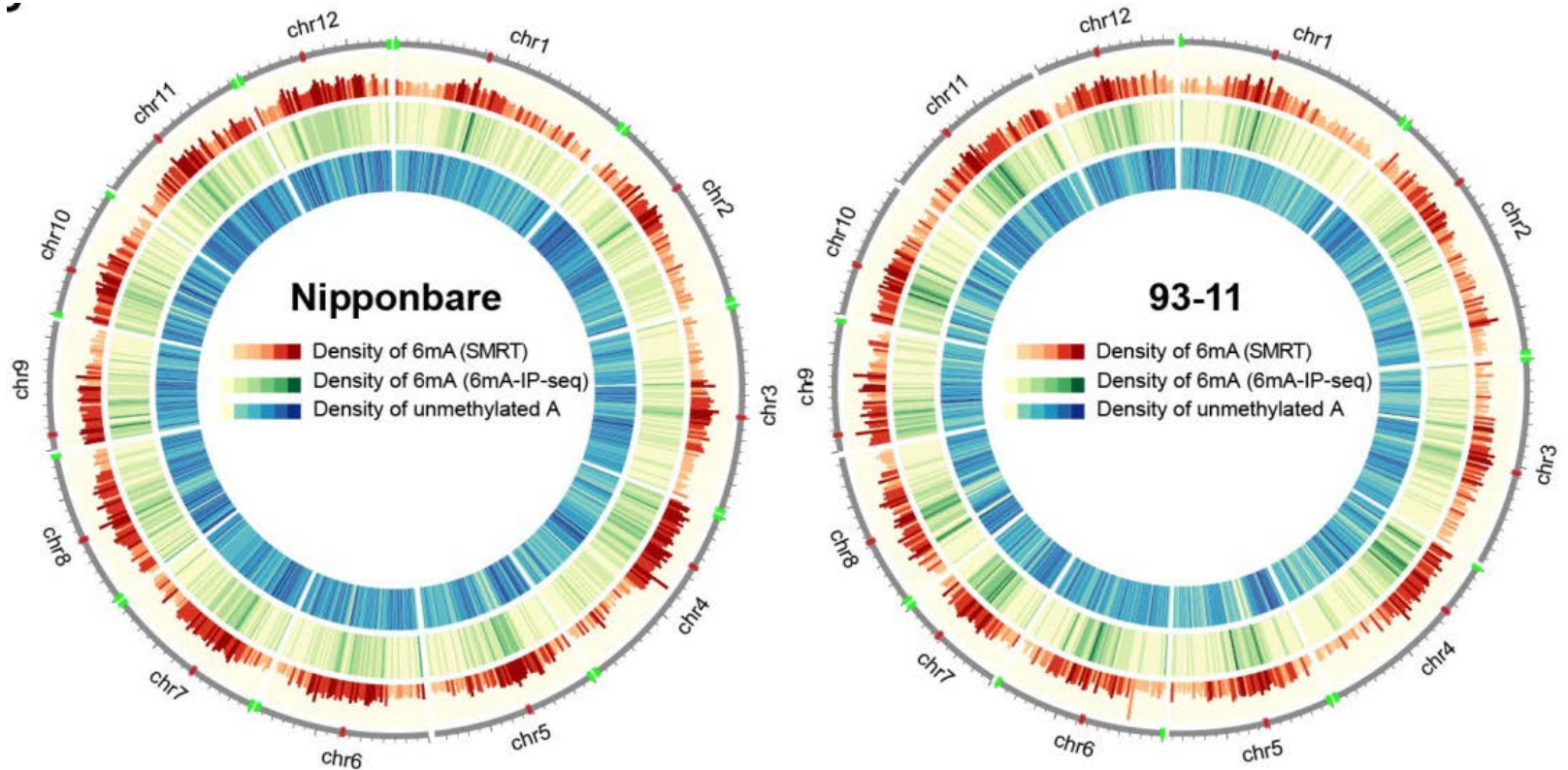
LC-MS/MS



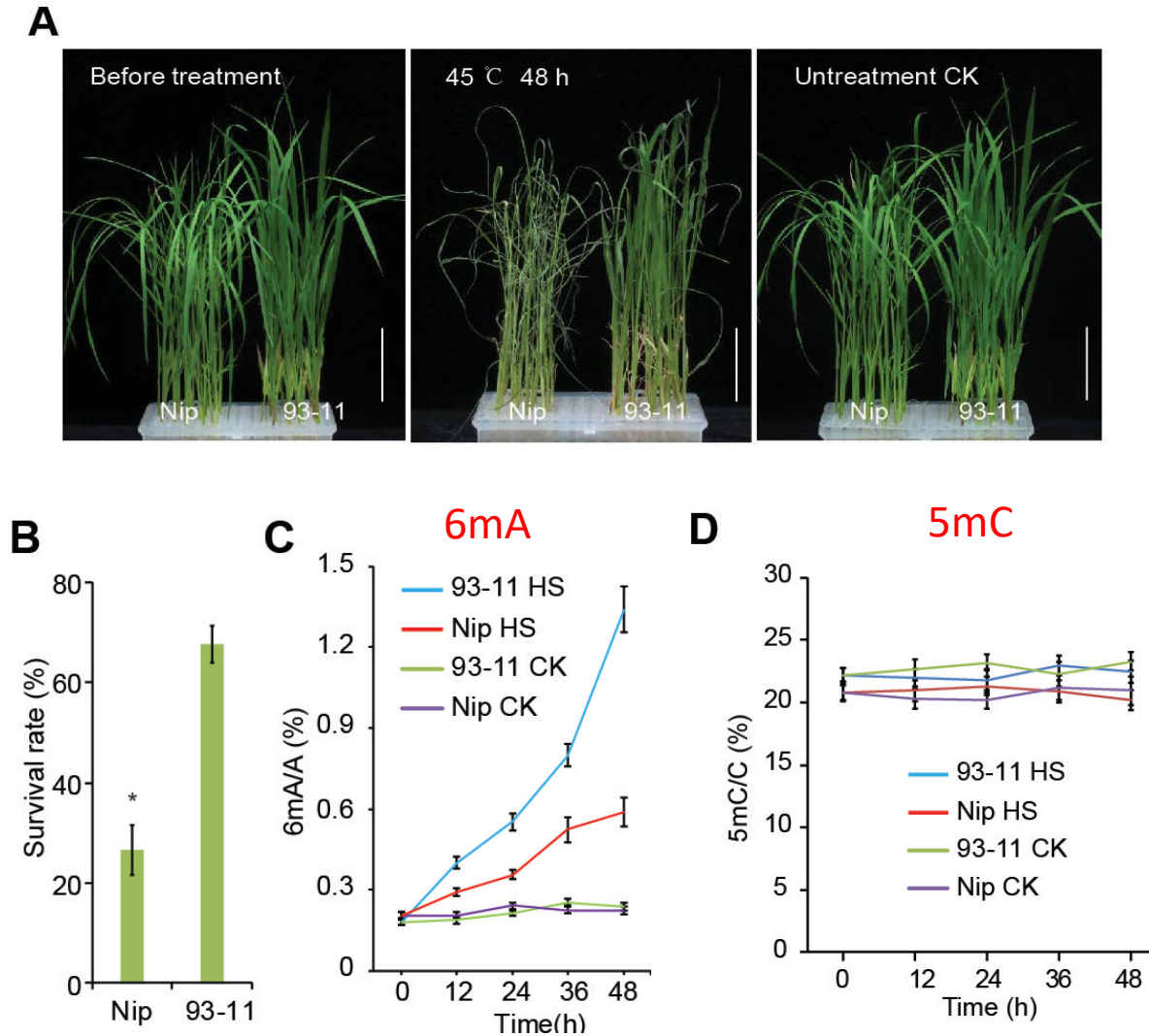
Strand-Specific Map of 6mA in *Arabidopsis*

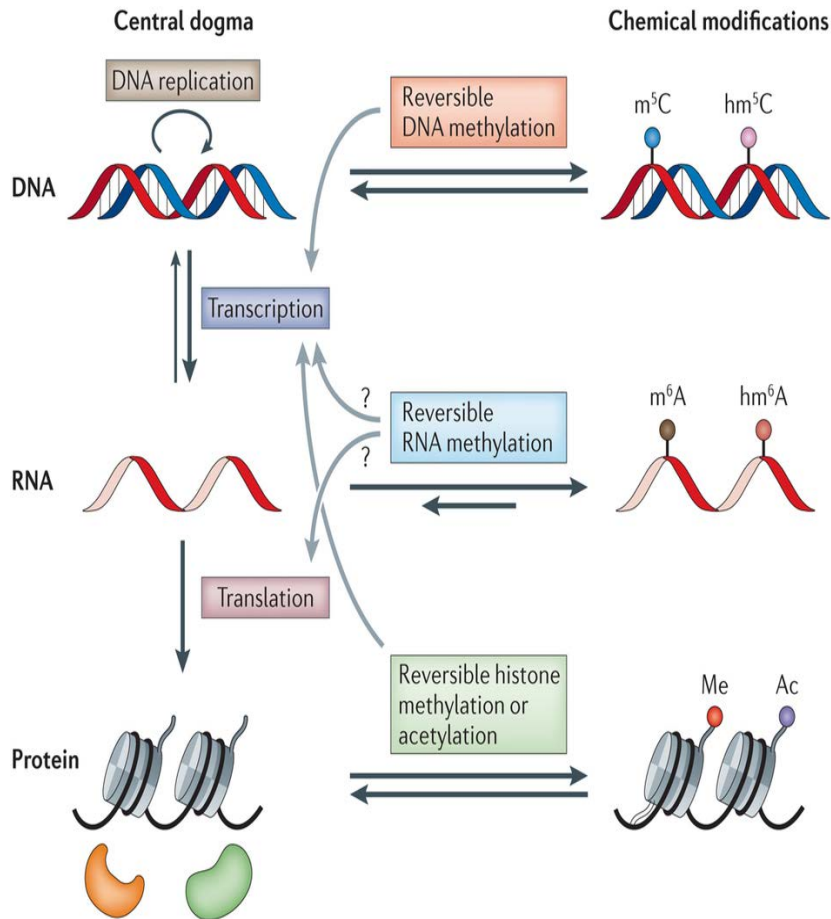


Widespread 6mA Methylation in Rice



植物温度响应的表观遗传调控机制

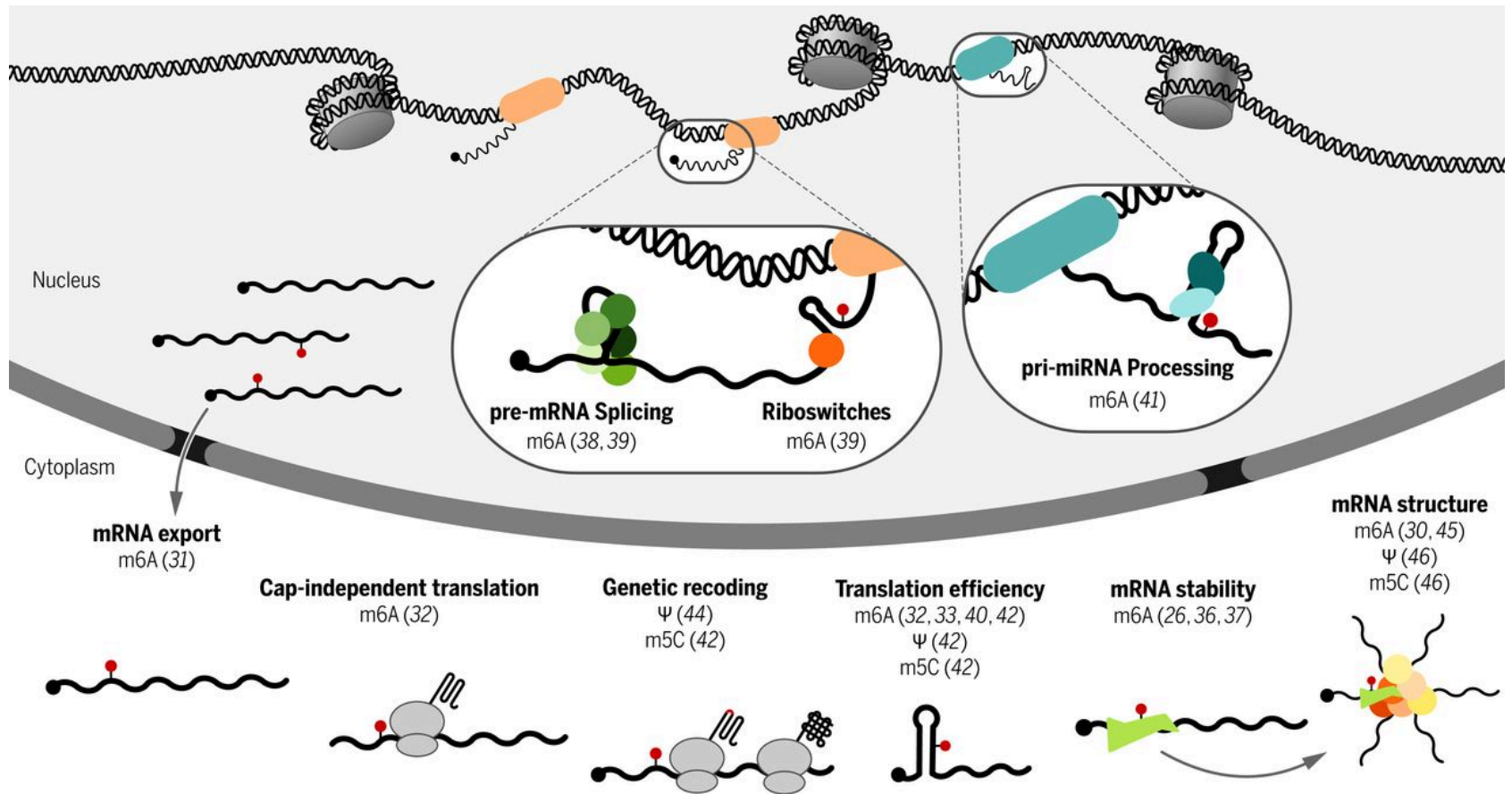




- DNA Methylation
- RNA Methylation
- Histone Modification
- nc RNA
- Chromo remodeling

