中国机构CNS月报

03月刊

生物探索出品

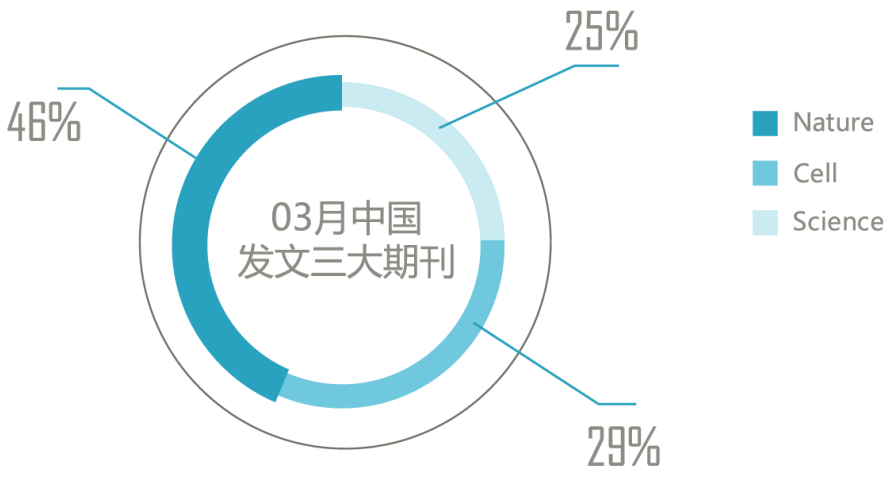
目　录

一、导语

令国内科研界振奋的是，自然系列期刊在 2012 年的论文统计显示，发文 140 篇论文的中国科学院超过日本东京大学排名亚洲机构第一位，这也是 Nature Index 统计以来中国科研机构首次排名第一，反映出中国顶尖科研机构在数量上领跑亚洲。据生物探索统计，2013 年 3 月份中国科研机构在 Nature、Cell 和 Science 三大系列期刊的总发文量是 28 篇，同比增长了 7.7%，而前三个月发文 96 篇，同比增长了 4.3%。

在生物学领域，三大期刊（Cell、Nature 和 Science）及其子刊，简称 CNS，倍受中国研究人员推崇，他们希望凭借 CNS 在学术界的威望将中国最尖端、最前沿的研究成果向全世界传达。这些研究动态可谓是中国科研机构的最高水平。作者希望对此进行统计，以便于从发文成果追踪国内科研经费动向，同时，生物医药圈内的研究人员和学生可实时了解中国顶尖研究人员从事研究的的领域和方向。

二、3 月份中国机构发文 CNS 三大期刊



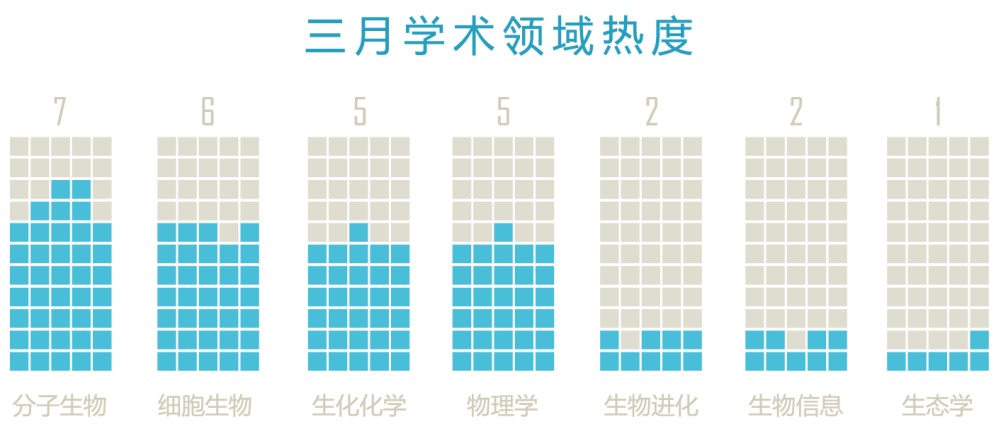
（饼状图表示期刊论文百分数）

2013 年 3 月份中国研究机构在三大系列期刊共发表 28 篇论文，包括 Nature 系列 13 篇、Cell 系列 8 篇和 Science 系列 7 篇。其中 Nature 主刊和 Science 主刊的发文量分别是 4 篇和 7 篇。

值得注意的是，3 月份 Cell 主刊没有发表 1 篇中国机构的研究论文，而 Science 主刊却包揽了 7 篇所接受的中国机构论文。从饼状图上可看出，Nature 系列期刊贡献了中国研究机构一半的 CNS 发文量，这延续了自 CNS 创刊以来该期刊发表的中国机构的论文数量处于高位的趋势，反映出中国研究机构青睐于 Nature 系列期刊。

继 1 月份和 2 月份港台地区分别发表 5 篇和 2 篇 CNS 论文之后，3 月份仅有香港大学发表 1 篇自然通讯论文。而大陆地区贡献了 28 篇 CNS 论文中的 27 篇，反映出其研究机构在 CNS 论文方面处于主体地位。

三、3 月份学术领域热度

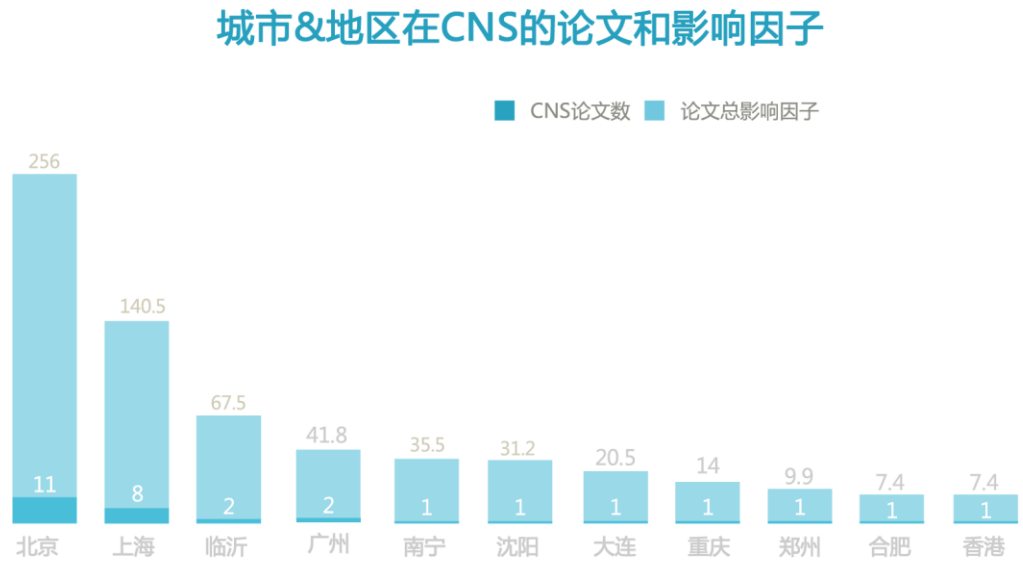


（柱状图反映论文数量/篇）

在 3 月份 CNS 刊登的中国研究论文中，分子生物和细胞生物以 7 篇和 6 篇分别列于第一位和第二位，生物化学和物理学以 5 篇共同列于第三位，而上个月物理学还占据第一的位置。此外，在上图 7 个学术分类中，Cell 系列刊和 Science 系列刊都占有 3 个，而 Nature 系列刊却涉及 5 个，表明 Nature 系列刊覆盖的学术范围最广。

以基因组为对象的生物信息学研究持续成为热点，近 7 个月内中国研究机构都有关于基因组测序的 CNS 论文发表。3 月份发表在 Nature 主刊的 2 篇生物信息学论文分别讲到粗山羊草和小麦这 2 个物种的基因组。

