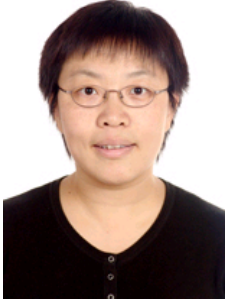




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搜索



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学习经历：（从大学开始）

1984—1988	北京大学生物系	学士
1988—1991	中国农业大学生物学院	硕士
1993—1997	北京大学生命科学学院	博士

工作经历

1991—1993	北京大学生命科学学院	助教
1993—1997	北京大学生命科学学院	讲师
1995—1996	英国John Innes Centre	访问学者
1997—1998	美国华盛顿州立大学生化研究所	博士后
1999—2003	美国加州大学洛杉矶分校	助理研究员
2003—今	中科院遗传与发育生物学研究所	研究员

获奖情况

- 2008年获得美国杜邦青年科学家奖
- 2006年“百人计划”终期评估中获得优秀
- 2003年获国家杰出青年基金
- 2002年入选中科院“百人计划”

主要研究领域

表观遗传学(Epigenetics)指的是研究基因功能的变化,这种变化在有丝分裂和/或减数分裂中是可以遗传的,与一般遗传学不同的是,所研究的基因不存在DNA序列上的改变。从广义上讲,表观遗传学控制基因功能主要包括以下三个方面:基因本身的DNA甲基化;基因所在的核小体上的组蛋白的共价修饰、染色质核小体的重塑和核小体变种以及近年来发现的小分子RNA介导的转录和转录后水平的基因沉默。随着表观遗传调控机理研究的深入和相关研究技术的突破,在基因组水平上研究各种植物、不同发育阶段和各种生长条件的表观遗传图谱的表观遗传组学正在蓬勃兴起,为揭示高等植物生长发育的分子机理提供了新手段和新思路。本实验室运用拟南芥和水稻为材料,研究组蛋白修饰以及小的非编码RNA如何影响基因表达以及植物发育,主要研究方向为组蛋白甲基化对拟南芥开花时间的调控和水稻小RNA合成调控及其对植物发育的机理研究。



拟南芥中的组蛋白甲基化与开花时间调控的分子机理研究

在真核生物的细胞核中，许多细胞生理活动都以染色体为模板来进行。作为染色体的组分之一，组蛋白延伸出来的 N 末端可以发生多种翻译后修饰，这些修饰的不同组合构成了在 DNA 序列之外的另一个层面上的遗传信息并发挥着重要功能。在动物中，人们鉴定了一些催化组蛋白甲基化与去甲基化过程的酶，编码这些酶的基因分属于几个重要的基因家族。组蛋白甲基化是组蛋白修饰当中最为重要也是最为复杂的一种修饰。对组蛋白 H3、H4 上赖氨酸残基甲基化的进一步研究证明，组蛋白甲基化在维持染色体功能以及各种细胞生理活动的调控过程中发挥着重要作用，其中包括对染色体结构和基因表达的调节、异染色质的形成、基因印记、基因组稳定性和其他重要的细胞生理活动。另外，精氨酸的甲基化和去甲基化的重要作用也逐渐被证明，研究表明，精氨酸甲基化参与了转录调控、RNA 加工、核运输、DNA 损伤的响应以及信号转导等过程。最近，人们发现了一大类赖氨酸和精氨酸去甲基化酶，这些酶都含有一个保守的 JmjC 结构域。甲基化的动态平衡是通过甲基化和去甲基化这两个过程的控制来实现的。在拟南芥的基因组中存在着许多含有 SET 结构域蛋白、蛋白质精氨酸甲基转移酶以及含有 JmjC 结构域的蛋白。我们通过生物化学和反向遗传学的手段鉴定出了一些新的组蛋白甲基转移酶和去甲基化酶，并试图借此来理解组蛋白甲基化在植物发育过程中所发挥的重要作用。

开花时间对于植物是非常重要的，植物通过响应外源环境和内源的信号，在合适的时间开花，才能尽可能成功地繁殖后代。目前的研究已经证实，植物开花时间受光周期通路、赤霉素 (GA) 通路、春化通路和自主通路的调控。已有研究表明，包括乙酰化、赖氨酸甲基化和泛素化在内的组蛋白修饰在植物开花时间的调控中发挥着重要作用。在拟南芥中，蛋白质精氨酸甲基化作为一种翻译后修饰，也参与了植物开花时间的调控。我们之前的工作已经证实拟南芥中，AtPRMT5 (protein arginine methyltransferase)、AtPRMT10、AtPRMT4a/4b 以及 AtHAC1 (histone acetyltransferase) 通过抑制 FLC 的表达促进开花。本实验室研究的主要方向之一是研究组蛋白修饰的重要因子在调控拟南芥开花时间中的分子机理。



高等植物中 small RNA 的合成途径调控机理研究

RNA 沉默在植物发育过程中的作用是近期研究关注的焦点。miRNA 和 siRNA 是两类具有调节功能的 RNA 小分子，在发育调控、基因组稳定性和病毒防御方面发挥重要作用。miRNA 和 siRNA 很相似，但其起源、形成过程不同。DICER 或者 DICER-LIKE (DCL) 在 miRNA 和 siRNA 生物合成途径中发挥关键作用，小分子 RNA 成熟后会整合到不同的 RISC 复合体 (RNA-Induced Silencing Complexes) 中发挥作用。

水稻 (*Oryza sativa* L.) 作为世界上最重要的农作物之一，是进行单子叶植物基因组学和分子生物学研究的模式物种。水稻中存在多个 DCL 蛋白，其功能在单双子叶植物分化之前就已经分化。本研究组以水稻为模式生物，重点研究水稻小分子 RNA 的合成途径，期望阐释 small RNA 在水稻发育过程中的调控网络。

本研究组从水稻中鉴定了一批新的 miRNA，如 OsmiR528, OsmiR529 和 OsmiR530 等；获得了 OsDCL1IR 和 OsDCL4IR 两个功能缺失突变体，证明 OsDCL1 和 OsDCL4 在水稻发育过程中发挥重要作用。进一步研究发现，OsDCL1 对 miRNA 的累积起主要作用；OsDCL4 主要负责对 21nt siRNA 进行加工。本研究组的长期研究目标之一是以水稻为模式生物，深入研究 small RNA 合成途径的分子机理和小分子 RNA 在水稻发育过程中的重要作用。

PUBLICATIONS (* Corresponding authors):

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- Shengben Li, Lin Liu, Xiaohong Zhuang, Yu Yu, Xigang Liu, Xia Cui, Lijuan Ji, Zhiqiang Pan, **Xiaofeng Cao**, Beixin Mo, Fuchun Zhang, Natasha Raikhel, Liwen Jiang, and Xuemei Chen (2013). MicroRNAs inhibit the translation of target mRNAs on the endoplasmic reticulum in *Arabidopsis*. *Cell*, 153, 562 – 574.
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- Xiekui Cui, Ping Jin, Xia Cui, Lianfeng Gu, Zhike Lu, Yongming Xue, Liya Wei, Jianfei Qi, Xianwei Song, Ming Luo, Gynheung An and **Xiaofeng Cao*** (2013). Control of

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