Fu et al., 2014, *Nat Rev Genet*

Diverse molecular functions of m6A, Ψ, and m5C in coding RNAs.

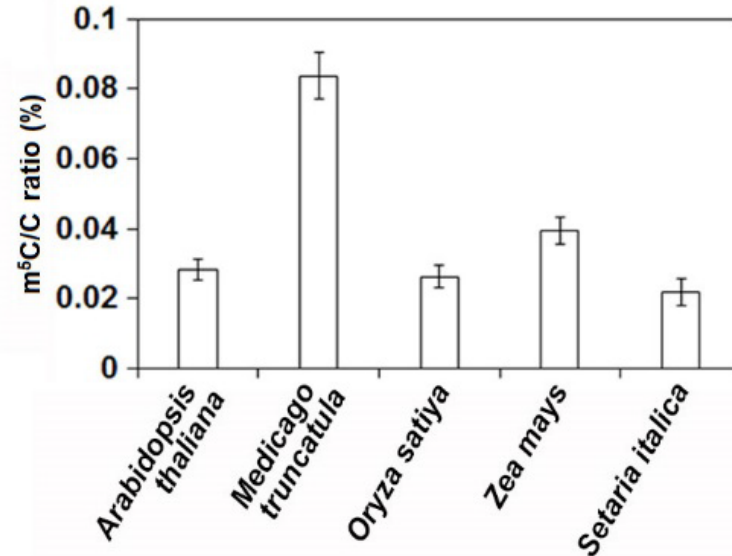
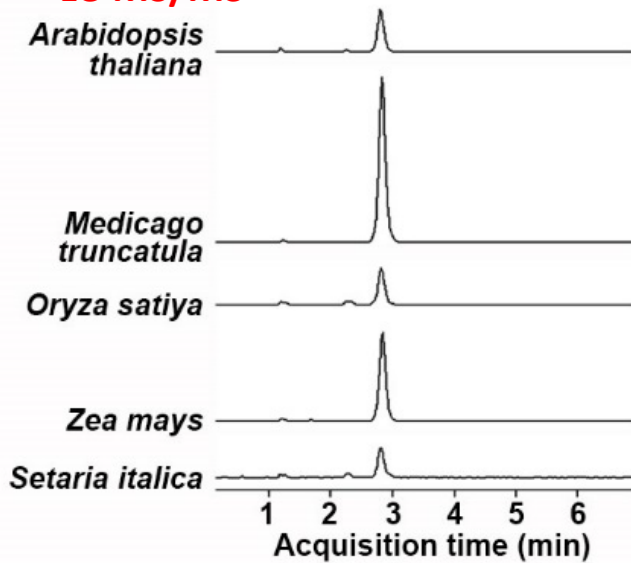


植物mRNA m5C甲基化检测

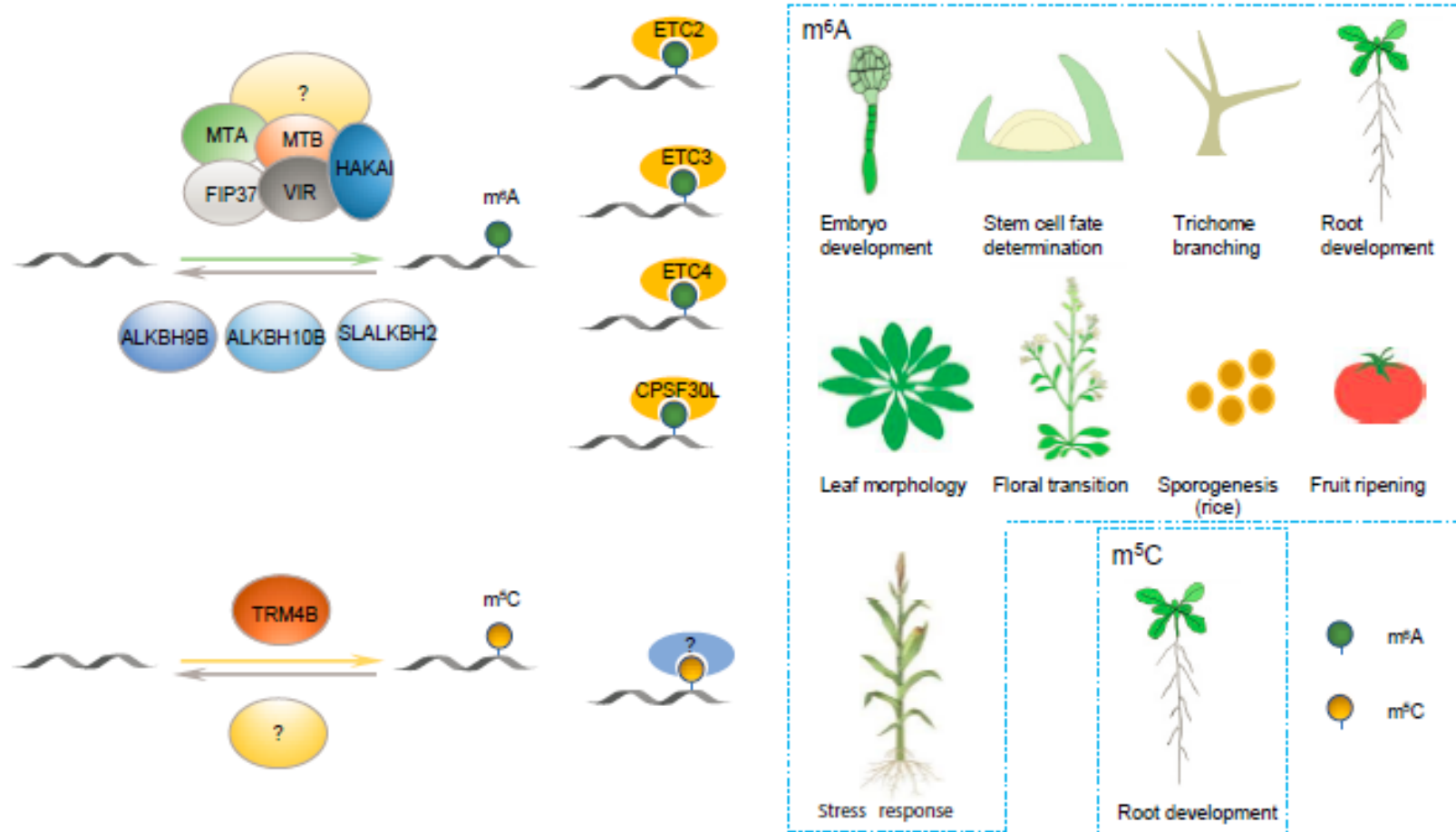


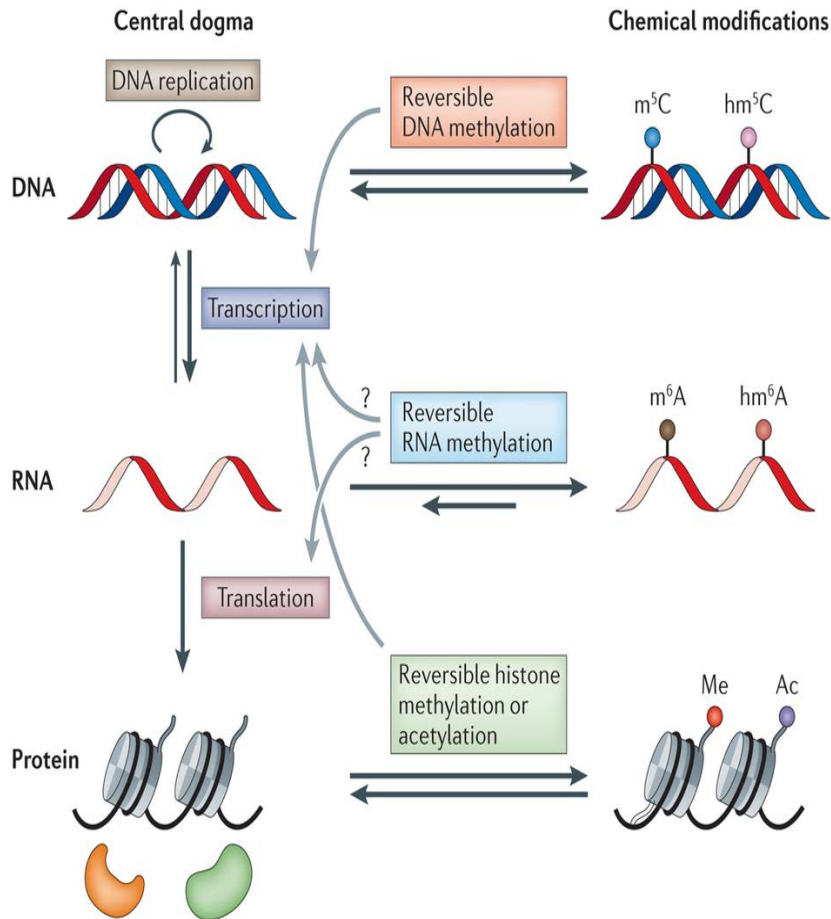
From Website

LC-MS/MS



RNA 甲基化调控植物发育和胁迫性

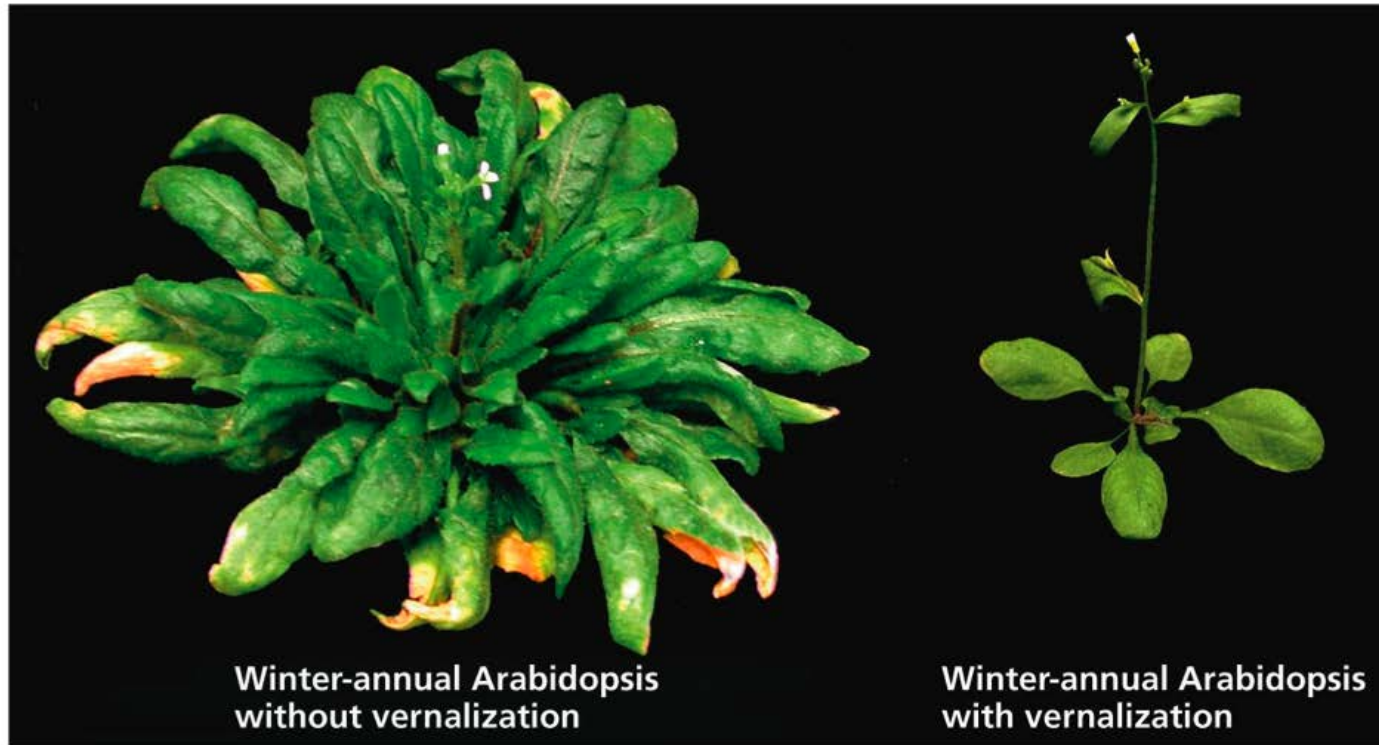




- DNA Methylation
- RNA Methylation
- **Histone Modification**
- nc RNA
- Chromo remodeling