四、3 月份城市&地区在 CNS 的论文和影响因子



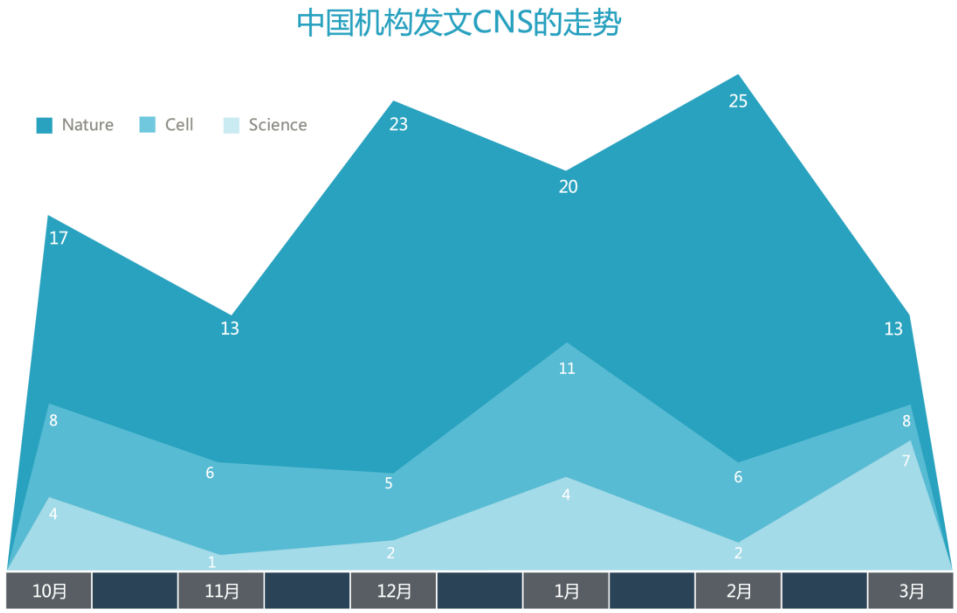
（影响因子源自 MedSci 查询系统，取小数点后一位）

从城市&地区来看，3 月份 CNS 论文影响因子超过 100 分的有北京和上海两地，北京以 256 分卫冕排行榜，较上月涨幅达 60.3 %。上海在 2 月份和 3 月份都排在第 2 位，其论文数由之前的 7 篇上升至 8 篇。从上图可以看出，北京的 CNS 论文影响因子遥遥领先其它城市&地区。

在 3 月份，除北京和上海外，其它城市发表的 CNS 论文数都不多，临沂和广州发表 2 篇，而发表 1 篇的有 7 个城市，它们是南宁、沈阳、大连、重庆、郑州、合肥和香港。

对城市&地区的 CNS 影响因子统计，生物探索网站希望向用户提供关于地区研究水平的一项指数，让科研人员在从事各自研究领域的同时选择较高的研究平台和学术氛围。此外，由于论文来自不同的经费项目，因此城市&地区的 CNS 影响因子能从一个方面反映国家经费的分配比例。

五、3 月份中国机构发文 CNS 的走势



（数据统计源自 NCBI 网站 Pubmed）

在 2012 年 10 月至 2013 年 3 月之间中国机构发文 CNS 的统计结果中，数据表明：Nature 及其子刊发表的中国研究论文数量处于高位，总计 111 篇，其中 2 月最高达到 25 篇；相反，Science 及其子刊发表的中国研究论文数量处于低位，总计 20 篇，其中 11 月最低下落至 1 篇。

Nature 系列期刊的数量最多，它覆盖的学术类别和影响因子也较多，这是中国研究论文发表在 Nature 系列刊最多的原因之一；另一原因可能是，Nature 系列期刊对中国机构的研究成果认可度高，从 Nature 在上海设立编辑部一事可以看出，它对中国机构研究成果的重视。

六、3 月份 CNS 发文机构论文量统计

研究机构	CNS 论文		
	3 月份发文量	近 5 年总数	总数
中国科学院上海生命科学研究院	1	64	92
清华大学	4	61	76
复旦大学	3	32	40
香港大学	1	26	32
中国科技大学	1	24	31
北京生命科学研究所	1	15	25
中国协和医科大学	1	20	23
中国科学院遗传与发育生物研究所	2	16	19
中山大学	1	13	16
第二军医大学	1	11	14
中国科学院大学	2	8	8
华东师范大学	2	8	8
中国农业科学院	1	8	8
中国科学院植物研究所	1	4	6
临沂大学	2	4	4
西南大学	1	4	4
中国极地研究中心	1	2	2
大连理工大学	1	2	2
中国科学院沈阳应用生态研究所	1	1	1
华南农业大学	1	1	1
广西大学	1	1	1
郑州大学第一附属医院	1	1	1
中国石油大学	1	1	1

（数据源于NCBI网站Pubmed）

从 3 月份 CNS 中国机构论文总数榜单上看，排名前三的分别中国科学院上海生命科学研究院、清华大学和复旦大学。在本月发文量上，超过 1 篇的研究机构是清华大学（4 篇）、复旦大学（3 篇）、中国科学院遗传与发育生物研究所（2 篇）、中国科学院大学（2 篇）、华东师范大学（2 篇）和临沂大学（2 篇）。其中中国科学院大学上月发文 4 篇，是当月最高发文量的学术机构。

在 3 月份 CNS 论文的统计数据中，中国机构近 5 年发表的 CNS 论文总数全都不低于其 CNS 论文总数的一半，这表明近 5 年来中国机构发文 CNS 的速度和数量增加较快。3 月份，中

国科学院沈阳应用生态研究所和华南农业大学都是首次发文 CNS。除首次发文 CNS 的研究机构外，中国科学院大学、华东师范大学、中国农业科学院、临沂大学、西南大学、中国极地研究中心和大连理工大学的 CNS 论文全都在近 5 年内。

七、3 月份 CNS 论文通讯作者的项目数和经费

研究机构	通讯作者	项目金额/万	项目数/个
清华大学	薛其坤	1971.2	13
中国科学院古脊椎动物与古人类研究所	周忠和	1383.9	7
中国科学院植物研究所	种康	1336.8	10
清华大学	施一公	1005.5	5
中国科学院遗传与发育生物学研究所	李振声	720	4
华南农业大学	刘耀光	712	7
中国科学院古脊椎动物与古人类研究所	徐星	651	5
西南大学	罗凌飞	562	4
清华大学	王亚愚	490	3
中国科技大学	吴缅	473	5
深圳华大基因研究院	王俊	470	3
中国农业科学院	何中虎	455.3	16
大连理工大学	曲景平	427	5
复旦大学	雷群英	399	6
中国农业科学院	贾继增	317.6	2
华东师范大学	翁杰敏	316	3
中国科学院遗传与发育生物学研究所	凌宏清	300	6
中国科学院遗传与发育生物学研究所	刘佳佳	261	4
中国科学院遗传与发育生物学研究所	张爱民	164	3
中国科学院物理研究所	何珂	117	2
中国科学院上海生命科学院	周兆才	115	2

（数据源于 NSFC）

对于 3 月份中国机构发文 CNS 的 25 位通讯作者（统计量不完全），国家自然科学基金项目提供了详细的项目金额和数量。清华大学的薛其坤教授以 1971.2 万元高举榜首，项目数为 13 个；中国科学院古脊椎动物与古人类研究所的周忠和院士和中国科学院植物研究所的种康研究员以 1383.9 万和 1336.8 万分列第二、三名，他们的项目数分别为 7 和 10 个。

排名前 10 的通讯作者分别来自北京（7 位）、广州（1 位）、合肥（1 位）和重庆（1 位），其中，北京地区 7 位通讯作者位于项目金额榜前十位之内，这反映出北京位列 3 月份 CNS 中

国机构影响因子之首的经费基础。

八、3 月份最受关注的媒体采访

Science 杂志对话中国国家自然科学基金委员会新晋主任杨卫

刚接任了中国国家自然科学基金委员会(NSFC)主任一职的杨卫，3 月份接受了顶级科学期刊《科学》（Science）在其就任后的首次采访。在采访中，他向 Science 谈及了关于改善 NSFC 经费管理，加强学术诚信，以及铲除不端行为方面的计划。专访内容如下：

