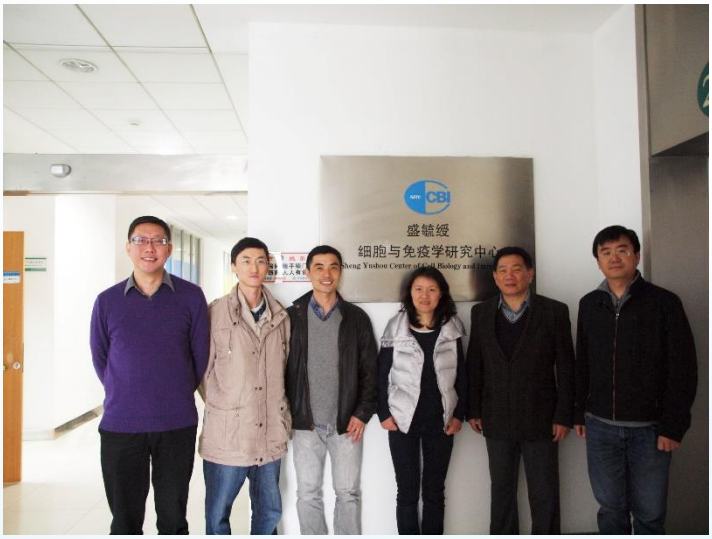
目　　录

一、“盛毓绶细胞与免疫学研究中心”中心简介

“盛毓绶细胞与免疫学研究中心”是在“盛毓绶基金会”和上海交通大学的大力支持下，于 2012 年正式成立于生命科学与技术学院之框架中。“中心”的宗旨为结合学校生命健康领域学科发展规划和需要，为能够解决生命科学与人体健康相关领域的重大科学问题，进一步增强交大生命学科的整体实力，通过组建细胞与免疫学研究方向，促进生物化学、微生物学、细胞生物学、遗传学等学科的交叉和协作发展，辐射带动整个生物学一级学科的快速发展，吸引凝聚更多的优秀人才，引领上海交大生命学科走向世界一流水平。

目前，我们已从国内外引进了五名青年学者。他们分别在肿瘤免疫学，神经生物学，细胞自噬和表观遗传学等领域中崭露头角，颇有建树。我们希望今后能聚集更多的海内外优秀学术人才，为上海交大和中国的生物医学研究和应用领域的发展做出我们特有的贡献。



二、会议通知

“盛毓绥细胞与免疫学研究中心”定于 2016 年 7 月 7 日至 2016 年 7 月 9 日在上海交通大学举办第一届遗传与医学学术研讨会。会议将围绕免疫学、肿瘤治疗、神经系统疾病、自噬等领域的最新进展举行报告和探讨。会议将邀请国内外 10 位专家作相关的学术汇报，增进中心科学家和同行的交流与合作，把握国际遗传和疾病研究的最新进展，为青年学者提供学术交流的平台，为广大科研工作者提供科研交流的机会。

一、 主办单位：

上海交通大学生命科学技术学院“盛毓绥细胞与免疫学研究中心”

二、 会议组织委员会：

马小京　孙涛　　谢志平　于明　杨选明　魏芳

三、 会议成员（姓名拼音字母顺序排列）：

Hao Jiang，林鑫华，黄灿华，马小京，邵峰，孙涛，许执恒，谢志平，于明，杨选明，朱冰，张传茂

四、 会议秘书处：

谢云　Tel: 021-34207401；15962176366；E-mail:xieyun8891@sjtu.edu.cn

三、会议须知

3.1 会议地址

上海交通大学闵行校区 学术活动中心（上海市闵行区东川路 800 号）

联系方式：021-54740800

3.2 会议交通

1. 从上海浦东国际机场到上海交通大学闵行校区：

出租：约 165 元，全程约 50 分钟；

公交：2 号线转 1 号线转 5 号线，至东川路站下车，换乘江川 3 路/闵行 26 路，全程约 150 分钟。

2. 从虹桥国际机场到上海交通大学闵行校区：

出租：约 90 元，全程约 40 分钟；

公交：10 号线转 4 号线转 1 号线转 5 号线，至东川路站下车，换乘江川 3 路/闵行 26 路，全程约 90 分钟。

3. 从上海火车站到上海交通大学闵行校区：

出租：约 120 元，全程约 60 分钟；

公交：1 号线转 5 号线，至东川路站下车，换乘江川 3 路/闵行 26 路，全程约 90 分钟。

4. 从上海南站到上海交通大学闵行校区：

出租：约 75 元，全程约 30 分钟；

公交：1 号线转 5 号线，至东川路站下车，换乘江川 3 路/闵行 26 路，全程约 60 分钟。

3.3 会议住宿

人员	地点
参会专家	上海交通大学闵行校区 学术活动中心
夏令营学生	上海交通大学思源门附近 海友快捷酒店

3.4 会议用餐

时间		地点	方式
7 月 7 日（夏令营学生）	午餐	交大第一餐饮、交大第二餐饮	餐券制
	晚餐	交大第一餐饮、交大第二餐饮	餐券制
7 月 8 日	早餐	酒店自助	餐券制
	午餐	大智居自助	餐券制
	晚餐	交大第一餐饮、交大第二餐饮	餐券制 专家为桌餐
7 月 9 日（夏令营学生）	早餐	酒店自助	餐券制
	午餐	交大第一餐饮、交大第二餐饮	餐券制

3.5 会议赞助

1. 盛毓绶基金会

2. BD 驻上海办事处

四、会议日程

2016 年 7 月 7 日 星期四

09:00-11:30	夏令营学生报到（上海交通大学生命科学技术学院 2-217 谢云）
11:30-14:00	午餐
14:00-17:00	各课题组组织夏令营学生参观实验室
17:30	晚餐