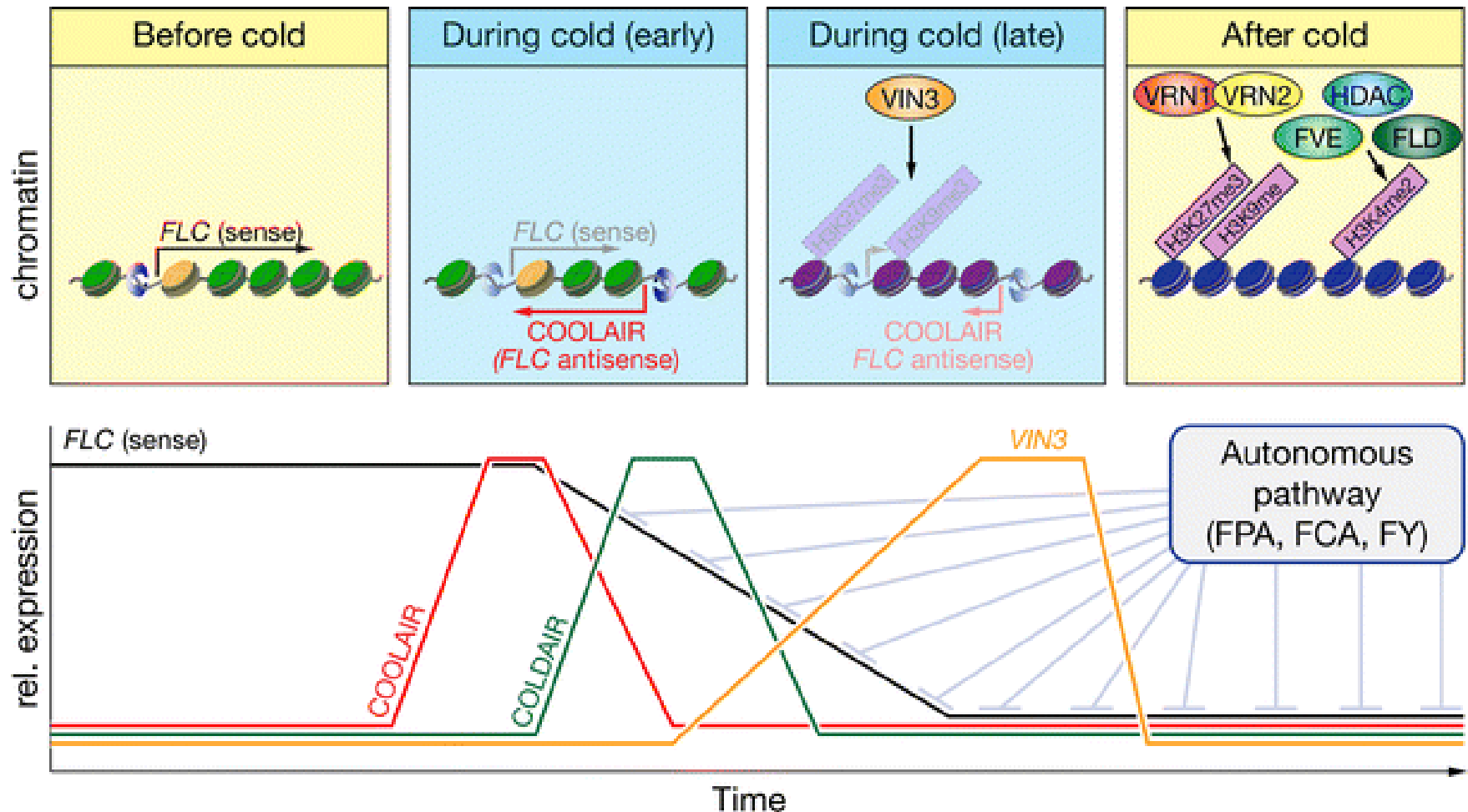
Fu et al., 2014, *Nat Rev Genet*

春化作用是指某些植物必须经历一段时间的持续低温，才能由营养生长阶段转入生殖阶段生长的现象。



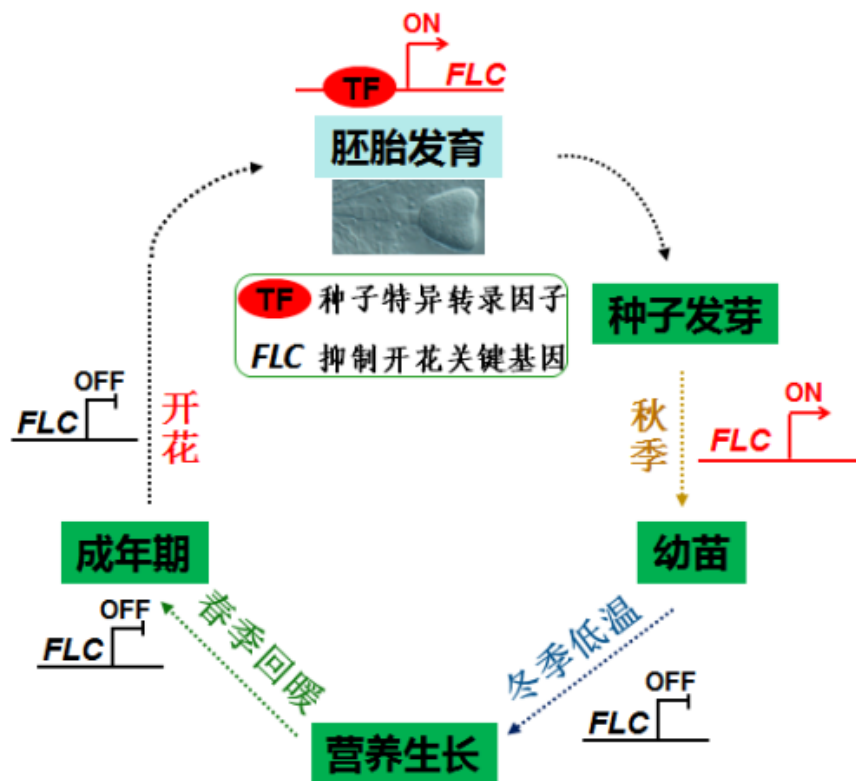
植物如何响应并记忆长时间的低温处理即春化作用一直是表观遗传学和发育生物学研究的热点。

FLC表达响应季节变化的表观遗传调控机制



Vernalization leads to the stable repression of *FLC* by a plant PcG mechanism that results in increased abundance of H3K27me3 at the *FLC* locus.

组蛋白甲基化调控越冬植物“春化作用”



Nature Plant, 2016

Nature Genetics, 2016

Nature, 2017

Plant Journal, 2018

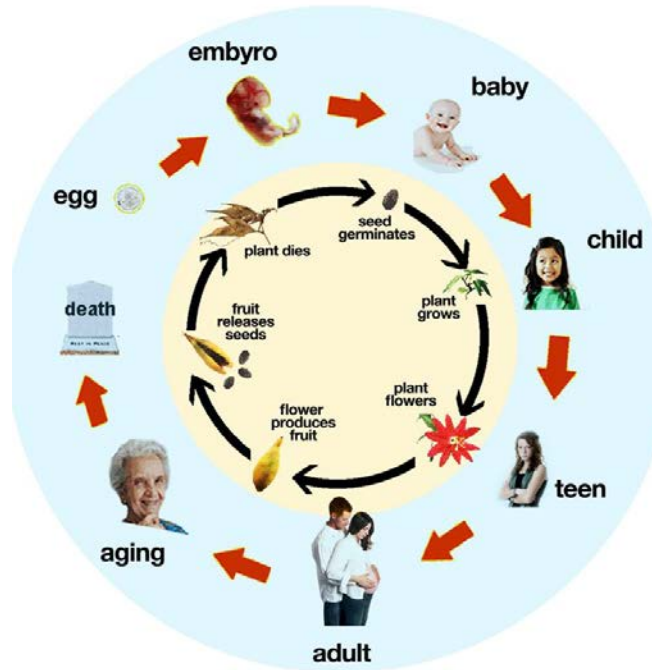
Nature Genetics, 2018

Nature Plant, 2018

Molecular Plant, 2019

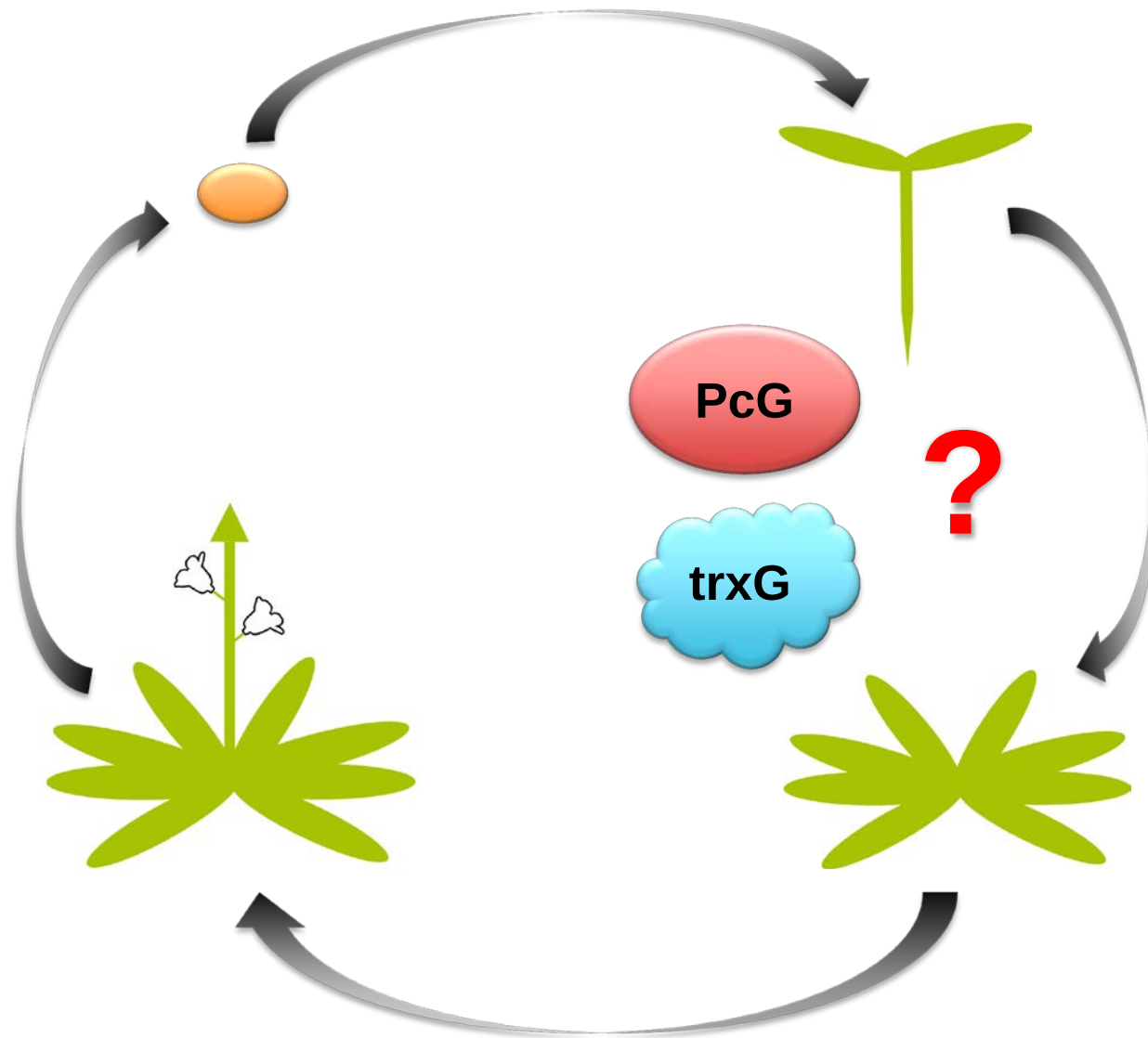
Nature Plant, 2019

“这项研究不仅具有重要的理论意义，同时也为其在作物花期调控的生产应用提供了新的作用靶点。将研究结果运用到农作物生产上，能提升农作物种子产量，对季节性花卉的培育也有重要意义。”