问：在你的前任、生物学家陈宜瑜（Chen Yiyu）的 9 年任期内，NSFC 的预算提高了近 7 倍。你打算如何说服中央政府以这种水平继续增加资金投入？

杨：我们预计未来 5 年预算将保持两位数增长。尽管增长幅度相比过去 9 年不会那样显著，我们仍然预计增长速率会高于中国的 GDP（国内生产总值）增长速率（2013 年预计为 7.5%）。

当前中国的预算只有美国国家科学基金会的 40%。在中国我们还没有与美国国立卫生研究院（NIH）相当的机构，NSFC 生命科学部只占据总预算的三分之一，这一部门不得不独自与预算达到 20 亿美元的 NIH 竞争。通过这样比较，NSFC 的预算要远远少于美国基础科学总经费。中国 2012 年的 GDP 大约是美国的一半；中国的 R&D（科学研究与试验发展）总社会支出去年约为 165 亿美元，也是美国的大约一半。就这些比率而言，美国的基础科学经费要高于 NSFC 的预算。

中国必须从一个经济强国向技术强国转变，然后成为科学和文化强国。为了实现这一目标，我们还需要许多的科学家，我们需要说服政府为 NSFC 提供更多的资金。

问：NSFC 正在落实哪些政策，以提高科研诚信，减少经费申请和项目审查中的不端行为？

杨：NSFC 授权一个独立的委员会监督科研诚信。在过去 3 年里，该委员会每年收到大约 200 个学术不端指控。考虑到在同一时期内，呈送的研究计划增长了 16%，指控与计划的相对数量略有减少。去年，委员会在 200 个指控中，发现了 19 个学术不端案例，占所有指控的 10%。

委员会已经确定了五类学术不端行为。第一是夸大证书。例如，一位研究人员预期在 6 月获得博士学位，在 3 月呈送申请书时就使用了博士称号。还有，有时候，伪造协作者的签名来扩大项目范围。这是最大的类别。我们已经制定了培训材料，警告人们不要犯这类学术不端。我们还有专门的负责机构，他们有义务教育新研究人员书写申请书时的良好行为。

第二类是剽窃。一些拷贝自他们自己过去的计划书，另一些是抄袭他人的计划书。我们正使用软件来反复查对新呈送的计划书和在过去 5-10 年我们的旧计划书档案。

第三类是项目管理者选择评审者，以支持与他们有良好关系的申请人。一些评审人以严厉著称，而一些则相对温和。项目管理者有可能会为他们的朋友选择温和的评审者。我们正在考虑如何解决这一问题。例如，我们正在建立评审者的平均评分数据库。一个项目管理者可以为一个特定计划选择 7-10 名评审者。如果分数很高，就可能表明选择了一组非常温和的评审者。如果平均评分非常低，那么就有可能选择了一组非常严厉的评审者。我们可以建立一些界限，如果评审者在这一界限之外，我们将对这些计划投入更多的关注。

第四类是审查信息泄露。我的同事曾告诉我关于我们的数据库被频繁访问的事情，其中包括了所有的计划相关信息。我们正在考虑设立一个警报机制，标记异常频繁的数据库访问，追踪信息系统的注册和访问。

最后一类是伪造 NSFC 经费的进度报告。

问：在 2011 年，NSFC 25 周年庆时，一个国际审查小组鉴别了可以改进的操控领域。这些问题正在如何得到解决？

杨：我的所有前辈们一直致力使 NSFC 成为负责任的学术中心。我们也知道，还有改进的空间。

首先是我们的小职员，他们要处理数量日益增长的经费申请。NSFC 目前有约 200 名正式员工，占 NSF 总人数的 10%。我们可以说 NSFC 是非常高效的。我们自己的经营预算是 2 亿人民币，只占我们预算资金总额的 1%，员工工资只占我们经营预算的 15%。

另一方面，资金管理员工队伍不足或许会破坏 NSFC 巧实力（smart power）可能的放大效应。即我的意思是，纵使相比于我们管理的金额，我们的成本非常的小，我们的附加值可能是不

够的。一种办法就是招聘业余资金管理者来充实 NSFC 的学术构架。当前，我们雇佣了约 200 名临时项目管理者来处理经费申请。

我们还实施了一项新的方案来减少申请数量。如果某人连续两年无法成功获得申请，他需要停一年才能再次申请。这或许有助于减少呈送计划的总数量，给予申请人时间思考如何改进他们的研究，或是寻找新的方向。

2012 年，我们收到了 178,000 份呈送计划，有 38,000 个获得批准。批准率大约为 20%。这是一个很好的比率，因为我们不希望批准率太高，这意味着低选择性。而批准率太低，看起来又像是在赌博。

NSFC 一直以来都对处于职业早期阶段的年轻研究人员给予经费资助。现在我们将早期职业经费的资格条件扩大到博士后。自 2012 年开始，NSFC 启动了一个新类别，每年选择多达 400 名优秀的年轻研究人员，向他们提供为期 3 年的，总额为 100 万人民币的经费。

我们也在考虑将间接成本导入预算表中。自去年起，我们开始允许研究机构，而非中央政府制定最终预算。

国际同行评审是一个值得遵循的线路。我们有可能也会尝试让国际专家参与制定 NSFC 经费指南。我们将加大对国际协作的支持。我们希望能够实现实在的协作，而不是仪式上的。

英文原文:New Head of China's NSF Speaks Out

九、专家精选

Preservation of ovarian follicles reveals early evolution of avian reproductive behaviour. (临沂大学&中国科学院古脊椎动物与古人类研究所)

中国科学院古脊椎动物与古人类研究所的周忠和院士（左图）和临沂大学等处的研究人员，在古代鸟类化石中发现了发育卵细胞的第一个化石痕迹，从而揭示出了 1.2 亿年前鸟类与其祖先分离的一个重要特征。像现代的鸟类一样，这些祖先鸟类将它们的功能性卵巢减少至一个，有别于它们的恐龙近亲。相关研究发表在《Nature》期刊上。

在该论文中，研究人员们研究了热河鸟（*Jeholornis*，保留了诸如长尾骨等古老特征的一种原

始鸟）的一个化石标本，以及属于另一个灭绝鸟类群——反鸟类(Enantiornithines)的一对化石。根据周忠和院士和共同作者们所说，所有三个化石都保存有多个成熟的卵泡（ovarian follicle）。研究人员还指出，似乎所有的卵泡都分布在三只鸟类身体的左侧，就像在现代近亲鸟类中一样。与之相反，一件窃蛋龙类（oviraptorosaur）（一种有羽毛和喙的兽脚类恐龙）化石的髋部包含左右分布的两个卵子，每个卵子分别在一个卵巢和输卵管中发育，这表明非鸟类恐龙有两个功能性卵巢和输卵管，这与现代鳄鱼很相似。

周忠和的同事们说，热河鸟和两个反鸟类比较接近从非鸟类恐龙向现代鸟类的“过渡”。这表明从爬行动物的两个卵巢及输卵管转变为一个卵巢和输卵管似乎与飞行适应（体重减轻）相关。这也是多数生物学家们长期以来一直持有的观点。

Structural Mechanism of CCM3 Heterodimerization with GCKIII Kinases（中国科学院上海生命科学研究院）

中科院上海生科院生化与细胞所周兆才（左图）和张雷研究组的最新研究，阐述了脑海绵状血管瘤因子 3（CCM3）与 GCKIII 激酶异源二聚化的分子机制，并揭示了 GCKIII 被招募到 STRIPAK 复合物后如何调控生理功能。相关研究发表在 Cell 杂志《Structure》期刊上。

在本项研究中，周兆才研究组的张萌，史竹兵和焦石等人通过解析 CCM3 与 GCKIII 家族激酶 MST4 异源二聚体的晶体结构，分析两者的相互作用界面，确定了两者相互作用的关键位点。通过比较 CCM3-MST4 异源和同源二聚体的结构，揭示了 CCM3 和 GCKIII 激酶通用的二聚化模式，并阐述了关键残基对同源或异源二聚化的差异化影响。此外，CCM3 上 N 端二聚化结构域与 C-端 FAT 结构域之间的一段柔性的连接序列在介导 CCM3 同源和异源二聚体装配和解聚中起着关键作用。细胞学实验结合突变研究表明，CCM3 与 MST4 异源二聚体协同促进细胞迁移和细胞增殖。基于 CCM3 与 GCKIII 家族不同成员相互作用模式的相似性，以及 CCM3 在促生长和促凋亡通路发挥的差异化功能，