2016 年 7 月 8 日 星期五

08:30-9:00	专家学生签到
	主持人：孙涛
09:00-9:20	蔡威副校长致辞，中心主任马小京致辞
9:20-9:45	Cytosolic anti-bacterial immunity: sensing and execution 邵峰 院士 北京生命科学研究所
9:45-10:10	The UBR5 Ubiquitin Protein Ligase, Genetics, Breast Cancer, and Immune Response 马小京 教授 上海交通大学
10:10-10:20	茶歇
	主持人：于明
10:20-10:45	Epigenetic Regulation of stem cell fate determination and tumorigenesis Hao Jiang Assistant Professor University of Alabama at Birmingham
10:45-11:10	Molecular mechanisms of promoter-proximal pausing release of RNA polymerase II in human cells 于明 特别研究员 上海交通大学
11:10-11:35	Establishment and Maintenance of Epigenetic Information 朱冰 研究员 中科院生物物理所
11:35-14:00	午餐
	主持人：杨选明

14:00-14:25	Type I Interferons: Bridging Innate and Adaptive Anti-tumor Immunity 杨选明　特别研究员 上海交通大学
14:25-14:50	Zika Virus Disrupts Neural Progenitor Development and Leads to Microcephaly in Mice 许执恒　研究员 中国科学院遗传与发育生物学研究所
14:50-15:15	Functions of noncoding RNAs in neural stem cell development and neurological disorders 孙涛　特聘教授 上海交通大学
15:15-15:30	茶歇
	主持人：谢志平
15:30-15:55	Proper Mitotic Spindle Assembly is Essential for Accurate Chromatids Separation in Mammalian Cells 张传茂　教授 北京大学
15:55-16:20	氧化应激与氧化还原信号调控 黄灿华 教授　四川大学
16:20-16:45	Regulation of Autophagy by Novel Pathways 谢志平　特别研究员 上海交通大学
16:45-17:10	Mechanisms of intestinal stem cell regulation and homeostasis 林鑫华　特聘教授　复旦大学
17:10	晚餐

2016 年 7 月 9 日 星期六

08:30-10:30	夏令营学生面试总结评比
10:30-11:00	午餐后散会

五、专家介绍及会议摘要

特邀专家：邵峰 院士

人物简介

邵峰，男，1996 年毕业于北京大学技术物理系应用化学专业；1999 年获得中科院生物物理所硕士学位；2003 年获得美国密歇根大学医学院博士学位；2005 年在哈佛大学医学院完成博士后。现为中国科学院院士，北京生命科学研究所学术副所长、资深研究员。

研究方向

实验室的研究兴趣集中在病原细菌感染宿主和宿主先天性免疫防御的分子机制。对于细菌感染来说，通过特殊的分泌系统向宿主细胞中注入毒素效应蛋白是病原细菌普遍采用的重要致病机制。这些效应蛋白往往以非常有效的方式作用于宿主信号转导中的关键分子，使其发生功能紊乱。效应蛋白的作用有利于细菌宿主中的生存和进一步感染。研究以多种临床上常见的病原菌（Shigella,Salmonella, Enteropathogenic E. coli, Legionella 以及 Burkholderia）为模式，着眼于发现并揭示效应蛋白在抑制真核细胞重要信号转导通路中的一些新的、较为普遍的生物化学机制。

实验室最近的研究工作在这方面取得了一系列的突破和发现。1)来源于 Shigella, Salmonella 和植物假单胞杆菌的 OspF 家族三型分泌系统效应蛋白通过一种崭新的磷酸化苏氨酸裂合酶的活性，特异性地、不可逆地“去磷酸化”宿主 MAPK 激酶并使其失活，从而抑制宿主细胞因子的表达。2) Legionella 的四型分泌系统效应蛋白 LegK1 能模拟宿主中的 IKK 激酶而磷酸化 IκBa 蛋白，并诱导其被泛素化和降解，进而激活 NF-κB 通路并对巨噬细胞凋亡产生抑制作用。3)三型分泌系统效应蛋白 CHBP（Burkholderia）和 Cif（Enteropathogenic E. coli）特异性地修饰（脱氨）泛素和泛素样蛋白 NEDD8 中 Gln-40。这种修饰能有效地阻断宿主泛素-蛋白酶体通路并导致诸如细胞周期等重要细胞生理过程发生功能紊乱。

同时，我们也对宿主巨噬细胞如何通过其先天性免疫系统来拮抗病原微生物感染的机制感兴趣。我们将结合生物化学、细胞生物学以及小鼠遗传学等多种手段来研究和阐明炎症小体被激活的生化机制。

Cytosolic anti-bacterial immunity: sensing and execution

Feng Shao

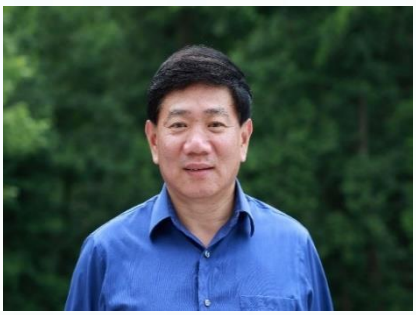
National Institute of Biological Sciences, Beijing