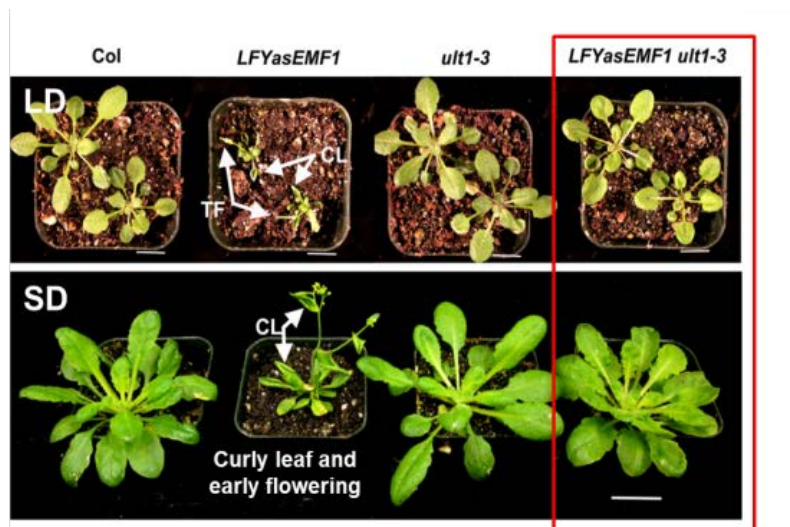
- 无论植物、动物还是人类，生长发育都是从胚胎发生
- 各个时期都按照遗传学上设定的标准和程序进行
- 每个时期都占有一生的某一部分、都有它自己特定的外形和功能特征
- **基因组一致**

生长发育在时间和空间上如何被精确地调控？

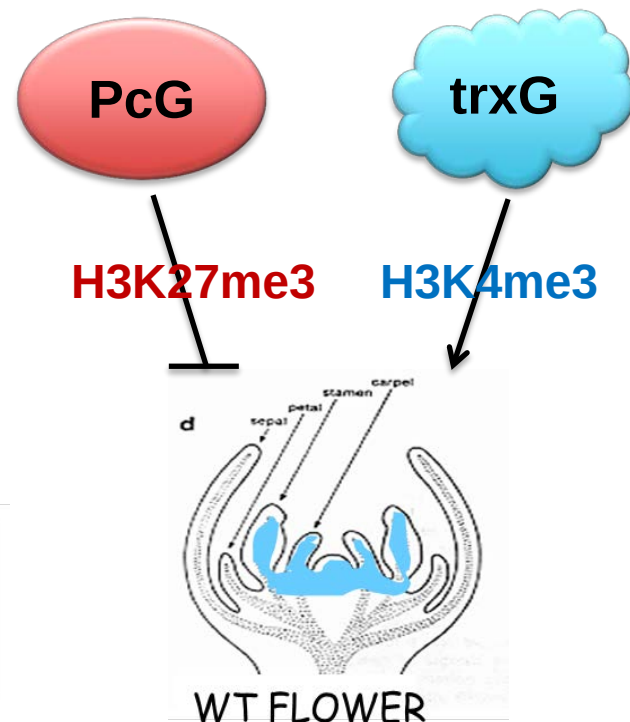
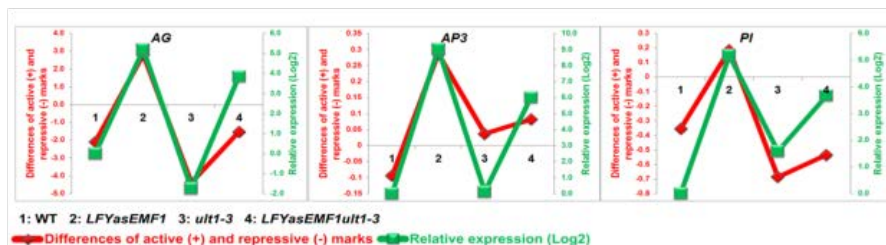


组蛋白甲基化的动态平衡确保植物处于正常的营养生长期

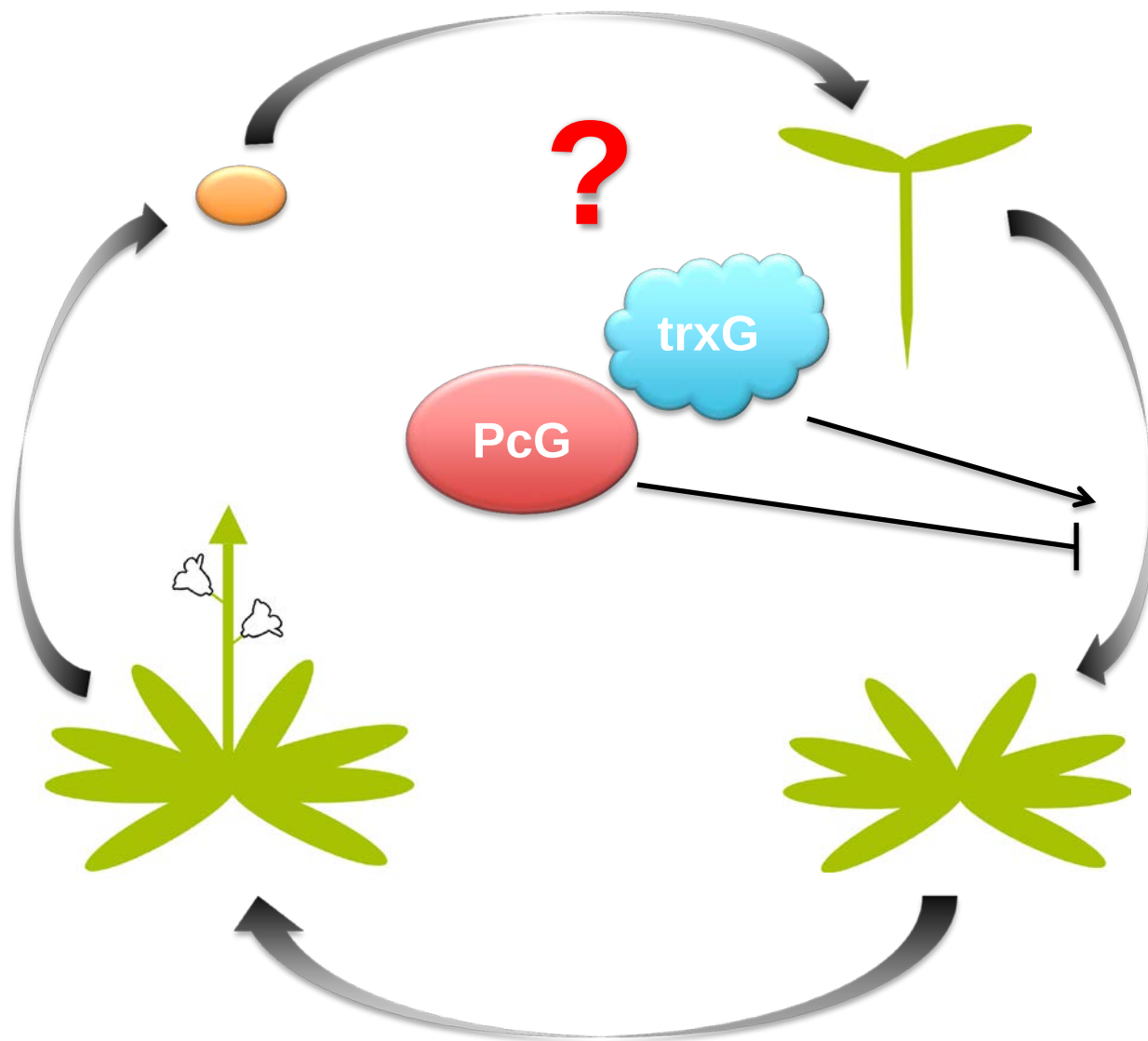
ULT1突变回复由于EMF1突变造成的早花和卷叶表型。



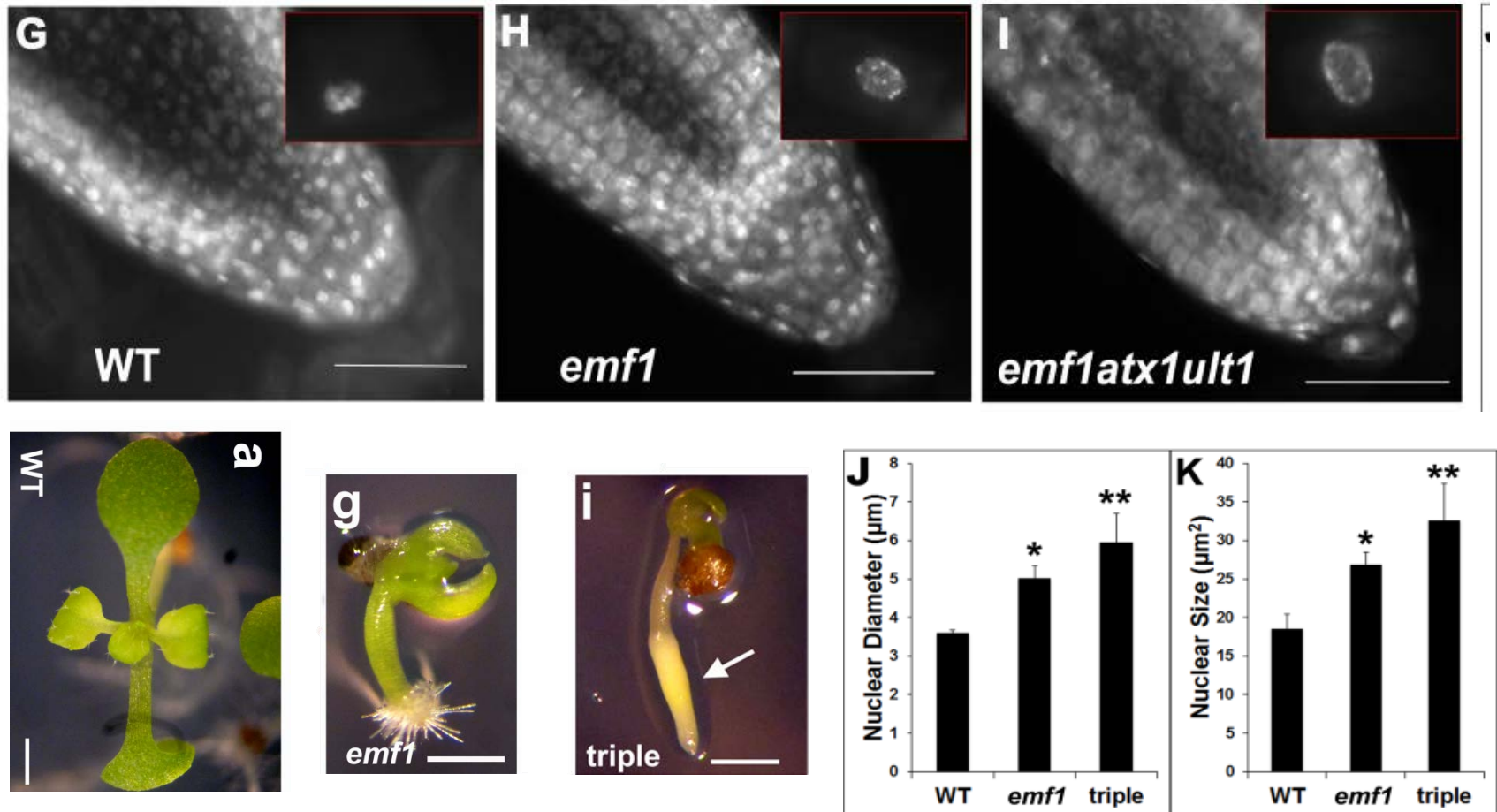
花发育基因的表达和高H3K4me3、低H3K27me3水平密切相关。



花器官发育基因: AG, AP1, AP3, PI, SEP1, SEP2, SEP3
开花基因: FLC, FT, AGL, SPL3, SPL4, TFL, CO