研究人员推测 CCM3 以相同的方式与不同的 GCKIII 家族激酶结合，从而调控不同的信号通路。这一工作为深入研究 CCM3-GCKIII 的生物学功能奠定了坚实基础。

A detrimental mitochondrial-nuclear interaction causes cytoplasmic male sterility in rice.（华南农业大学）

华南农业大学生命科学学院刘耀光教授（左图）课题组经过 10 年艰苦钻研，成功克隆三系杂交稻广泛利用的野败型细胞质雄性不育基因，并首次基于核质基因互作阐明了不育发生的分子机理。相关研究发表在《Nature Genetics》期刊上。

研究发现，不育系的 WA352 mRNA 表达虽然是组成型的，WA352 蛋白只在花药特定时期（花粉母细胞期）的绒毡层特异积累，并与核基因编码的线粒体定位蛋白 COX11 进行互作。研究发现，COX11 具有消除活性氧的功能，是真核生物保守的一个新的细胞程序性凋亡（PCD）的抑制因子。这个蛋白互作干扰了 COX11 的正常功能，导致花药绒毡层线粒体的活性氧爆发和细胞色素 c 释放到细胞浆（这是 PCD 的诱导因素），提前启动 PCD 控制的绒毡层降解，从而产生花粉败育。而 2 个恢复基因 Rf3 与 Rf4 以不同机理抑制 WA352 表达而恢复育性。论文还揭示了 WA352 是一个在野生稻线粒体基因组经多次重组事件产生的年轻新基因；我国育种家用不同的栽培稻和野生稻材料育成的多种类型水稻不育系如岗型、印水型，矮败型等不育系也含有相同的 WA352 基因，表明它们与野败型属同一 CMS 类型。也就是说，绝大部分的三系杂交稻都是利用基于 WA352 基因的雄性不育不育系。

刘耀光课题组研究成果不仅从分子遗传基础角度揭示了杂交稻雄性不育的机理，同时，以大量翔实的科学依据推翻了美国科学家提出的能量代谢缺陷导致雄性不育的假说。该研究受到科技部重大基础研究计划（973）和国家自然科学基金的支持。

The interaction between OsMADS57 and OsTB1 modulates rice tillering via DWARF14.（中国科学院植物研究所&中国科学院大学）

中国科学院植物研究所副所长的种康教授（左图）研究组发现了四个基因组成嵌合阻抑网络控制水稻产量性状分子机制，即水稻 MADS57 与 TB1 之间相互作用、miR444a 负调控以及对 D14 (Dwarf14)的靶向作用，这对于水稻产量研究具有重要意义。相关成果公布在《Nature Communications》期刊上。

在这篇文章中，研究人员以水稻突变株系和转反义株系为材料，解析了 MADS57 的功能及分子机理。研究人员发现一种激活突变体 mads57-1 和 MADS57 过表达突变株系显示分蘖增多，而 MADS57 转反义株系则分蘖较少。证实了 MADS57 具有控制营养器官侧芽分化和分蘖形成的功能。遗传和分子生物学实验证实，MADS57 直接与独脚金内酯（新激素）受体基因 D14 启动子上 CarG 模体结合，抑制了 D14 的转录。MADS57 可受到 miR444a 的负调控，导致 MADS57 表达抑制。此外，研究人员证实水稻 TCP 家族成员 TB1 与 MADS57 蛋白互作，可削弱 OsMADS57 对 D14 转录的抑制作用。

郭思义博士和徐云远研究员是该文共同第一作者，揭示了由 miRNA、MADS 和 TCP 型转录因子及酯酶 D14 构成的水稻分蘖数调控的 miMTD（miRNA/MADS/TCP/D14）分子网络之崭新机制，拓展了传统上认为的花器官基因 MADS 的新功能，加深了人们对侧芽器官分化和分蘖形成分子调控网络的了解，在水稻高产分子设计育种方面具有重要的应用潜力。

PtdIns(4)P regulates retromer-motor interaction to facilitate dynein-cargo dissociation at the trans-Golgi network.（中国科学院遗传与发育生物学研究所&中国科学院大学）

细胞内的运输系统将大量需要运输的物质分拣、包装到膜状的囊泡结构中，动力蛋白/分子马达（molecular motor）利用水解 ATP 产生的能量驱动囊泡在细胞骨架充当的轨道上移动，高效精确地将各种货物定向运输到相应的亚细胞结构。对于货物识别机制的研究发现，以微管细胞骨架为轨道驱动逆向运输的 dynein/dynactin 动力蛋白复合体中某些亚基可通过囊泡表面的介导分子（cargo adaptor）特异性识别相应

的货物。而胞内运输领域另一个重大问题，即当货物到达靶细胞器时，动力蛋白识别靶膜并将货物精确卸载的分子机制尚不明晰。

SNX6 是 dynein/dynactin 的货物介导分子，它通过与 dynein/dynactin 亚基 p150Glued 和 retromer 亚基 SNX1 分别直接作用，将动力蛋白复合体与 retromer 介导的囊泡货物连接，介导从胞内体(endosome)到反式高尔基体（trans-Golgi network）的逆向运输。中国科学院遗传与发育生物学研究所分子发育生物学国家重点实验室刘佳佳（左图）研究组通过与中国科技大学田长麟以及中国科学院生物物理研究所龚为民课题组的合作，发现 SNX6 的 PX 结构域不仅能与 p150Glued 结合，而且与高尔基体膜富含的磷脂 PtdIns4P 有弱亲合力。当高尔基体膜中的 PtdIns4P 被去除后，retromer 介导的囊泡货物 CI-MPR 在高尔基体附近区域大量积累，说明 PtdIns4P 在 dynein/dynactin 的囊泡货物卸载中具有重要的调控作用。进一步研究发现，PtdIns4P 对 SNX6 和 p150Glued 的结合具有负调控作用，并能促进 retromer 和 dynein/dynactin 这两个蛋白质复合体的解离。这些结果表明高尔基体膜中的磷脂通过抑制动力蛋白-货物相互作用而促进动力蛋白在靶膜精确释放囊泡货物。不仅如此，他们还发现 PtdIns4P 通过抑制货物介导分子 SNX4 和 dynein 之间的结合调控另一种囊泡货物 transferrin 及其受体从胞内体到内吞循环体(endocytic recycling compartment)的逆向运输，提示靶膜中的磷脂对动力蛋白-货物相互作用的调控可能是货物卸载的普遍机制。

该项研究发表在《Nature Cell Biology》期刊上。刘佳佳实验室博士研究生牛洋为该论文的第一作者，该研究得到了国家自然科学基金委、科技部和中国科学院的资助。

十、3 月份论文列表

1、Nature 及其子刊

Draft genome of the wheat A-genome progenitor Triticum urartu.[链接]

通讯作者：凌宏清 李振声 张爱民 王俊（中国科学院遗传与发育生物学研究所&深圳华大基因研究院）Nature. Epub 2013 Mar 24.

Bread wheat (Triticum aestivum, AABBDD) is one of the most widely cultivated and consumed food crops in the world. However, the complex polyploid nature of its genome makes genetic and functional analyses extremely challenging. The A genome, as a basic genome of bread wheat and other polyploid wheats, for example, T. turgidum (AABB), T. timopheevii (AAGG) and T. zhukovskyi (AAGGA(m)A(m)), is central to wheat evolution, domestication and genetic improvement. The progenitor species of the A genome is the diploid wild einkorn wheat T. urartu, which resembles cultivated wheat more extensively than do Aegilops speltoides (the ancestor of the B genome) and Ae. tauschii (the donor of the D genome), especially in the morphology and development of spike and seed. Here we present the generation, assembly and analysis of a whole-genome shotgun draft sequence of the T. urartu genome. We identified protein-coding gene models, performed genome structure analyses and assessed its utility for analysing agronomically important genes and for developing molecular markers. Our T. urartu genome assembly provides a diploid reference for analysis of polyploid wheat genomes and is a valuable resource for the genetic improvement of wheat

专家点评：有关专家指出，小麦 A 基因组测序和基因组图谱绘制的完成，将为研究小麦驯化史提供一个全新的视角，并为多倍体小麦基因组的测序分析提供了二倍体基因组参照序列。注释出的基因信息和分子标记有助于加速小麦的遗传改良，对保障粮食安全和农业可持续发展具有重要作用。

A detrimental mitochondrial-nuclear interaction causes cytoplasmic male sterility in rice.[链接]

通讯作者：刘耀光（华南农业大学&广西大学）Nat Genet. 2013 Mar 17.