Inflammatory caspases including caspase-1, 4, 5 and 11 are critical for cytosolic defenses against bacterial infections. Caspase-1 is activated by canonical inflammasomes mediated by a scaffold that senses the infection. We identify the NAIP family of NLR proteins as inflammasome receptors for bacterial flagellin as well as the type III secretion apparatus. Pyrin, encoded by the familial Mediterranean fever disease gene, forms a canonical inflammasome complex upon bacterial modifications/inactivation of host Rho GTPases, such as glucosylation by *C. difficile* cytotoxin TcdB and deamidation by *B. cenocepacia*. We also discover that caspase-4/5 in human and caspase-11 in mice are cytosolic receptors for bacterial LPS, playing a critical role in anti-bacterial defense and septic shock. LPS binding to the CARD domain induces oligomerization and activation of caspase-4/5/11. Common to inflammatory caspases activation is pyroptosis, a programmed necrotic cell death. Using genome-wide CRISPR/Cas9 screens we identify GSDMD as a pyroptosis substrate for all inflammatory caspases. GSDMD$^{-/-}$ cells resist pyroptosis induction by both canonical inflammasome agonists and cytosolic LPS. IL-1β release is also inhibited in GSDMD$^{-/-}$ cells. The caspases cleave the linker between the Gasdermin-N and -C domains in GSDMD, releasing the autoinhibition on Gasdermin-N that harbors intrinsic pyroptosis-inducing activity. GSDMD belongs to a large Gasdermin family; other family members are not cleaved by inflammatory caspases but share the autoinhibition. These findings are of significant insights into inflammatory caspases-mediated immunity/diseases and also suggest a new paradigm for understanding pyroptosis and programmed necrosis.

Key words: Pyroptosis, Inflammasome, LPS, flagellin, bacterial infection.

特邀专家：马小京 教授

人物简介



1987 年获英国爱丁堡大学分子遗传学专业博士学位，先后在美国宾夕法尼亚大学担任高级研究员、康奈尔大学担任终身教授，长期从事探索免疫学领域的基础研究，在揭示免疫反应细胞和分子作用机制及开创新的探测技术方法手段方面取得了突出成绩。在 Nature Immunology, Immunity, J. Experimental Medicine, J.Immunology 等高水平国际期刊杂志发表 SCI 论文 80 余篇，相关研究成果的独特与创新性被 Nature 和 Cell、Nature Reviews Immunology 等进行专题报导和评论。曾荣获 Young Investigators Award by International Cytokine Society、Howard Temin Award (NCI/NIH)等奖励。现为上海交通大学“盛毓绶细胞与免疫学研究中心”主任。

研究方向

我们组致力于研究细胞因子的基因表达及其在炎症疾病中的免疫反应。目前的研究领域包括以下几个方面：

在凋亡细胞被巨噬细胞和树突状细胞吞噬的过程中，调节 IL-23 基因表达的分子机制，及其对红斑狼疮中 Th17 细胞发育的影响。

在抗原呈递细胞 APCs 中，NOD2 调节 IL-12 基因表达的分子机制，及 IL-12 介导的炎性肠病。

肿瘤细胞产生的新型分子抑制树突状细胞诱导的 T 细胞活化及 T 细胞介导的抗肿瘤免疫的分子及细胞机制。

在三阴性乳腺癌中，CCL5 对髓样抑制细胞发育的作用及机制。

在败血症和中枢神经系统中，progranulin 通过调节 IL-10 调控炎症的作用及机制研究。

The UBR5 Ubiquitin Protein Ligase, Genetics, Breast Cancer, and Immune Response

Xiaojing Ma
School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, Shanghai

Breast cancer (BC) is a leading cause of mortality among women in the Western world. Approximately 15-20% of BC is the so-called "triple negative" (TN) type for the absence of estrogen receptor (ER), progesterone receptor (PR) and HER-2/neu (ErbB2). A 2007 study of more than 50,000 women with all stages of BC found that 77% of women with TNBC survived at least 5 years, whereas 93% of women with other forms of breast cancer were found to survive at least five years. Clearly, more therapeutic modalities are needed for TNBC.

We applied next generation sequencing to a number of human TNBC specimens with the objective to identify potential "driver" genes for TNBC development and pathogenesis. One of the hits that was identified for its significant amplifications at the genomic DNA level and verified at the mRNA level for overexpression over the surrounding normal breast tissues was an E3 ubiquitin protein ligase named UBR5. To explore UBR5's functional importance in TNBC, we studied this gene in great details in a syngeneic murine model of transplanted TNBC, which expresses very high levels of UBR5. We took the approach to "knockout" UBR5 in tumor cells via the CRISPR/Cas9 system and confirmed that it was inactivated by more than 95% at the mRNA and protein levels in several selected clones. Subsequently, we carried out a series of in vitro and in vivo experiments comparing the behavior and responses of the WT and KO tumor cells. There were dramatic differences in tumor growth and lung metastasis. We observed that the KO tumors exhibited decreased proliferation and angiogenesis, increased apoptosis, and altered epithelial mesenchymal transition (EMT). One of the most strikingly affected genes critically involved in EMT is E-cadherin whose expression in KO tumors was completely abrogated. In addition, we also observed marked increases in the number of activated dendritic cells (DCs) in the tumor-draining lymph nodes and tumor-infiltrating cytotoxic T cells in mice carrying UBR5 KO tumors. Finally, as a confirmation of our study, a large clinical data mining survey/analysis published at the end of 2015 in Molecular Cancer Research reveals that UBR5 amplifications occur in more than 20% of ovarian and breast cancers, in more than 10% of liver, prostate and bladder cancers. In addition, BC patients carrying genetic mutations in UBR5 have significantly reduced survival rates compared to those without the alterations. Thus, targeting UBR5 in TNBC will likely be a much more effective therapeutic strategy than currently available treatment regimens for this deadly disease.