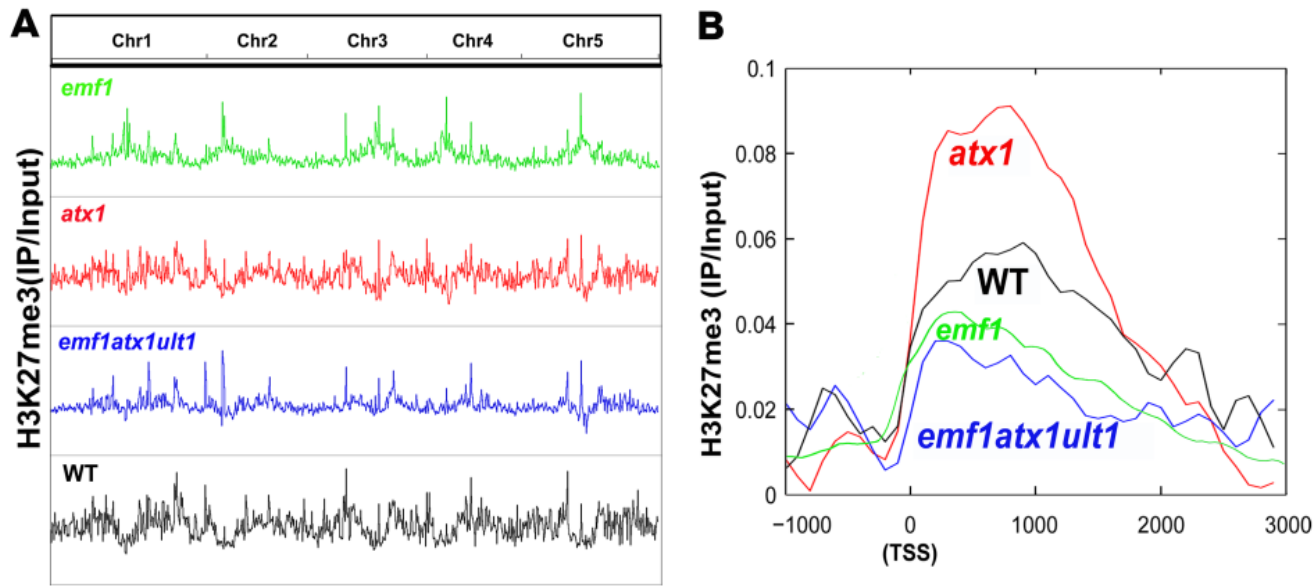


组蛋白甲基化影响染色体动态结构

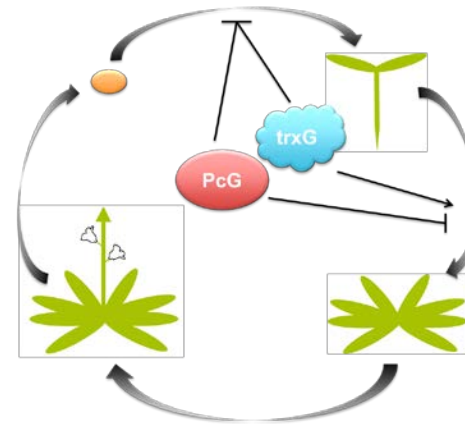
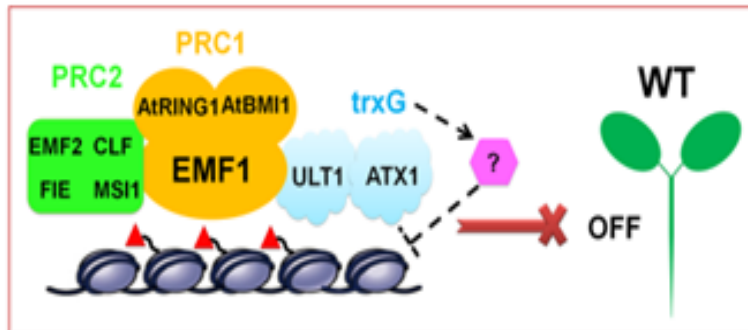


The nuclear diameter and size was significantly increased in the triple mutants compared to WT.

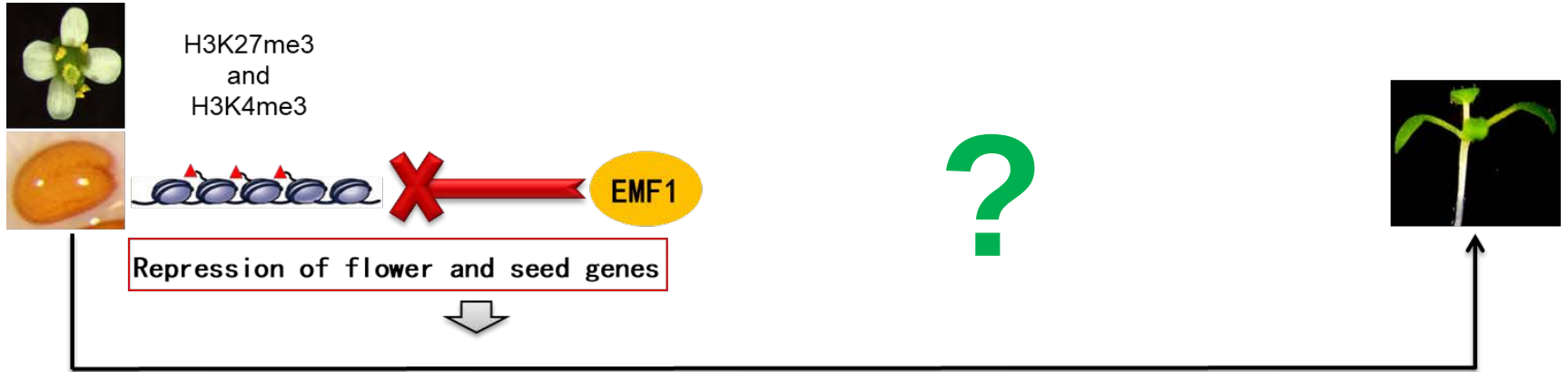
组蛋白甲基化（H3K27me3）调控苗期的正常生长



联合抑制种子发育基因：ABI3，LEC1，LEC2，LTP



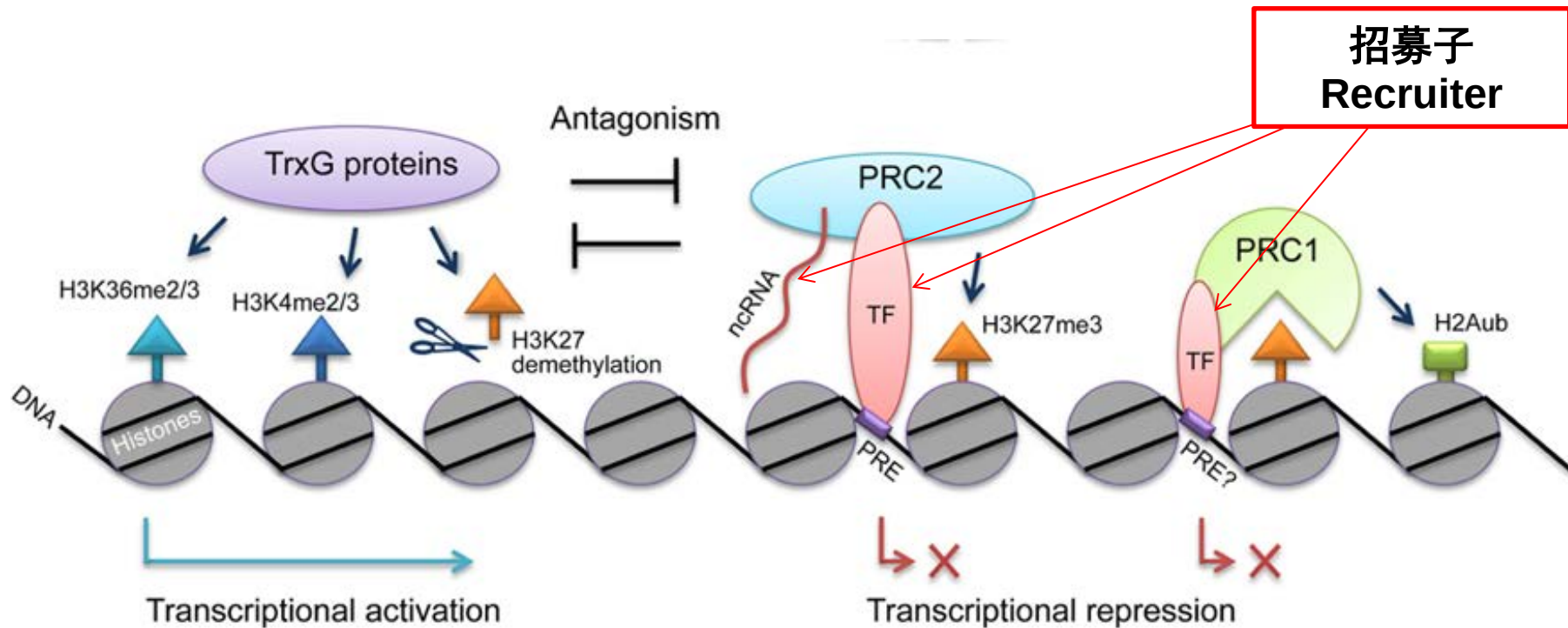
Moon et al., 2003
Myriam et al., 2008
Kim et al., 2010, 2012
Pu et al., 2013, 2015



种子萌发后:

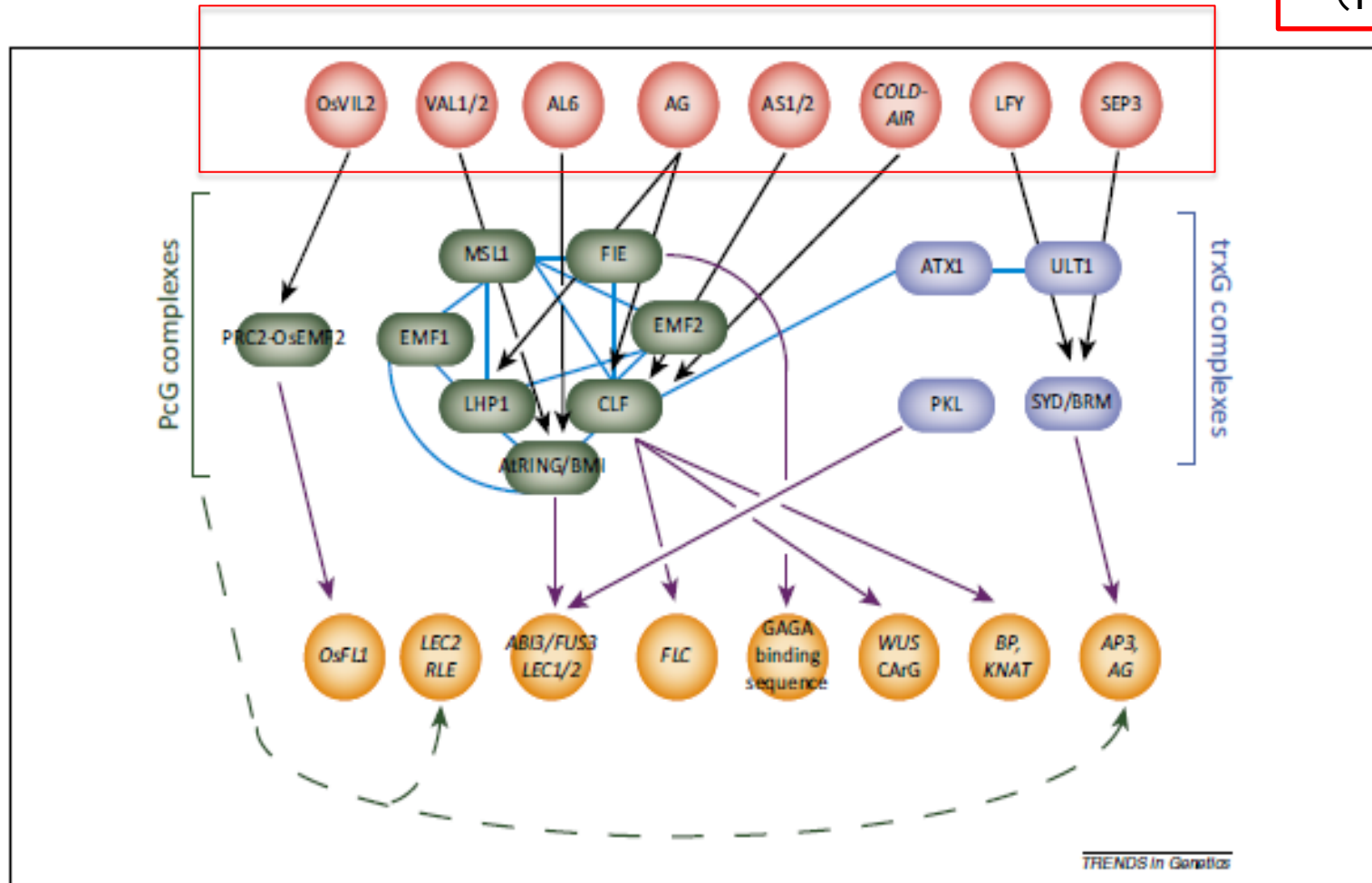
1. 抑制: 种子发育程序, 花发育程序
2. 促进: 叶绿体发育, 光合作用, 能量积累