Plant cytoplasmic male sterility (CMS) results from incompatibilities between the organellar and nuclear genomes and prevents self pollination, enabling hybrid crop breeding to increase yields. The Wild Abortive CMS (CMS-WA) has been exploited in the majority of 'three-line' hybrid rice production since the 1970s, but the molecular basis of this trait remains unknown. Here we report that a new mitochondrial gene, WA352, which originated recently in wild rice, confers CMS-WA

because the protein it encodes interacts with the nuclear-encoded mitochondrial protein COX11. In CMS-WA lines, WA352 accumulates preferentially in the anther tapetum, thereby inhibiting COX11 function in peroxide metabolism and triggering premature tapetal programmed cell death and consequent pollen abortion. WA352-induced sterility can be suppressed by two restorer-of-fertility (Rf) genes, suggesting the existence of different mechanisms to counteract deleterious cytoplasmic factors. Thus, CMS-related cytoplasmic-nuclear incompatibility is driven by a detrimental interaction between a newly evolved mitochondrial gene and a conserved, essential nuclear gene.

专家点评：复旦大学生命科学学院的马红教授在 Nature Genetics 邀请下写专题评述时称之为雄性植物的生育能力战斗。对细胞质雄性不育水稻的新线粒体基因进行分析，揭示了核编码蛋白的抑制作用以及核育性恢复因子之间对立性。在天然野生稻种中存在这些基因表明了它们在生育上具有选择性优势。

Aegilops tauschii draft genome sequence reveals a gene repertoire for wheat adaptation. [链接]

通讯作者：贾继增　刘旭　何中虎　毛龙　王俊（中国农业科学院&深圳华大基因研究院）Epub 2013 Mar 24.

About 8,000 years ago in the Fertile Crescent, a spontaneous hybridization of the wild diploid grass Aegilops tauschii (2n = 14; DD) with the cultivated tetraploid wheat Triticum turgidum (2n = 4x = 28; AABB) resulted in hexaploid wheat (T. aestivum; 2n = 6x = 42; AABBDD). Wheat has since become a primary staple crop worldwide as a result of its enhanced adaptability to a wide range of climates and improved grain quality for the production of baker's flour. Here we describe sequencing the Ae. tauschii genome and obtaining a roughly 90-fold depth of short reads from libraries with various insert sizes, to gain a better understanding of this genetically complex plant. The assembled scaffolds represented 83.4% of the genome, of which 65.9% comprised transposable elements. We generated comprehensive RNA-Seq data and used it to identify 43,150 protein-coding genes, of which 30,697 (71.1%) were uniquely anchored to chromosomes with an

integrated high-density genetic map. Whole-genome analysis revealed gene family expansion in Ae. tauschii of agronomically relevant gene families that were associated with disease resistance, abiotic stress tolerance and grain quality. This draft genome sequence provides insight into the environmental adaptation of bread wheat and can aid in defining the large and complicated genomes of wheat species.

Identification of NUB1 as a suppressor of mutant Huntingtin toxicity via enhanced protein clearance. [链接]

通讯作者：鲁伯埙（复旦大学）Nat Neurosci. 2013 Mar 24.

Huntington's disease is caused by expanded CAG repeats in HTT, conferring toxic gain of function on mutant HTT (mHTT) protein. Reducing mHTT amounts is postulated as a strategy for therapeutic intervention. We conducted genome-wide RNA interference screens for genes modifying mHTT abundance and identified 13 hits. We tested 10 in vivo in a Drosophila melanogaster Huntington's disease model, and 6 exhibited activity consistent with the in vitro screening results. Among these, negative regulator of ubiquitin-like protein 1 (NUB1) overexpression lowered mHTT in neuronal models and rescued mHTT-induced death. NUB1 reduces mHTT amounts by enhancing polyubiquitination and proteasomal degradation of mHTT protein. The process requires CUL3 and the ubiquitin-like protein NEDD8 necessary for CUL3 activation. As a potential approach to modulating NUB1 for treatment, interferon-β lowered mHTT and rescued neuronal toxicity through induction of NUB1. Thus, we have identified genes modifying endogenous mHTT using high-throughput screening and demonstrate NUB1 as an exemplar entry point for therapeutic intervention of Huntington's disease.

PtdIns(4)P regulates retromer-motor interaction to facilitate dynein-cargo dissociation at the trans-Golgi network.[链接]

通讯作者：刘佳佳（中国科学院遗传与发育生物学研究所）Nat Cell Biol. Epub 2013 Mar 24.

The molecular mechanisms for the retrograde motor dynein-dynactin to unload its cargoes at their final destination remain to be elucidated. In this study, we have investigated the regulatory mechanism underlying release of retromer-associated cargoes at the trans-Golgi network (TGN). We report that phosphotidylinositol-4-phosphate (PtdIns(4)P), a Golgi-enriched phosphoinositide, negatively regulates the protein-protein interaction between the p150(Glued) subunit of dynein-dynactin and the retromer component SNX6. We show that PtdIns(4)P specifically facilitates dissociation of retromer-mediated membranous cargoes from the motor at the TGN and uncover an important function for PtdIns(4)P in the spatial control of retrograde vesicular trafficking to the TGN membrane. PtdIns(4)P also regulates SNX4-mediated retrograde vesicular trafficking to the endocytic recycling compartment by modulating its interaction with dynein. These results establish organelle-specific phosphoinositide regulation of motor-cargo interaction as a mechanism for cargo release by molecular motors at target membrane.

PKA-induced dimerization of the RhoGAP DLC1promotes its inhibition of tumorigenesis and metastasis. [链接]

通讯作者：（香港大学 ）Nat Commun. 2013 Mar 19;4:1618.

Deleted in Liver Cancer 1 (DLC1) is a tumour suppressor that encodes a RhoGTPase-activating protein (RhoGAP) and is frequently inactivated in many human cancers. The RhoGAP activity of DLC1 against Rho signalling is well documented and is strongly associated with the tumour suppressor functions of DLC1. However, the mechanism by which the RhoGAP activity of DLC1 is regulated remains obscure. Here, we report that phosphorylation of DLC1 at Ser549 by cyclic AMP-dependent protein kinase A contributes to enhanced RhoGAP activity and promotes the activation of DLC1, which suppresses hepatoma cell growth, motility and metastasis in both in vitro and in vivo models. Intriguingly, we found that Ser549 phosphorylation induces the dimerization of DLC1 and that inducible dimerization of DLC1 can rescue the tumour suppressive and RhoGAP activities of DLC1 containing a Ser549 deletion. Our study establishes a novel regulatory mechanism for DLC1 RhoGAP activity via dimerization induced by protein kinase A signaling

Ammonia formation by a thiolate-bridged diiron amide complex as a nitrogenase mimic.[链接]

通讯作者：曲景平（大连理工大学）Nat Chem. Epub 2013 Mar 17.

Although nitrogenase enzymes routinely convert molecular nitrogen into ammonia under ambient temperature and pressure, this reaction is currently carried out industrially using the Haber-Bosch process, which requires extreme temperatures and pressures to activate dinitrogen. Biological fixation occurs through dinitrogen and reduced NxHy species at multi-iron centres of compounds bearing sulfur ligands, but it is difficult to elucidate the mechanistic details and to obtain stable model intermediate complexes for further investigation. Metal-based synthetic models have been applied to reveal partial details, although most models involve a mononuclear system. Here, we report a diiron complex bridged by a bidentate thiolate ligand that can accommodate HN=NH. Following reductions and protonations, HN=NH is converted to NH3 through pivotal intermediate complexes bridged by N2H3(-) and NH2(-) species. Notably, the final ammonia release was effected with water as the proton source. Density functional theory calculations were carried out, and a pathway of biological nitrogen fixation is proposed.