特邀专家：Hao Jiang Assistant professor

人物简介

1996 Tsinghua University, Beijing B.S.

2005 Johns Hopkins University School of Medicine, Baltimore Ph.D. (with Stephen Desiderio)

2010 The Rockefeller University, New York Post-doc (with Robert G. Roeder)

2011- University of Alabama at Birmingham, Assistant professor

2016- University of Alabama at Birmingham, Associate Scientist.

研究方向

My lab studies roles of histone modifications, with a particular focus on histone H3K4 methylation, in the regulation of gene expression in stem cell fate determination. The central properties of the embryonic stem cells lie in their continuous self-renewal while maintaining the potential to differentiate into all types of cells in the organism. It has recently been demonstrated that various types of differentiated cells can be reverted to the pluripotent state or can be converted to one another. Controlling the stability and plasticity of cell identity is obviously crucial for animal development and physiology, and is also pivotal for regenerative medicine. With a few exceptions, all cells in an organism share the same genome, but they do have different epigenomes and gene expression patterns. Therefore, at the heart of the cell identity control is the control of gene expression. Epigenetic mechanisms including the covalent chemical modifications on histones are increasingly recognized as a fundamental and prevalent means to regulate gene expression. In a simplistic view, histone H3K4 methylation is generally associated with gene activation, while H3K27 methylation with gene repression. However, it is still difficult today to give definitive answers to some simple yet fundamental questions including: Is H3K4 methyl mark functionally critical for transcription? If yes, then to what extent does it impact on animal physiology?

Epigenetic Regulation of stem cell fate determination and tumorigenesis

Hao Jiang

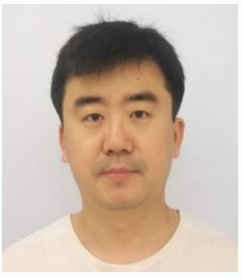
University of Alabama at Birmingham, USA

The broad interest of my laboratory is how gene regulation at the chromatin, transcriptional, and post-transcriptional levels controls the stability and plasticity of animal cell identity, how dysregulation of these mechanisms lead to diseases especially cancer, and how we may develop novel molecules to combat these diseases based on these mechanisms. One major direction of our research has to do with the functional role of the Dpy30 subunit of the Set1/Mll complexes in regulating stem cell fate determination and tumorigenesis. We have shown that Dpy30 is dispensable for embryonic stem (ES) cell maintenance, but is critical for the two-way cell-fate transitions between the ES and differentiated cells. Using a *Dpy30* conditional KO mouse model we recently generated, we have shown a critical role of Dpy30 in the fate specification of neural stem cells and hematopoietic stem cells (HSCs), as well as the long-term maintenance of HSCs, via epigenetic regulation of the expression of multiple key chromatin and transcription modulators. Moreover, we have recently shown that Dpy30 reduction significantly repressed the *Eμ-Myc*-driven lymphomagenesis by inducing B cells apoptosis without affecting normal physiology. These results suggest a key role of Dpy30 in a “non-oncogene addiction” pathway and may be targeted for cancer treatment. I will also present our latest progress in developing inhibitors of Dpy30 for potential cancer treatment.

Keywords: Histone methylation, Dpy30, stem cell maintenance and differentiation, cancer.

特邀专家：于明 特别研究员

人物简介



1996－2000　本科，微生物学，内蒙古大学生命科学学院

2000－2005　博士，生物化学与分子生物学，北京大学生命科学学院

2005－2007　博士后，Department of Immunobiology, Yale University School of Medicine (with Tian Chi)

2007－2010　博士后，Boston Children’s Hospital, Harvard Medical School (with Alan B. Cantor)

2010－2015　博士后，Laboratory of Biochemistry & Molecular Biology, The Rockefeller University (with Robert G. Roeder)

2016~至今　特别研究员，上海交通大学生命科学技术学院。

研究方向

血细胞发育和癌症的转录调控。主要利用基因组学技术、分子遗传学技术和蛋白质组学技术来阐明转录调控因子 PAF1 complex（Yu et al., Science, 2015）、Super Elongation Complex、MLL1、GATA1（Yu et al., Molecular Cell, 2009）和 RUNX1（Yu et al., Molecular Cell, 2012; Yu et al., PNAS, 2008）在生理条件下调控血细胞的发育的分子机理以及与它们相关的转录失调诱发癌症的分子机理。

Molecular mechanisms of promoter-proximal pausing release of RNA polymerase II in human cells

Ming Yu

Sheng Yushou Center of Cell Biology and Immunology, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, Shanghai

Around seventy-five percent of the genes in a given type of animal cells have paused RNA polymerase II (Pol II) 30-50 nucleotides downstream of their transcriptional start sites (TSSs). Paused Pol II release is a critical step of transcriptional regulation. It is currently believed that paused Pol II release is dependent on the kinase activity of P-TEFb. MLL1 is one of the histone 3 lysine 4 methyltransferases in human cells. MLL fusion genes, arising from the break of MLL1 and the fusion of its 5’ fragment in frame to one of the fusion partner genes, cause mixed lineage leukemias (MLLs). Some of the major fusion partners of MLL1, including AF4, AFF4, AF9, ENL, and ELL, were recently found to be subunits of a multiprotein complex, which also contains P-TEFb. Considering that ELL and P-TEFb are known elongation factors, the complex was named the super elongation complex. Yet, roles of AF4, AFF4, AF9, and ENL in transcriptional regulation and the molecular mechanisms underlying the corresponding MLL fusion proteins-mediated persistent gene activation remain unclear. I will present our latest findings.