表观遗传调控模块： Recruiter, Writer, Reader, Eraser



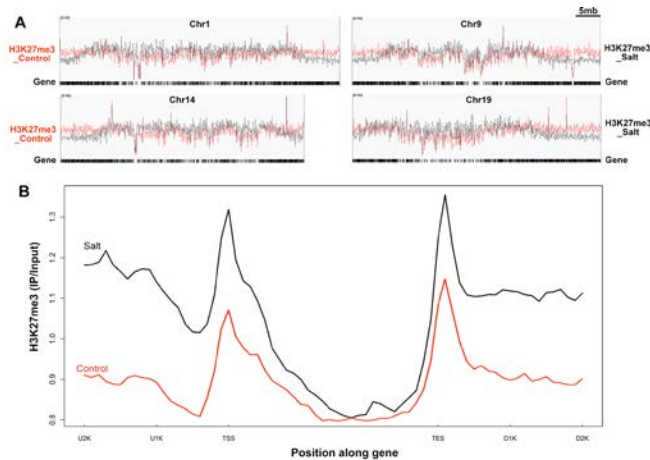
植物特异的招募子？

招募子
(Recruiter)

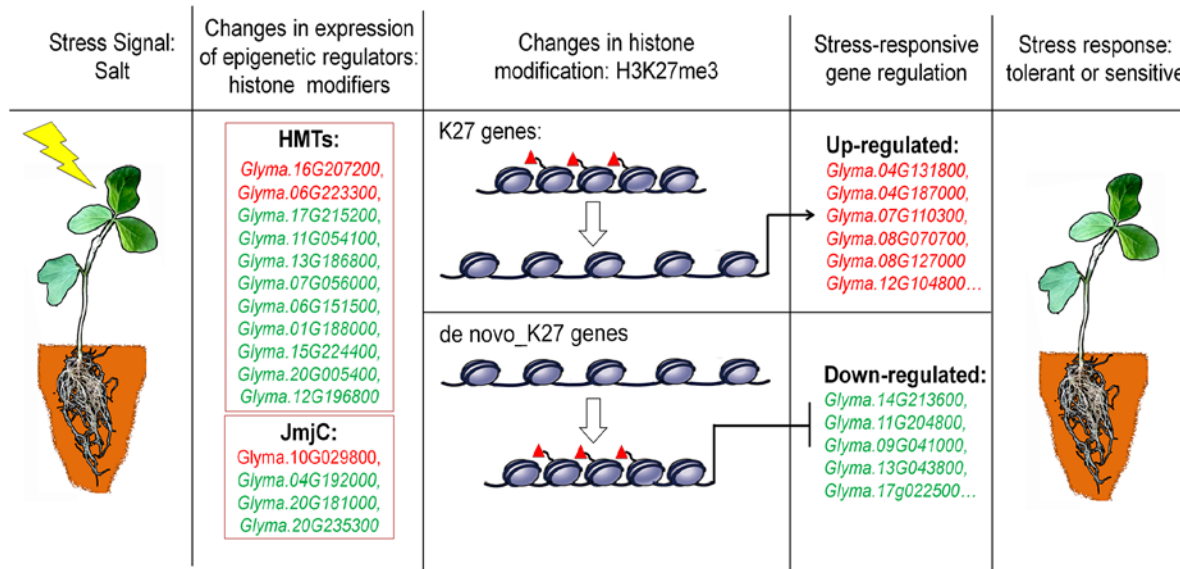


(Pu and Sung., 2015)

环境适应性的组蛋白甲基化调控机制



- 绘制了大豆组蛋白甲基化全基因组图谱
- 揭示了作物响应环境信号的调控机制
- 鉴定了表观遗传调控回路元件和模块



Pu *et al.*, 2013
 Sun *et al.*, 2019
 Yu *et al.*, 2020

- I. 表观遗传学概念以及发展历史
- II. 表观遗传学研究进展
- III. 表观遗传智能设计育种技术

Epigenetics and crop improvement

Nathan M. Springer

Microbial and Plant Genomics Institute, Department of Plant Biology, University of Minnesota, Saint Paul, MN 55108, USA

CellPress
PARTNER JOURNAL

Molecular Plant
Review Article

Crop Epigenomics: Identifying, Unlocking, and Harnessing Cryptic Variation in Crop Genomes

Lexiang Ji^{1,2,3}, Drexel A. Neumann^{1,3} and Robert J. Schmitz^{1,*}

Review

Epigenetics for Plant Improvement: Current Knowledge and Modeling Avenues

Philippe Gallusci,^{1,8,*} Zhanwu Dai,^{1,8,*} Michel Génard,²
Arnaud Gauffretau,³ Nathalie Leblanc-Fournier,⁴
Céline Richard-Molard,⁵ Denis Vile,⁶ and
Sophie Brunel-Muguet^{7,8,*}

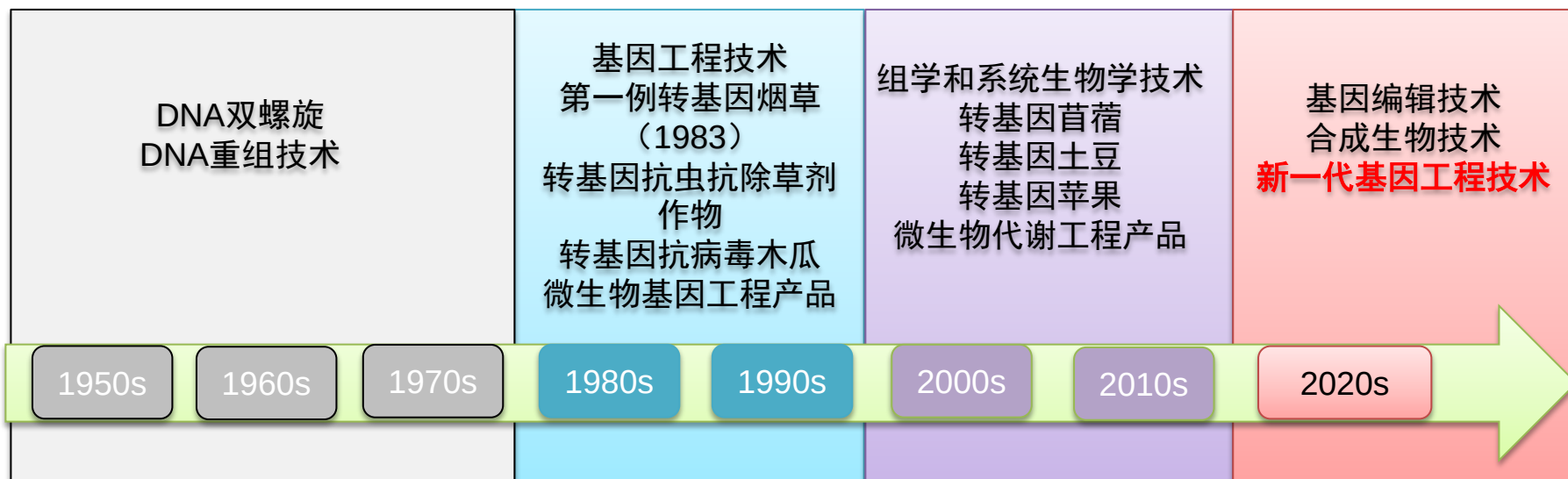
REVIEWS



Exploiting induced and natural epigenetic variation for crop improvement

Nathan M. Springer¹ and Robert J. Schmitz²

新一代基因工程技术引领现代农业发展



当前，随着生物组学、系统生物学和合成生物学等前沿学科高度交叉融合并不断取得重大突破，**推动新一代农业基因工程技术更加精确、定向和智能。**

Targeted DNA demethylation *in vivo* using dCas9–peptide repeat and scFv–TET1 catalytic domain fusions

Targeted DNA demethylation of the *Arabidopsis* genome using the human TET1 catalytic domain

Javier Gallego-Bartolomé^{a,1}, Jason Gardiner^{a,1}, Wanlu Liu^{a,b,1}, Ashot Papikian^{a,c,1}, Basudev Ghoshal^a, Hsuan Yu Kuo^a, Jenny Miao-Chi Zhao^a, David J. Segal^d, and Steven E. Jacobsen^{a,e,2}

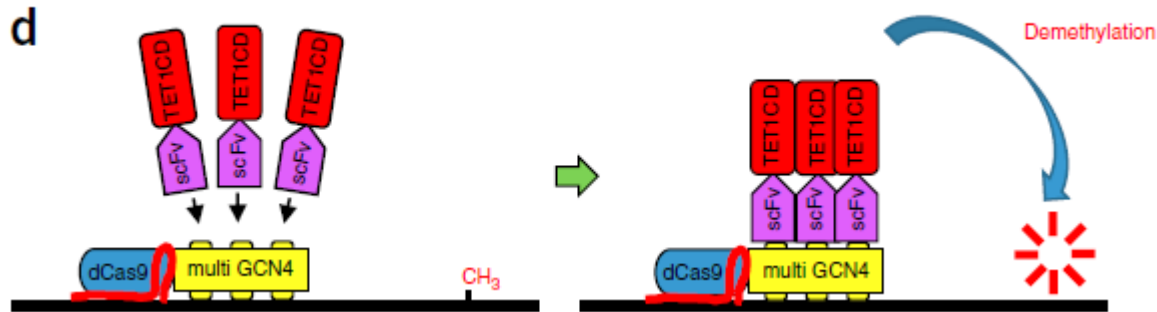
ARTICLE

DOI: 10.1038/s41467-018-03289-7

OPEN

TET-mediated epimutagenesis of the *Arabidopsis thaliana* methylome

Lexiang Ji¹, William T. Jordan², Xiuling Shi², Lulu Hu^{3,4,5}, Chuan He^{3,4,5} & Robert J. Schmitz²



“Finally, we have developed a CRISPR/dCas9-based targeted demethylation system using the TET1cd and a modified SunTag system. Similar to the ZF–TET1cd fusions, the SunTag–TET1cd system is able to target demethylation and activate gene expression when directed to the *FWA* or *CACTA1* loci. Our study provides tools for targeted removal of 5mC at specific loci in the genome with high specificity and minimal off-target effects”.