Preservation of ovarian follicles reveals early evolution of avian reproductive behaviour. [链接]

通讯作者：周忠和 邹晶梅 （临沂大学）Nature.Mar 28;495(7442):507-11

The two groups of archosaurs, crocodilians and birds, form an extant phylogenetic bracket for understanding the reproductive behaviour of dinosaurs. This behaviour is inferred from preserved nests and eggs, and even gravid individuals. Data indicate that many 'avian' traits were already present in Paraves--the clade that includes birds and their close relatives--and that the early evolution of the modern avian form of reproduction was already well on its way. Like living neornithine birds, non-avian maniraptorans had daily oviposition and asymmetrical eggs with

complex shell microstructure, and were known to protect their clutches. However, like crocodilians, non-avian maniraptorans had two active oviducts (one present in living birds), relatively smaller eggs, and may not have turned their eggs in the way that living birds do. Here we report on the first discovery of fossilized mature or nearly mature ovarian follicles, revealing a previously undocumented stage in dinosaur reproduction: reproductively active females near ovulation. Preserved in a specimen of the long bony-tailed Jeholornis and two enantiornithine birds from the Early Cretaceous period lacustrine Jehol Biota in northeastern China, these discoveries indicate that basal birds only had one functional ovary, but retained primitive morphologies as a result of their lower metabolic rate relative to living birds. They also indicate that basal birds reached sexual maturity before skeletal maturity, as in crocodiles and paravian dinosaurs. Differences in follicular morphology between Jeholornis and the enantiornithines are interpreted as forming an evolutionary gradient from the reproductive condition in paravian dinosaurs towards neornithine birds. Furthermore, differences between the two enantiornithines indicate that this lineage might also have evolved advanced reproductive traits in parallel to the neornithine lineage.

Isolation and culture of endothelial cells, pericytes and perivascular resident macrophage-like melanocytes from the young mouse ear. [链接]

通讯作者：Xiaorui Shi（郑州大学第一附属医院） Nat Protoc. Epub 2013 Mar 14.

This protocol describes a growth medium-based approach for obtaining cochlear endothelial cells (ECs), pericytes (PCs) and perivascular resident macrophage-like melanocytes (PVM/Ms) from the stria vascularis of mice aged between P10 and P15 (P, postnatal day). The procedure does not involve mechanical or enzymatic digestion of the sample tissue. Explants of stria vascularis, 'mini-chips', are selectively cultured in growth medium, and primary cell lines are obtained in 7-10 d. The method is simple and reliable, and it provides high-quality ECs, PVM/Ms and PCs with a purity >90% after two passages. This protocol is suitable for producing primary culture cells from organs and tissues of small volume and high anatomical complexity, such as the inner ear capillaries. The highly purified primary cell lines enable cell culture-based in vitro modeling of

cell-cell interactions, barrier control function and drug action.

The interaction between OsMADS57 and OsTB1 modulates rice tillering via DWARF14. [链接]

通讯作者：种康（中国科学院植物研究所）Nat Commun. 2013;4:1566.

Rice tillering is a multigenic trait that influences grain yield, but its regulation molecular module is poorly understood. Here we report that OsMADS57 interacts with OsTB1 (TEOSINTE BRANCHED1) and targets D14 (Dwarf14) to control the outgrowth of axillary buds in rice. An activation-tagged mutant osmads57-1 and OsMADS57-overexpression lines showed increased tillers, whereas OsMADS57 antisense lines had fewer tillers. OsMIR444a-overexpressing lines exhibited suppressed OsMADS57 expression and tillering. Furthermore, osmads57-1 was insensitive to strigolactone treatment to inhibit axillary bud outgrowth, and OsMADS57's function in tillering was dependent on D14. D14 expression was downregulated in osmads57-1, but upregulated in antisense and OsMIR444a-overexpressing lines. OsMADS57 bound to the CArG motif [C(A/T)TTAAAAAG] in the promoter and directly suppressed D14 expression. Interaction of OsMADS57 with OsTB1 reduced OsMADS57 inhibition of D14 transcription. Therefore, OsMIR444a-regulated OsMADS57, together with OsTB1, target D14 to control tillering. This regulation mechanism could have important application in rice molecular breeding programs focused on high grain yield.

UHRF1 targets DNMT1 for DNA methylation through cooperative binding of hemi-methylated DNA and methylated H3K9.[链接]

通讯作者：翁杰敏（华东师范大学）Nat Commun. 2013;4:1563.

Epigenetic inheritance of DNA methylation in mammals requires a multifunctional protein UHRF1, which is believed to recruit DNMT1 to DNA replication forks through a unique hemi-methylated CpG-binding activity. Here we demonstrate that the UHRF1 mutants deficient in

binding either hemi-methylated CpG or H3K9me2/3, but not both, are able to associate with pericentric heterochromatin, recruit Dnmt1 and partially rescue DNA methylation defects in mouse Uhrf1 null ES cells. Furthermore, we present evidence that the flip out of the methylated cytosine induced by UHRF1 binding is unlikely essential for subsequent DNA methylation by DNMT1. Together, our study demonstrates that UHRF1 can target DNMT1 for DNA maintenance methylation through binding either H3K9me2/3 or hemi-methylated CpG, and that the presence of both binding activities ensures high fidelity DNA maintenance methylation. In addition, our study indicates that UHRF1 mediates cross-talk between H3K9 methylation and DNA methylation at the level of DNA methylation maintenance.

Siva1 inhibits p53 function by acting as an ARF E3 ubiquitin ligase. [链接]

通讯作者：梅一德 吴缅（中国科技大学）Nat Commun. 2013;4:1551.

The tumour suppressor alternative reading frame (ARF) is one of the most frequently mutated proteins in human cancer. It has been well established that ARF is able to stabilize and activate p53 by directly inhibiting Mdm2. ARF-mediated p53 activation in response to oncogenic stress is thought to be an important determinant of protection against cancer. However, little is known regarding the control of ARF in cells. Here, we show that Siva1 is a specific E3 ubiquitin ligase of ARF. Siva1 physically interacts with ARF both in vitro and in vivo. Through direct interaction, Siva1 promotes the ubiquitination and degradation of ARF, which in turn affects the stability of p53. Functionally, Siva1 regulates cell cycle progression and cell proliferation in an ARF/p53-dependent manner. Our results uncover a novel regulatory mechanism for the control of ARF stability, thereby revealing an important function of Siva1 in the regulation of the ARF-Mdm2-p53 pathway.

Allosteric signaling and dynamics of the clamshell-like NMDA receptor GluN1 N-terminal domain. [链接]

通讯作者：Pierre Paoletti（华东师范大学）Nat Struct Mol Biol.　Epub 2013 Mar 3.

N-methyl-D-aspartate receptors (NMDARs), neuronal glutamate-gated ion channels, are obligatory heterotetramers composed of GluN1 and GluN2 subunits. Each subunit contains two extracellular clamshell-like domains with an agonist-binding domain and a distal N-terminal domain (NTD). The GluN2 NTDs form mobile regulatory domains. In contrast, the dynamics of GluN1 NTD and its contribution to NMDAR function remain poorly understood. Here we show that GluN1 NTD is neither static nor functionally silent. Perturbing the conformation of GluN1 NTD affects both receptor gating and pharmacological properties. GluN1 NTD undergoes structural rearrangements that involve hinge bending and large twisting and untwisting motions, allowing for new intra- and intersubunit contacts. GluN1 NTD acts in trans with GluN2 NTD to influence binding of glutamate but, notably, not of GluN1 coagonist glycine. Our work uncovers a dynamic role of GluN1 NTD in controlling NMDAR function through new interdomain allosteric interactions.