Key words: human, RNA polymerase II, transcriptional elongation, leukemogenesis

特邀专家：朱冰 研究员

人物简介

朱冰，男，1992 年毕业于浙江大学生物科学技术系；1995 年从中国水稻研究所获得遗传学硕士学位；1999 年从中国科学院上海植物生理研究所获得分子遗传学博士学位；1999-2002 年在瑞士弗雷德里克-米歇尔研究所作博士后（with Jean-Pierre Jost）；2002-2006 年在美国霍华德-休斯医学院/新泽西医学与牙医学大学作博士后（with Danny Reinberg）；2006-2014 年在北京生命科学研究所（NIBS）担任研究员、高级研究员；2012 年起开始担任 Howard Hughes Medical Institute（HHMI）International Early Career Scientist；2014 年受聘为中国科学生物物理研究所，现为中科院生物物理所研究员、博士生导师。

研究方向（表观遗传学的可塑性和可继承性）

多细胞生物的多种细胞类型拥有同一基因组体，却各不相同，并拥有各自独特的基因表达谱。这被认为是由表观遗传学机制实现的对 DNA 承载的遗传信息的精细调控。表观遗传学信息需要同时具有可塑性和一定的可继承性，以确保不同类型细胞可以得到分化，又可以在分化后维持稳定。本实验室的研究兴趣为：

1. 表观遗传信息的建立与维持机制

多种组蛋白修饰和 DNA 甲基化是经典表观遗传现象的重要调控因子，本实验室试图通过结合生物化学，定量蛋白质组学，高通量基因组分析和高通量筛选来鉴定并理解参与表观遗传信息的建立与维持的新机制。

2. 染色质修饰酶的活性调节

大量的染色质修饰酶已被鉴定，但对它们催化活性的调节机理研究较少。染色质修饰酶常被认为是机械性的催化机器，然而近期的研究表明染色质修饰酶更可能是聪明的艺术家，可以视基因转录状态的不同和染色质环境的不同调节自己的活性，以谱写不同的修饰曲调。对染色质修饰酶活性调节的研究不仅有助于对表观遗传学机制的理解，也有助于更好的设计干预染色质修饰酶活性的小分子化合物。因为多个染色质修饰酶被认为是潜在的药物靶标。

Establishment and Maintenance of Epigenetic Information

Bing Zhu

Institute of Biophysics, Chinese Academy of Sciences

DNA is unarguably the carrier of genetic information. However, DNA sequence alone cannot explain how hundreds of cell types in a complex multi-cellular organism, such as a human individual can possess distinct transcription programs, while sharing the same genetic information. This is believed to be achieved by fine-tuning our genetic information with a so-called “epigenetic” system. To fulfill the two basic tasks challenging the multi-cellular organisms, epigenetic system must simultaneously offer dual characteristics, “Plasticity & Inheritability”. Plasticity allows the transformation of one genome into hundreds of epigenomes and transcriptomes, whereas inheritability permits the maintenance of every single epigenome and its corresponding transcriptome.

We are interested in several dimensions of the epigenetic system. Primarily, we would like to understand how epigenetic information is inherited during mitotic divisions and how epigenetic information is established during germ cell maturation and stem cell differentiation. In this seminar, I will highlight some of our recent progresses along these directions.

Keywords: Epigenetics, DNA methylation, histone modification, germ cell maturation, mitotic inheritance

特邀专家：杨选明 特别研究员

人物简介

1998.9-2002.7　北京大学生命科学学院 理学学士

2002.9-2009.5　中国科学院生物物理研究所感染与免疫研究中心 博士

2009.6-2014.6　美国芝加哥大学病理学系 博士后

2014.6-2014.10　美国芝加哥大学 助理研究员

2014.11 至今　上海交通大学生命科学技术学院 特别研究员

研究方向

课题组研究侧重于肿瘤免疫学和肿瘤免疫治疗，研究成果发表于 Nature Medicine, PNAS, Cancer Cell, Cell Host & Microbe，Molecular Therapy 和 Journal of Immunology 等杂志。

免疫治疗在抗感染与肿瘤治疗中有着重要的作用和非常广泛的临床应用前景。尤其是肿瘤免疫治疗，在近期获得了飞速的发展，被 Science 杂志评为 2013 年十大突破科技进展中的第一位。本实验室从基础肿瘤免疫学入手，着手于发现新的抗肿瘤机理和靶点，发展新的肿瘤免疫疗法，具体方向如下：

1.研究肿瘤微环境中的各种细胞组分对肿瘤免疫的抑制机理，发现新的肿瘤治疗靶点；

2.发展基于抗体的靶向肿瘤免疫治疗手段；

3.发展基于 T 细胞修饰的细胞过继性肿瘤治疗手段；

Type I Interferons: Bridging Innate and Adaptive Anti-tumor Immunity

Xuanming Yang

Sheng Yushou Center of Cell Biology and Immunology, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, Shanghai

Antibodies (Abs) that preferentially target oncogenic receptors have been increasingly used for cancer therapy, but tumors often acquire intrinsic Ab-resistance after prolonged and costly treatment. Here, we arm the Ab with IFNb? and observed that it is more potent than first generation of Ab for controlling Ab-resistant tumors. This strategy controls Ab-resistance by re-bridging suppressed innate and adaptive immunity in tumor microenvironment. Mechanistically, Ab-IFNb therapy primarily and directly targets intra-tumoral dendritic cells, which re-activate CTL by increasing antigen cross presentation within the tumor microenvironment. Additionally, blocking PD-L1, which is induced by Ab-IFNb treatment, overcomes treatment-acquired resistance and completely eradicates established tumors. Therefore, it establishes a next-generation Ab-based immunotherapy that targets and eradicates established Ab-resistant tumors.