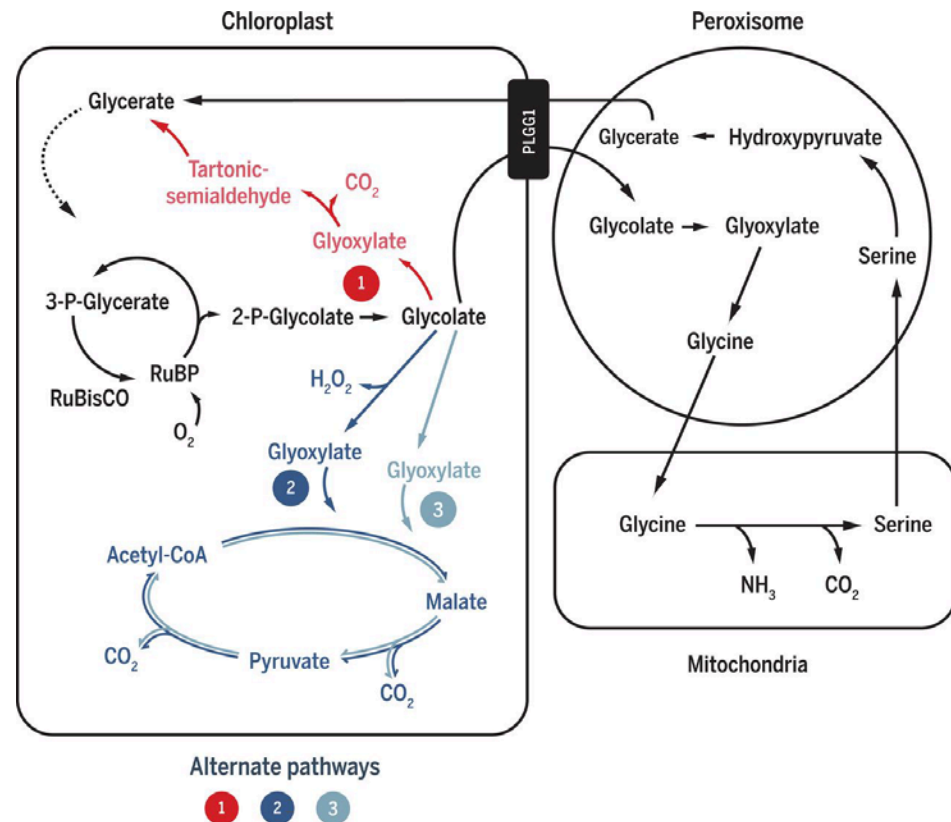
Synthetic glycolate metabolism pathways stimulate crop growth and productivity in the field

人工设计“光呼吸”路径的高光效烟草



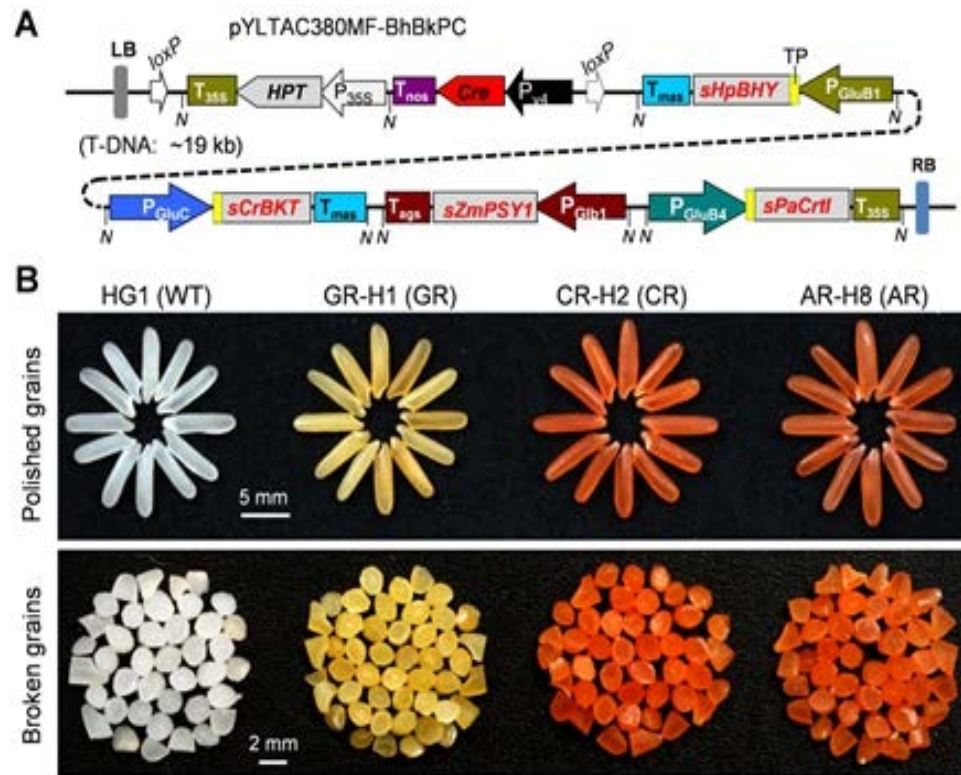
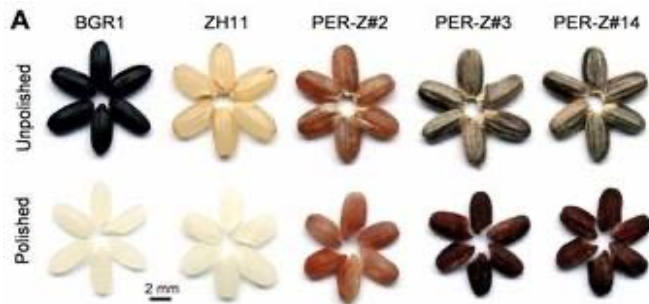
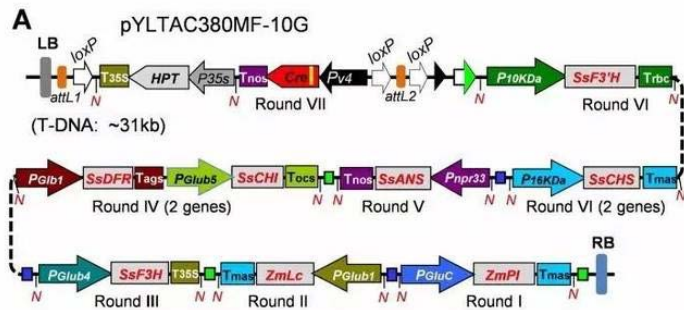
经合成生物技术改造缩短“光呼吸”路径的烟草生长更快、更高、茎部更粗大，比对照多产出40%的生物量。研究人员将尝试改造水稻、大豆、马铃薯、西红柿、茄子等农作物。

South *et al.*, *Science* **363**, eaat9077 (2019)



伊利诺伊大学研究人员人工设计出3条额外的“光呼吸”替代路径，大大缩短了“光呼吸”原本迂回复杂的反应路径。

合成生物学创制水稻新种质



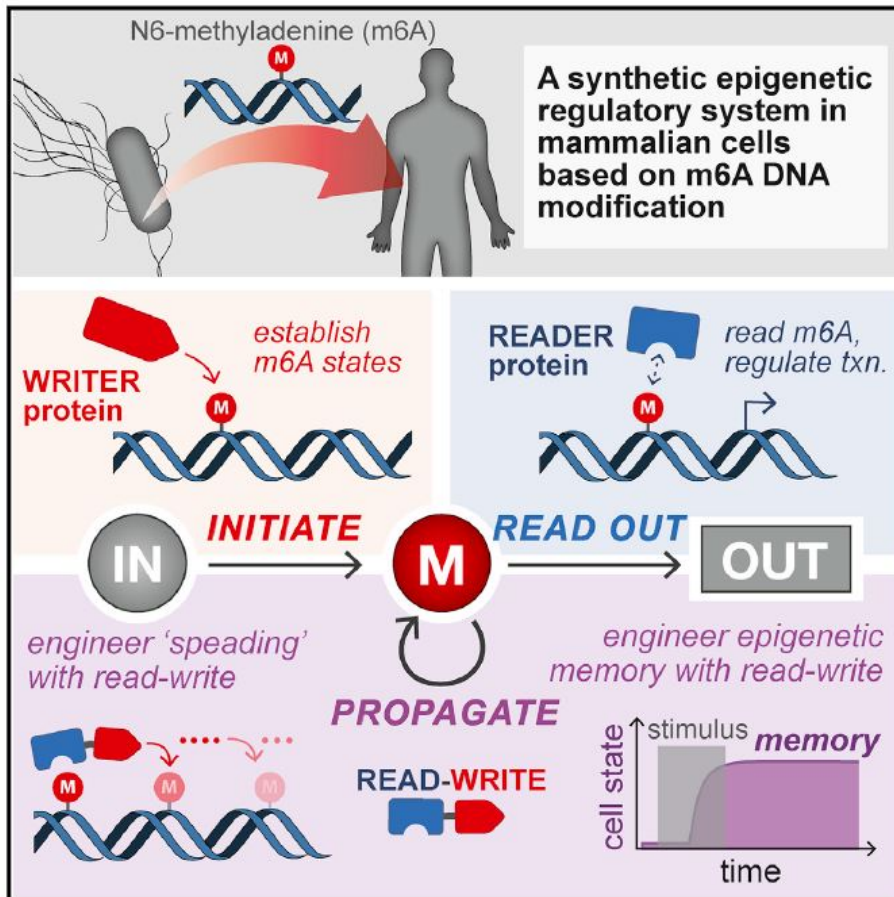
胚乳富含花青素的水稻新种质 “紫晶米”

胚乳富含虾青素的水稻新种质 “赤晶米”

Zhu et al, 2017, 2018, Molecular Plant

Engineering Epigenetic Regulation Using Synthetic Read-Write Modules

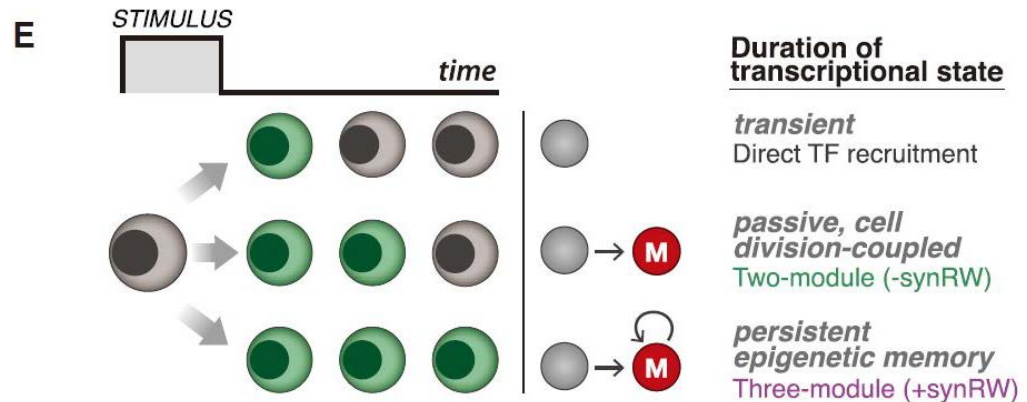
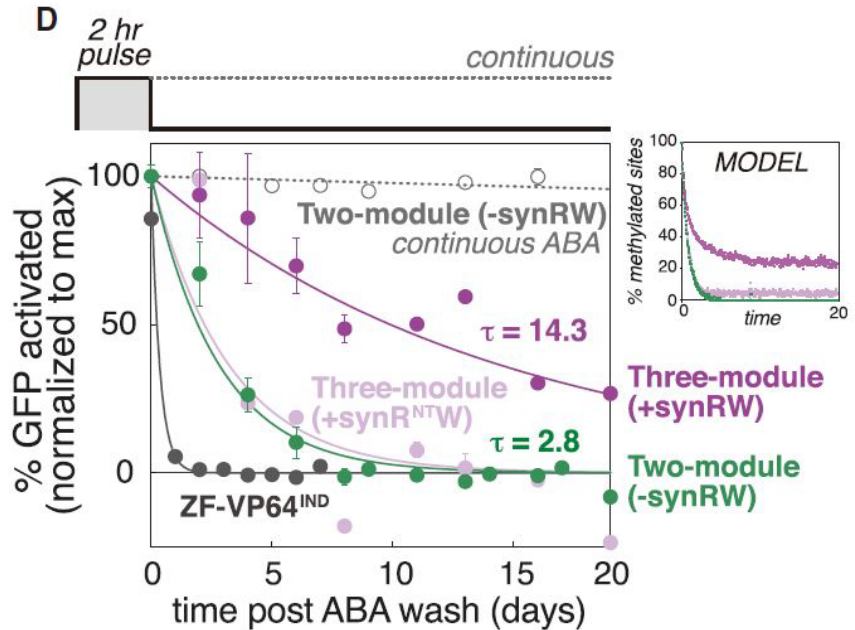
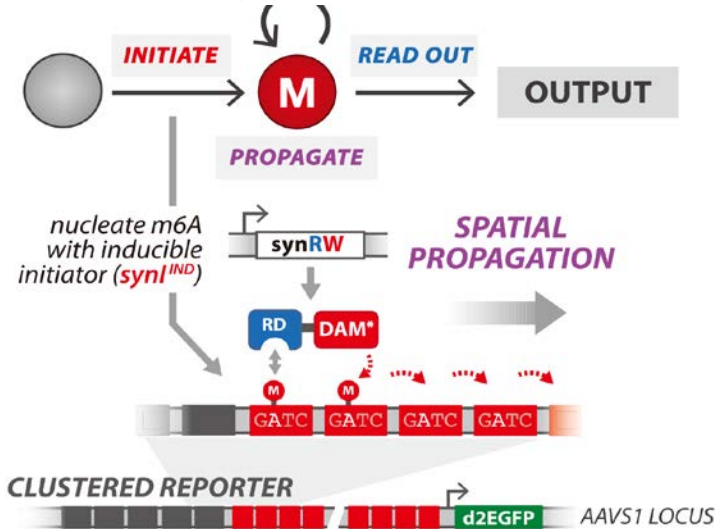
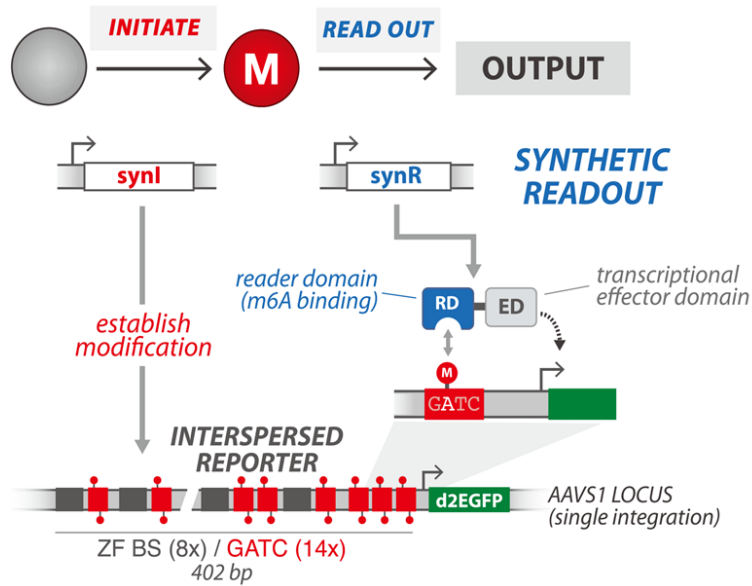
利用人工合成的“编写器和阅读器”调控表观遗传学