2、Cell 及其子刊

R-2-Hydroxyglutarate as the Key Effector of IDH Mutations Promoting Oncogenesis. [链接]

通讯作者：管坤良（复旦大学）Cancer Cell. 2013 Mar 18;23(3):274-6

The tumor-associated isocitrate dehydrogenase (IDH) mutants are unique in that they have lost their normal catalytic activity and gained a novel function to produce R-2-hydroxyglutarate (R-2-HG). A recent study now shows that R-2-HG can reversibly promote leukemogenesis in vitro, suggesting a therapeutic potential of targeting mutant IDH1 and IDH2.

专家点评：管坤良教授在 Cancer Cell 上发表评述性文章，介绍了 R-2-HG 的研究新机制，指出 R-2-HG 能可逆的诱发白血病，这为靶向 IDH1 和 IDH2 的治疗方法提出了新证据。他还指出 IDH 突变基因的作用是独一无二的，因为它们失去了正常的催化活性，变成了另外一种新功能：诱导产生 R-2-HG，这不仅表明 R-2-HG 能在体外可逆诱导白血病发生，而且也为靶向 IDH1 和 IDH2 的治疗方法提出了新证据。

Endogenous miRNA Sponge lincRNA-RoR Regulates Oct4, Nanog, and Sox2 in Human Embryonic Stem Cell Self-Renewal. [链接]

通讯作者：（第二军医大学）Dev Cell. Epub 2013 Mar 28.

The embryonic stem cell (ESC) transcriptional and epigenetic networks are controlled by a multilayer regulatory circuitry, including core transcription factors (TFs), posttranscriptional modifier microRNAs (miRNAs), and some other regulators. However, the role of large intergenic noncoding RNAs (lincRNAs) in this regulatory circuitry and their underlying mechanism remains undefined. Here, we demonstrate that a lincRNA, linc-RoR, may function as a key competing endogenous RNA to link the network of miRNAs and core TFs, e.g., Oct4, Sox2, and Nanog. We show that linc-RoR shares miRNA-response elements with these core TFs and that linc-RoR prevents these core TFs from miRNA-mediated suppression in self-renewing human ESC. We suggest that linc-RoR forms a feedback loop with core TFs and miRNAs to regulate ESC maintenance and differentiation. These results may provide insights into the functional interactions of the components of genetic networks during development and may lead to new therapies for many diseases.

Structural Mechanism of CCM3 Heterodimerization with GCKIII Kinases.[链接]

通讯作者：张雷　周兆才（中国科学院上海生命科学院）Structure. 2013 Mar 26. pii: S0969-2126(13)00055-5.

Mutation of CCM3 causes cerebral cavernous malformations of the vasculature, leading to focal neurological deficits, seizures, and hemorrhagic stroke. CCM3 can heterodimerize with GCKIII kinases (MST3, MST4, and STK25) to regulate cardiovascular development. Here, we provide direct experimental evidence to prove that CCM3 heterodimerizes with GCKIII in a manner structurally resembling the CCM3 homodimerization. Structural comparison revealed the mechanism and critical residues that drive CCM3-GCKIII heterodimerization versus homodimerization. A flexible linker was identified for CCM3, which mediates a large-scale conformational rotation of the FAT domain relative to the dimerization domain. The conformational flipover of FAT domain removes steric locking in the CCM3 homodimer and allows its disassembly and subsequent heterodimerization with GCKIII. CCM3 forms a stable complex with MST4 in vivo to promote cell proliferation and migration synergistically in a manner dependent on MST4 kinase activity. Collectively, our work offers a structural basis for further functional study.

Cryo-EM Structure of a Molluscan Hemocyanin Suggests Its Allosteric Mechanism. [链接]

通讯作者：赵华（中山大学）Structure. 2013 Mar 26. pii: S0969-2126(13)00075-0.

Hemocyanins are responsible for transporting O2 in the arthropod and molluscan hemolymph. Haliotis diversicolor molluscan hemocyanin isoform 1 (HdH1) is an 8 MDa oligomer. Each subunit

is made up of eight functional units (FUs). Each FU contains two Cu ions, which can reversibly bind an oxygen molecule. Here, we report a 4.5 Å cryo-EM structure of HdH1. The structure clearly shows ten asymmetric units arranged with D5 symmetry. Each asymmetric unit contains two structurally distinct but chemically identical subunits. The map is sufficiently resolved to trace the entire subunit Cα backbone and to visualize densities corresponding to some large side chains, Cu ion pairs, and interaction networks of adjacent subunits. A FU topology path intertwining between the two subunits of the asymmetric unit is unambiguously determined. Our observations suggest a structural mechanism for the stability of the entire hemocyanin didecamer and 20 "communication clusters" across asymmetric units responsible for its allosteric property upon oxygen binding.

Lysine-5 Acetylation Negatively Regulates Lactate Dehydrogenase A and Is Decreased in Pancreatic Cancer. [链接]

通讯作者：熊跃 雷群英 管坤良（复旦大学）Cancer Cell. Epub 2013 Mar 21.

Tumor cells commonly have increased glucose uptake and lactate accumulation. Lactate is produced from pyruvate by lactate dehydrogenase A (LDH-A), which is frequently overexpressed in tumor cells and is important for cell growth. Elevated transcription by c-Myc or HIF1α may contribute to increased LDH-A in some cancer types. Here, we show that LDH-A is acetylated at lysine 5 (K5) and that this acetylation inhibits LDH-A activity. Furthermore, the K5-acetylated LDH-A is recognized by the HSC70 chaperone and delivered to lysosomes for degradation. Replacement of endogenous LDH-A with an acetylation mimetic mutant decreases cell proliferation and migration. Importantly, K5 acetylation of LDH-A is reduced in human pancreatic cancers. Our study reveals a mechanism of LDH-A upregulation in pancreatic cancers.

Replacement of Oct4 by Tet1 during iPSC Induction Reveals an Important Role of DNA Methylation and Hydroxymethylation in Reprogramming. [链接]

通讯作者：蔡涛博士 高绍荣（中国协和医科大学&北京生命科学研究所）Cell Stem Cell. Epub 2013 Mar 14.

DNA methylation and demethylation have been proposed to play an important role in somatic cell reprogramming. Here, we demonstrate that the DNA hydroxylase Tet1 facilitates pluripotent stem cell induction by promoting Oct4 demethylation and reactivation. Moreover, Tet1 (T) can replace Oct4 and initiate somatic cell reprogramming in conjunction with Sox2 (S), Klf4 (K), and c-Myc (M). We established an efficient TSKM secondary reprogramming system and used it to characterize the dynamic profiles of 5-methylcytosine (5mC), 5-hydroxymethylcytosine (5hmC), and gene expression during reprogramming. Our analysis revealed that both 5mC and 5hmC

modifications increased at an intermediate stage of the process, correlating with a transition in the transcriptional profile. We also found that 5hmC enrichment is involved in the demethylation and reactivation of genes and regulatory regions that are important for pluripotency. Our data indicate that changes in DNA methylation and hydroxymethylation play important roles in genome-wide epigenetic remodeling during reprogramming.

EpCAM Is an Endoderm-Specific Wnt Derepressor that Licenses Hepatic Development. [链接]

通讯作者：罗凌飞（西南大学）Dev Cell 2013 Mar 11;24(5):543-53.

Mechanisms underlying cell-type-specific response to morphogens or signaling molecules during embryonic development are poorly understood. To learn how response to the liver-inductive Wnt2bb signal is achieved, we identify an endoderm-enriched, single transmembrane protein, epithelial-cell-adhesion-molecule (EpCAM), as an endoderm-specific Wnt derepressor in zebrafish. hi2151/epcam mutants exhibit defective liver development similar to prt/wnt2bb mutants. EpCAM directly binds to Kremen1 and disrupts the Kremen1-Dickkopf2 (Dkk2) interaction, which prevents Kremen1-Dkk2-mediated removal of Lipoprotein-receptor-related protein 6 (Lrp6) from the cell surface. These data lead to a model in which EpCAM derepresses Lrp6 and cooperates with Wnt ligand to activate Wnt signaling through stabilizing membrane Lrp6 and allowing Lrp6 clustering into active signalosomes. Thus, EpCAM cell autonomously licenses and cooperatively activates Wnt2bb signaling in endodermal cells. Our results identify EpCAM as the key molecule and its functional mechanism to confer endodermal cells the competence to respond to the liver-inductive Wnt2bb signal.