特邀专家：许执恒 研究员

人物简介

1989 年获上海第二军医大学医学学士系学位，1999 年获美国新泽西 Rutgers 大学博士学位。1999-2005 在美国哥伦比亚大学神经生物学和精神病中心做博士后及高级研究助理。先后获得美国 NIH 的 Ruth L. Kirschstein National Research Service Award (2002-03)及 Rutgers 大学 Bush Fellowship (1997-1999)和 Waksman Fellowship (1993-1997)，2005 年中国科学院“百人计划”入选者，2007 年国家杰出青年科学基金获得者。现为中国科学院遗传与发育生物学研究所研究员。

研究方向

利用本课题组在信号转导领域的优势，结合不同的模式动物，进行神经和肿瘤生物学研究，争取在阐明不同的重要疾病发生的分子机制方面有所突破。目前，我们的研究重点是 JNK，NFκB 和 AKT 信号通路，这些信号通路与肿瘤、神经发育及神经退行性疾病均密切相关。有关研究将为疾病的预防和治疗提供理论依据，同时为个体正常发育的分子机理提供新见解。

主要研究内容：

1) 用分子、生化和细胞生物学为手段研究不同蛋白激酶复合体在信号传导通路中的作用与调节机制，进一步揭示 JNK 信号传导通路在神经发育和肿瘤及神经退行性疾病病理过程中的意义。

2) 建立和利用基因操作小鼠模型研究小颅畸形、精神分裂症、自闭症和神经退行性疾病的发病机制。

Zika Virus Disrupts Neural Progenitor Development and Leads to Microcephaly in Mice

Zhiheng Xu

Institute of Genetics and Developmental Biology, Chinese Academy of Sciences.

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The link between Zika virus (ZIKV) infection and microcephaly has raised urgent global alarm. The historical African ZIKV MR766 was shown to infect cultured human neural precursor cells (NPCs), but unlike the contemporary ZIKV strains, is not believed to cause microcephaly. Here we investigated whether the Asian ZIKV strain SZ01 could infect NPCs in vivo and affect brain development. We found that SZ01 replicates efficiently in embryonic mouse brain by directly targeting different neuronal linages. ZIKV infection leads to cell cycle arrest, apoptosis and inhibition of NPC differentiation, resulting in cortical thinning and microcephaly. Global gene expression analysis of infected brains reveals upregulation of candidate flavirus entry receptors and dysregulation of genes associated with immune response, apoptosis and microcephaly. Our model provides the first evidence for a direct link between Zika virus infection and microcepahly, with potential for further exploration of the underlying mechanisms and treatment of ZIKV related pathological effects.

Keywords: Zika virus infection, neural precursor cells, microcepahly, immune response

特邀专家：孙涛 特聘教授

人物简介

2013—至今 特聘教授 上海交通大学，生命科学技术学院

2011—2013 副教授 康奈尔大学威尔医学院 细胞与发育生物学系

2005—2011 助理教授 康奈尔大学威尔医学院 细胞与发育生物学系

2002—2005 博士后 哈佛大学医学院 医学中心神经生物学系

2000—2002 博士后 哈佛大学医学院 癌症研究所小儿肿瘤科

1995—1999 神经生物学博士 伦敦大学学院

1991—1994 动物学硕士 中国科学院动物所 （北京）

1987—1991 动物学学士 厦门大学生物系 （厦门）

研究方向

实验室主要致力于研究非编码 RNA 在神经系统发育和神经系统疾病机理的研究。利用动物遗传学、分子生物学、干细胞培养和生物信息分析等手段，我们力图探究非编码 RNA（包括 microRNA，long noncoding RNA 等）在大脑发育中的作用，解析神经系统疾病的分子机理，寻找神经系统疾病早期诊断及治疗的新手段、新靶点。实验室研究成果发表在《Science》,《Cell》，《Cell Reports》,《Nature Reviews Neuroscience》，《PNAS》，《Current Biology》，《Development》，《Journal of Neuroscience》和《Journal of Cell Science》等杂志上。

Functions of noncoding RNAs in neural stem cell development and neurological disorders

Tao Sun

School of Life Sciences and Technology, Shanghai Jiao Tong University, Shanghai

Abnormal proliferation and differentiation of neural stem cells and neural progenitors in the developing cerebral cortex can cause brain malformation and result in dysregulation of brain function such as epilepsy and mental disability. Emerging evidence has shown that similar to protein coding genes, noncoding RNAs play critical roles in cortical development and are associated with the etiology of human neurological disorders. We have found that a specific group of microRNAs (miRNAs) is required for proper proliferation and differentiation of cortical neural progenitors. Knockout or knockdown of these miRNAs cause microcephaly in mice. These miRNAs are also essential for maintaining adult neural stem cell population in the hippocampus and are associated with mood disorders. Moreover, long noncoding RNAs (lncRNAs) are also required for neurogenesis in the developing cortex by interacting with transcription factors. Our studies have demonstrated crucial roles of noncoding RNAs in brain development and neurological disorders.

特邀专家：张传茂 教授

人物简介

1983 年～1986 年：南京农业大学硕士研究生

1989 年～1993 年：北京大学生命科学学院 博士研究生

1993 年 7 月～2001 年 8 月：北京大学生命科学学院副教授

2005 年 3 月至今 ：北京大学教育部长江特聘教授

2001 年 8 月至今 ：北京大学生命科学学院教授，博士生导师

研究方向

细胞核结构与功能、细胞周期调控研究（包括纺锤体装配机理研究，DNA 复制起始调控机理研究，核膜装配机理研究等）、Ran GTPase 在细胞核物质运输和细胞周期调控中的作用、肿瘤细胞生物学(肿瘤细胞增殖调节和增殖控制)