- 利用 DNA 6mA修饰在人类细胞中合成表观遗传调控系统
- 利用工程化的6mA“编写器(Writer)和阅读器(Reader)”构建调控回路
- Read-Write回路驱动表观修饰标记沿染色质进行传播
- Read-Write回路可以形成转录状态的表观遗传记忆

Highlight: 利用合成生物学的方法, 开发了可以从头建立和驱动表观遗传学系统。

三大模块(SynI+SynR+SynRW)组成调控回路 —产生表观遗传记忆



Review

Retrospective and perspective of plant epigenetics in China

Cheng-Guo Duan ^{a,*}, Jian-Kang Zhu ^{a,b,*}, Xiaofeng Cao ^{c,*}

REVIEW

National Science Review

3: 309–327, 2016

doi: 10.1093/nsr/nww042

MOLECULAR BIOLOGY & GENETICS

Special Topic: Rice Breeding



Epigenetic regulation and epigenomic landscape in rice

Xian Deng¹, Xianwei Song¹, Liya Wei^{1,2}, Chunyan Liu¹ and Xiaofeng Cao^{1,*}

REVIEW

Epigenomic landscape and epigenetic regulation in maize

Jia Yu¹ · Fan Xu¹ · Ziwei Wei² · Xiangxiang Zhang¹ · Tao Chen³ · Li Pu¹

水稻表观遗传数据库推进智能育种

eRice database

eRice
Rice Epigenetic & Epigenomic Database

HOME Gene Annotation BLAST Multi-JBrowse DNA Methylation 6mA AI Predictor Download

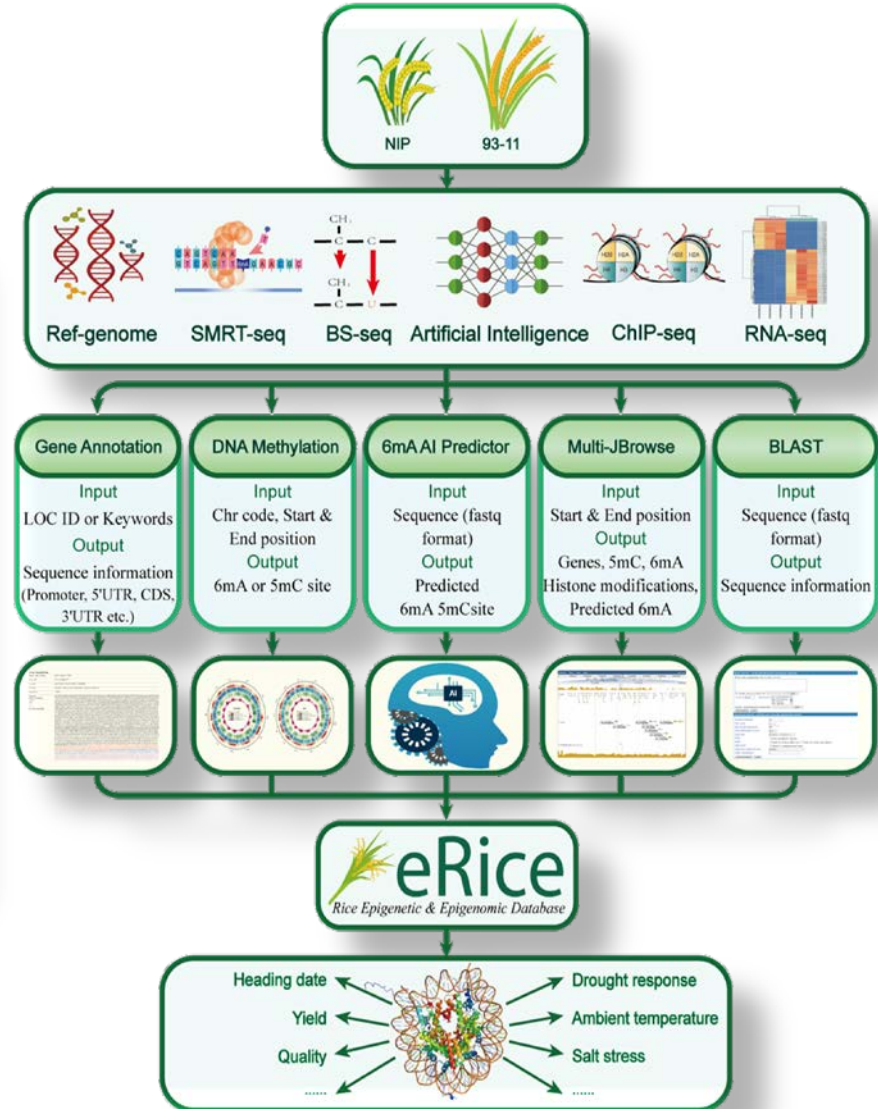
Welcome to eRice

News
 August 3, 2019
Improved eRice website design.
 May 1, 2019
Improved Genome Annotation
 March 25, 2019
Update 6mA AI Predictor.
 January 29, 2019
eRice v1.0 is online.
 November 17, 2018
A paper describing DNA 6mA methylation in rice and its association with gene expression, plant development and stress responses has been published on Molecular Plant.
 August 14, 2018
A review paper summarizing DNA 6mA methylation and RNA m6A in plant has been published on Molecular Plant.
 May 8, 2018
A paper describing DNA 6mA methylation in Arabidopsis thaliana has been published on Developmental Cell.

Rice Epigenomic & Genomic Annotation

Epigenetic marks played an essential role in various pathways, including transcription regulation, DNA replication and repair, development and differentiation as well as response to environmental factors. Thanks to single-molecule real-time (SMRT) sequencing, recent discovery of DNA N6-methyladenosine (6mA) methylation provided new insights into altering the activities and functions of developmental signals and stress responses.

In rice (*Oryza sativa*), genome-wide 6mA distribution at single-nucleotide resolution has been reported in two main and parental cultivars (Nipponbare, japonica group; 93-11, indica group), which were regarded as reference genomes of japonica and indica groups. Here, we have developed a species-specific epigenomic database, eRice (an Epigenomic & Genomic Annotation Database for Rice), to facilitate efficient epigenomic studies for both japonica and indica groups.



(Zhang et al., 2019)

人工智能技术在表观组学大数据分析和预测上展现广阔的应用潜力

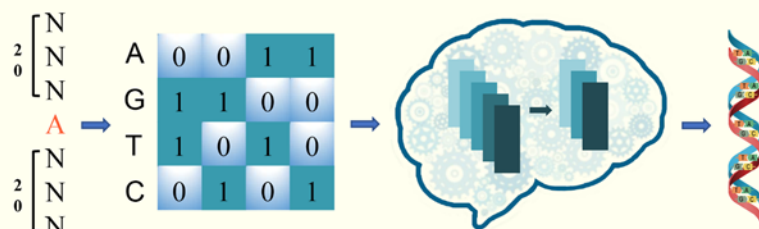


6mA Predictor Overview

Machine and deep learning approaches have been largely responsible for a recent paradigm shift in image and natural language processing, which are among the fundamental enablers of modern artificial intelligence advances such as facial recognition, speech recognition, and self-driving vehicles. These deep-learning methodologies have been applied to biology such as agriculture and genetics. Here, we first developed a deep learning models trained with previous released 6mA data for predicting and memorizing on both the motifs and the functional evolutionary history of 6mA in rice. With these deep learning of trained data, we tested 6mA in two Nip and 93-11 cultivars for predicting 6mA site from the whole rice genome region. The architectures will allow all rice researchers easily enquiry and predict the potential 6mA site on targeted genes or regions.

Type/Pater the gene sequence with the Fasta format below:

Predictor Reset



Component

Motif Search: Japonica group cultivar Nip Input keyword search Please entry the keyword

MOTIF	Logo	RC Logo	E-value	Type	Cultivar
DAGGYR			3.2e-17472	6mA	93-11
ANMGA			1.6e-5289	6mA	93-11
CATVYA			1.6e-2618	6mA	93-11
GAWGYA			1.5e-1684	6mA	93-11
TGRGTYR			5.7e-1052	6mA	93-11
GAKGYR			1.2e-13905	6mA	Nip
ANCBAA			2.2e-4890	6mA	Nip
AAGGYR			1.7e-2302	6mA	Nip
AAWBAK			1.4e-2185	6mA	Nip
CATRTR			3.0e-1268	6mA	Nip

(Zhang et al., 2019)

表观遗传智能设计育种

- 表观元器件的数据库
- 高效基因编辑技术
- 基因智能改造与定向表达体系
- 合成生物学技术手段

SMART Crop

Self-Monitoring, Adapted and Responsive Technology



- 整合不同胁迫响应回路，形成多种耐逆性
- 智能响应环境胁迫信号

致谢

Biotechnology Research Institute, CAAS

Haiyang Wang, Chunyi Zhang, Xiaofeng Gu,
Hao Lin, Lifang Niu, Tao Chen

Lab members: Fan Xu, WeiJun Guo, Jia Yu,
Daolei Zhang, Danyao Du, Yue Wu

Institute of Crop Sciences, CAAS

Jiaqiang Sun

Institute of Genetics and Developmental Biology, CAS

Yongboiao Xue, Zhukuan Cheng

Institute of Microbiology, CAS

Zhaosheng Kong

UC Berkeley

Renee Sung

Rosario Sanchez, Sang Yeol Kim

Yenny Rosali, Gilbert Garcia, Andrew Liu

Jennifer Fletcher

Purdue University

Joe Ogas

University of Nebraska

Zoya Avramova

IPMB, Academia Sinica, Taiwan

Oliver L.-F. Chen, Mao-Sen Liu, Tony Kuo

Funding:

CAAS Start-up Funding

China NSF

Beijing NSF



“未来农业” 青年科技讲坛

主办：中国农业科学院科技管理局

承办：中国农业科学院生物技术研究所

协办：中国农业生物技术学会 《生物技术通报》 aBIOTECH