Structural Basis of RIP1 Inhibition by Necrostatins.[链接]

通讯作者：施一公（清华大学）Structure. 2013 Mar 5;21(3):493-9

Necroptosis is a cellular mechanism that mediates necrotic cell death. The receptor-interacting serine/threonine protein kinase 1 (RIP1) is an essential upstream signaling molecule in tumor-necrosis-factor-α-induced necroptosis. Necrostatins, a series of small-molecule inhibitors, suppress necroptosis by specifically inhibiting RIP1 kinase activity. Both RIP1 structure and the mechanisms by which necrostatins inhibit RIP1 remain unknown. Here, we report the crystal structures of the RIP1 kinase domain individually bound to necrostatin-1 analog, necrostatin-3 analog, and necrostatin-4. Necrostatin, caged in a hydrophobic pocket between the N- and C-lobes of the kinase domain, stabilizes RIP1 in an inactive conformation through interactions with highly conserved amino acids in the activation loop and the surrounding structural elements. Structural comparison of RIP1 with the inhibitor-bound oncogenic kinase B-RAF reveals partially overlapping binding sites for necrostatin and for the anticancer compound PLX4032. Our study

provides a structural basis for RIP1 inhibition by necrostatins and offers insights into potential structure-based drug design.

3、Science 及其子刊

Hind wings in Basal birds and the evolution of leg feathers.[链接]

通讯作者：徐星（临沂大学）Science. 2013 Mar 15;339(6125):1309-12.

Recent discoveries of large leg feathers in some theropods have implications for our understanding of the evolution of integumentary features on the avialan leg, and particularly of their relevance for the origin of avialan flight. Here we report 11 basal avialan specimens that will greatly improve our knowledge of leg integumentary features among early birds. In particular, they provide solid evidence for the existence of enlarged leg feathers on a variety of basal birds, suggest that extensively scaled feet might have appeared secondarily at an early stage in ornithuromorph evolution, and demonstrate a distal-to-proximal reduction pattern for leg feathers in avialan evolution.

专家点评：论文通讯作者徐星称："这一研究成果"令人兴奋"，因为这些骨骼纤细的古老鸟类，留下几块化石有待深入研究。这些鸟类后肢羽毛的存在证实了早期鸟类演化过程中曾存在一个四翼阶段，并且后肢羽翼在鸟类飞翔起源中曾扮演过非常重要的角色，也就是说最早的鸟类曾经是用四个翅膀飞翔的。"

徐星还表示，这项研究中发现的鸟类来自白垩纪，约 1.2 亿年前，那时也存在恐龙。研究显示鸟类可能是在其进化中逐渐失去了长在其后肢上的羽毛，这种从四翼向双翼的转变可能是鸟类在其后肢获得了更多的鳞片，并且更多地用于地面行走时出现的。

参与了这篇论文审核工作的加州大学伯克利分校的 Kevin Padian 提出，"我不认为这些动物会拍打自己的腿飞行，还没有证据证明腿部的羽毛能增加飞行力，不过这是一次值得称赞的研究，因为研究表明了恐龙和原始鸟类中腿部羽毛如何随时间而演化的。"

Direct observations of the evolution of polar cap ionization patches. [链接]

通讯作者：张清和（中国极地研究中心）Science. 2013 Mar 29;339(6127):1597-600.

Patches of ionization are common in the polar ionosphere, where their motion and associated density gradients give variable disturbances to high-frequency (HF) radio communications, over-the-horizon radar location errors, and disruption and errors to satellite navigation and communication. Their formation and evolution are poorly understood, particularly under

disturbed space weather conditions. We report direct observations of the full evolution of patches during a geomagnetic storm, including formation, polar cap entry, transpolar evolution, polar cap exit, and sunward return flow. Our observations show that modulation of nightside reconnection in the substorm cycle of the magnetosphere helps form the gaps between patches where steady convection would give a "tongue" of ionization (TOI).

Topology-driven magnetic quantum phase transition in topological insulators. [链接]

通讯作者：何珂 王亚愚（清华大学）Science. 2013 Mar 29;339(6127):1582-6.

The breaking of time reversal symmetry in topological insulators may create previously unknown quantum effects. We observed a magnetic quantum phase transition in Cr-doped Bi2(SexTe1-x)3 topological insulator films grown by means of molecular beam epitaxy. Across the critical point, a topological quantum phase transition is revealed through both angle-resolved photoemission measurements and density functional theory calculations. We present strong evidence that the bulk band topology is the fundamental driving force for the magnetic quantum phase transition. The tunable topological and magnetic properties in this system are well suited for realizing the exotic topological quantum phenomena in magnetic topological insulators.

Environment and development. Measuring China's circular economy. [链接]

通讯作者：Yong Geng（中国科学院沈阳应用生态研究所）Science. 2013 Mar 29;339(6127):1526-7

Facing significant natural resource consumption, environmental degradation, and resulting public frustration, China's new administration heightened attention on ecological modernization, green growth, and low carbon development, with a national circular economy (CE) strategy (1). The 2012 Rio+20 United Nations Conference on Sustainable Development emphasized the need to develop indicators of progress that decouple economic growth and environmental burden (2). We describe how China presents unique opportunities to develop new environmental indicator systems for measuring and managing CE.

Experimental Observation of the Quantum Anomalous Hall Effect in a Magnetic Topological Insulator.[链接]

通讯作者：薛其坤 王亚愚 何珂（清华大学&中科院物理所）Science. Epub 2013 Mar 14.

The quantized version of the anomalous Hall effect has been predicted to occur in magnetic topological insulators, but the experimental realization has been challenging. Here, we report the

observation of the quantum anomalous Hall (QAH) effect in thin films of chromium-doped (Bi,Sb)2Te3, a magnetic topological insulator. At zero magnetic field, the gate-tuned anomalous Hall resistance reaches the predicted quantized value of h/e(2), accompanied by a considerable drop in the longitudinal resistance. Under a strong magnetic field, the longitudinal resistance vanishes, whereas the Hall resistance remains at the quantized value. The realization of the QAH effect may lead to the development of low-power-consumption electronics.

A transforming metal nanocomposite with large elastic strain, low modulus, and high strength.[链接]

第一作者：崔立山（中国石油大学）Science. 2013 Mar 8;339(6124):1191-4.

Freestanding nanowires have ultrahigh elastic strain limits (4 to 7%) and yield strengths, but exploiting their intrinsic mechanical properties in bulk composites has proven to be difficult. We exploited the intrinsic mechanical properties of nanowires in a phase-transforming matrix based on the concept of elastic and transformation strain matching. By engineering the microstructure and residual stress to couple the true elasticity of Nb nanowires with the pseudoelasticity of a NiTi shape-memory alloy, we developed an in situ composite that possesses a large quasi-linear elastic strain of over 6%, a low Young's modulus of ~28 gigapascals, and a high yield strength of ~1.65 gigapascals. Our elastic strain-matching approach allows the exceptional mechanical properties of nanowires to be exploited in bulk materials.

Evidence for Two Distinct Populations of Type Ia Supernovae.[链接]

通讯作者：王晓峰（清华大学）Science. Epub 2013 Mar 7.

Type Ia supernovae (SNe Ia) have been used as excellent standardizable candles for measuring cosmic expansion, but their progenitors are still elusive. Here, we report that the spectral diversity of SNe Ia is tied to their birthplace environments. We found that those with high-velocity ejecta are substantially more concentrated in the inner and brighter regions of their host galaxies than are normal-velocity SNe Ia. Furthermore, the former tend to inhabit larger and more luminous hosts. These results suggest that high-velocity SNe Ia likely originate from relatively younger and more metal-rich progenitors than do normal-velocity SNe Ia and are restricted to galaxies with substantial chemical evolution.