1. 发现 Ran GTPase 控制核膜装配(Science, 2000; Current Biology, 2011; Journal of Cell Science, 2012）。
2. 发现 Ran GTPase 控制纺锤体组装(Journal of Cell Science, 1999)。
3. 建立了应用相关蛋白质小球和细胞(包括卵细胞)提取物为材料的非细胞体系核膜重建模式(Current Biology, 2001, 2002; European Journal of Cell Biology,2002）。
4. 发现核膜物质运输相关蛋白 importin beta 参与核膜装配(Current Biology, 2002)。
5. 发现 Ran 调控核孔复合体装配(European Journal of Cell Biology, 2002)。
6. 发现 RCC1 在染色体上定位所产生的 Ran-GTP 梯度是纺锤体正确装配所需要的(Current Biology, 2002)。
7. 发现 Ran GTPase 通过调控核膜物质运输进而调控 DNA 复制(Journal of Cell Science,1998)。
8. 以实验证明细胞核纤层(Nuclear lamina)对细胞核结构的维持和 DNA 复制起重要调控作用(Journal of Cell Science,1996)。
9. 发现 Nucleoplasin 在非洲爪蟾卵提取物细胞凋亡过程中调控染色质的凝集(PNAS 2005)。
10. 发现 Aurora A/B, Plk1, Cdk1 等激酶综合调控纺锤体装配(PNAS，2009；Cell Research, 2008, 2011; Journal of Cell Science, 2009, 2013a, 2013b)。

Proper Mitotic Spindle Assembly is Essential for Accurate Chromatids Separation in Mammalian Cells

Chuanmao Zhang

Peking University

Accurate chromatids separation and cell division require assembly of a proper mitotic spindle in mammalian cells. Fail to assemble a proper mitotic spindle can result in aneuploidy that may be involved in aging and the formation of cancer or the cell death. A typical metaphase spindle, vaguely ellipsoid in cross section, is mainly composed of a well-organized microtubule mass and many microtubule-associated proteins (MAPs). The spindle microtubules connect in one end with one of the two opposite spindle poles and in another end with one of the paired kinetochores assembled at each side of the chromosome. The mitotic spindle is dynamic all the time under tight regulation of a number of key issues and many regulatory factors such as MAPs, mitotic kinases, Ran GTPase with its binding/effect proteins, and so on. For instances, first, serving as two spindle poles for the spindle assembly in mitosis, the centrosome must be duplicated once per cell cycle and the duplicated pairing centrosomes need to be timely separated; second, a proper connection of the spindle microtubules with the kinetochores must be established for the accurate chromatids separation; and third, the spindle size/length must be proper as it influences the chromosome positioning, the cytokinetic furrow induction, the following cell division, and the daughter cell size. Among the many factors that regulate the proper mitotic spindle assembly, the mitotic kinases take crucial roles for the spindle dynamics, the stepwise kinetochore formation, the spindle assembly checkpoint and the connection of the microtubules with the kinetochores. Ran GTPase and its binding/effect proteins are also crucial for the mitotic spindle assembly by regulating many aspects including the microtubule nucleation, the connection of the microtubules with the kinetochore, and the spindle size. Both the mitotic kinase and Ran GTPase systems are well-coordinated and can also regulate each other in performing their functions in the regulation of the mitotic spindle dynamics through affecting the function of MAPs, the microtubule nucleation, the centrosome duplication, and other processes. In this talk, I will mainly discuss the morphology construction and the dynamics of the mitotic spindle under regulation of the mitotic kinases and Ran with its binding proteins.

特邀专家：黄灿华 教授

人物简介

国家杰出青年科学基金获得者(2012）；国家重大科学研究计划（973 计划）“病毒诱导肿瘤发生的氧化还原蛋白质组研究”项目首席科学家；教育部长江学者特聘教授（2014）。国际学术刊物 PROTEOMICS 等编委委员。

2000 年在中国科学院获博士学位，随后在新加坡国立大学生物系从事博士后研究。2003 年 8 月被新加坡国立大学肿瘤研究所聘为 Research Scientist。2005 年 9 月回国任四川大学生物治疗国家重点实验室教授。回国以来以通讯作者在 Gastroenterology、Cancer Res (2 篇，含封面论文)、Autophagy (4 篇)、 Mol Cell Proteomics (5 篇)、Cell Death Differ、PLoS Pathogen 等学术刊物上发表 SCI 论文 50 余篇，其中 30 余篇论文影响因子大于 5.0，被引用 1400 余次。受邀请在 Mass Spectrom Rev、Med Res Rev、Expert Rev Proteomics (6 篇)等国际学术刊物上发表多篇关于系统生物学前沿综述。

研究方向

（1）系统生物学筛选药物靶标。

（2）病毒诱发癌变的分子机理。

氧化应激与氧化还原信号调控

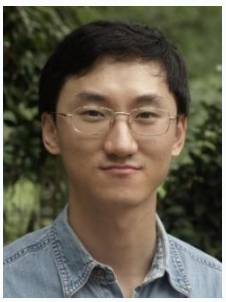
黄灿华

华西医院 生物治疗国家重点实验室

Cancer cells maintain their intracellular ROS concentrations at required levels for their survival. Changes in ROS concentrations can regulate biochemical signaling mechanisms that control cell function. It has been demonstrated that ROS regulate the cellular events through redox regulation of redox-sensitive proteins (redox sensors). Upon oxidative stress, redox sensors undergo redox modifications that cause the allosteric changes of these proteins and endow them with different functions. Understanding the altered functions of redox sensors and the underlying mechanisms is critical for the development of novel cancer therapeutics. Recently, a series of high-throughput proteomics approaches have been developed for screening redox processes. In this manuscript, we review these methodologies and discuss the important redox sensors recently identified that are related to cancer.

特邀专家：谢志平 特别研究员

人物简介



NSFC 优秀青年基金获得者

教育部新世纪优秀人才入选者

2014 年—至今，上海交通大学，生命科学技术学院，特别研究员

2009 年—2014 年，南开大学，医学院，副教授 (独立 PI)

2008 年—2009 年，美国 密歇根大学 安阿伯分校，生命科学研究所，博士后

2001 年—2008 年，美国 密歇根大学 安阿伯分校，分子细胞发育生物学系，博士

1997 年—2001 年，北京大学，生物化学与分子生物学系，中国经济研究中心，双学士

研究方向

细胞自噬(Autophagy)是对维持真核生物健康有关键作用的的一类亚细胞降解途径。该通路以囊泡运输的形式实现对胞内受损或冗余的大分子和细胞器的高效清除。研究表明，细胞自噬在生物体生长发育、免疫防御、细胞程序性死亡、肿瘤抑制等方面有非常重要的作用。本领域的研究兴起于上世纪 90 年代，现在是生命科学研究前沿发展最快的领域之一。

本实验室的研究主要包括利用现代分子生物学、细胞生物学方法，寻找作用于自噬体形成过程的新基因，进一步揭示自噬体形成的分子机理，理清上游信号转导网络对细胞自噬的调节作用，研究细胞自噬在疾病发生过程中的作用，探索通过干预细胞自噬减缓或治愈疾病的可行性。

Regulation of Autophagy by Novel Pathways

Zhiping Xie

School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, Shanghai

Autophagy is a basic function of eukaryotic cells. It is mainly responsible for the removal of obsolete or damaged organelles and protein aggregates, in particular under stress conditions. As both insufficient and excess autophagy lead to detrimental effects, maintaining adequate autophagy activity is of critical importance to the health at the cellular level. Our recent work has identified novel pathways involved in the regulation of autophagy under starvation.

Keywords: Autophagy, Regulation, Metabolism, Ubiquitin.

特邀专家：林鑫华　特聘教授

人物简介

国家首批“千人计划”海外高层次引进人才入选者。2016 年 7 月至今为复旦大学特聘教授，任复旦大学遗传学研究所所长。将组建“复旦大学细胞生物学与分子影像研究中心”跨院系平台并担任中心主任。1984 年毕业于杭州大学生物系 (现浙江大学)，获学士学位；1987 年毕业于中国科学院上海细胞生物学研究所，获硕士学位；1995 年 7 月毕业于美国华盛顿大学（Washington University），获分子遗传学博士学位；1995 年 5 月至 2000 年 4 月美国哈佛医学院做博士后研究；2000 年 4 月至 2009 年 7 月，历任美国辛辛那提大学儿童医院医学中心助理教授、副教授、教授；2009 年 7 月至 2016 年 6 月，任中国科学院动物研究所研究员。2007 年获得国家自然基金委海外杰出青年科学家奖（B 类），2008 年入选中组部“千人计划”资助，2010 年担任国家重大科学研究计划（973）首席科学家，2011 年担任膜生物学国家重点实验室动物所分室主任。目前担任中国细胞生物学会发育生物学分会会长、中国细胞生物学会北京分会副理事长、中国动物学会常务理事、任国际期刊 Developmental Dynamics、Fly 编委，担任《细胞生物学学报》副主编。曾获美国癌症协会学者奖、国家自然科学基金委海外杰出青年科学家奖、Basil O’Connor 学者奖、日本第十五届复合糖国际研讨会青年科学奖。

研究方向

研究领域着重于发育信号转导及干细胞生物学的研究。主要以果蝇和小鼠为模式动物，研究 Wnt、Hh 和 BMP 信号通路及其浓度梯度形成的作用机制和肠干细胞调控及稳态维持的机理；研究囊泡转运（Retromer）和蛋白修饰（泛素化）在发育信号转导中的作用机制；探讨细胞信号转导在干细胞以及相关疾病（如肿瘤、先天性缺陷）中的作用机制。林鑫华博士在细胞信号转导领域的研究成绩斐然。许多成果被 Nature 综述类杂志重点介绍；其对 Wnt/Wg 蛋白的分泌、分布以及信号转导的贡献获得发育生物学家们一致肯定；蛋白糖在形态发生素浓度梯度形成中的作用，被公认为是这一领域的重大发现；近年来有关肠干细胞领域的研究也获得同行专家的广泛关注和认可。是一位在模式动物遗传学、发育生物学和干细胞生物学领域有重要影响力的专家。

Mechanisms of intestinal stem cell regulation and homeostasis

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The Lin lab has been focused on the molecular mechanisms of morphogen gradient formation, cell signaling, stem cell-niche interaction using ***Drosophila*** and mouse as model systems. In the talk, I will present the recent studies of his lab on the molecular mechanisms regulating morphogen signaling and intestinal homeostasis. Adult tissue homeostasis is maintained by resident stem cells and their progeny. However, the underlying mechanisms controlling tissue homeostasis are not fully understood. Morphogens such as BMP, Hh and Wnt, are essential for developmental patterning. We demonstrated that trachea-derived Decapentaplegic(Dpp), the main BMP ligand in *Drosophila*, is essential for adult midgut homeostasis via organ-organ interaction. We showed that Debra-mediated Ci degradation is important for intestinal stem cell (ISC) proliferation in *Drosophila* adult midgut. We also demonstrated that Perlecan, an essential ECM molecule, is critical for maintaining gut stem cell activity possibly via stem cell-Matrix interaction. Recently, our lab has been focused on the mechanisms by which JAK/STAT pathway regulates ISC activity and homeostasis. Finally, I will also introduce our recent studies in intestinal homeostasis using mouse as a model system.