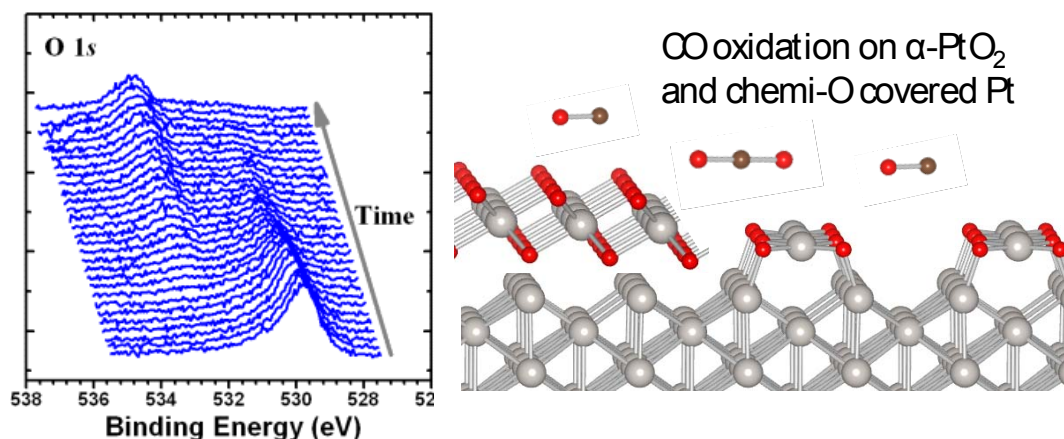


In situ Oxidation Study of Pt (110) and Its Interaction with CO

CO oxidation on transition-metal surfaces is one of the most thoroughly investigated systems in heterogeneous catalysis, due to its importance in automotive exhaust treatment and water-gas shift as well as its ability to shed light on fundamental catalyst properties. In particular, the study of CO oxidation on Pt (110) has received much attention over the last two decades. Self-sustained oscillations and spatiotemporal patterns form on this surface as well as a variety of surface oxides. Furthermore, there is still an ongoing debate regarding the influence of surface structure on CO oxidation kinetics. To fully understand and model these fascinating phenomena, in situ characterization of adsorbed oxygen and oxide phases of Pt (110) in O₂ and CO and under reaction conditions is required.

Progress has been made recently by an international cooperation led by theoretician Prof. Li Wei-Xue at Dalian Institute of Chemical Physics (DICP, China), Dr. Liu Zhi at Lawrence Berkeley National Laboratory (LBNL) and Prof. Bongjin S. Mun at Hanyang University (Korea), and the result has been published in *J. Am. Chem. Soc.* 133, 20319-20325 (2011). Using newly developed in-situ surface characterization techniques, ambient-pressure X-ray photoelectron spectroscopy (AP-XPS) at Advanced Light Source of LBNL and high pressure scanning tunneling microscopy (HP-STM) and density functional theory calculations, the teams found that at low oxygen pressure, only chemisorbed oxygen is observed on the Pt (110) surface. At higher pressure (0.5 Torr of O₂), nanometer-sized islands of multilayered α -PtO₂-like surface oxide form along with chemisorbed oxygen. Both chemisorbed oxygen and the surface oxide are removed in the presence of CO, and the rate of disappearance of the surface oxide is close to that of the chemisorbed oxygen at 270 K. The spectroscopic features of the surface oxide are similar to the oxide observed on Pt nanoparticles of a similar size, which provides an extra incentive to revisit some single-crystal model catalyst surfaces under elevated pressure using in situ tools.



This work was supported by National Natural Science Foundation of China, Department of Energy of United State and Korea Research Foundation.

Chinese Scientists Published a Paper on Prevention of Drug Craving and Relapse by Memory Retrieval-extinction Procedure in *Science*

With the financial support by the National Basic Research Program of China and the National Natural Science Foundation of China, the group led by professor Lin Lu from National Institute on Drug Dependence, Peking University found that a memory retrieval-extinction procedure prevent drug craving and relapse. The findings were published on *Science* Magazine on April 13th. Therewith, Professor Barry Everitt, a famous neurobiologist from University of Cambridge, wrote a comment about this finding that was published on the same issue.

Addiction was defined as a chronic, relapsing brain disorder. Recently, addiction was considered as aberrant memory that presents a pathological usurpation of the neural mechanisms underlying the normal learning and memory. The major problem in treatment of addiction is how to prevent drug craving even after long-term abstinence, during which the relapse occurs when the addicts re-exposed to drug-related cues (such as previous drug used context) or addictive drugs. Prior studies in rats and humans have shown that emotional memories are vulnerable to interference during reconsolidation: certain drugs given during reconsolidation can weaken the memory. The drugs don't erase actual memories of an event, only the emotional response to reminders of it. Unfortunately, most of these drugs have undesirable side effects or are not approved for human use. What's new in the work is that they've found a way to achieve the same effect without giving any drugs. In the studies, before each extinction session, the researchers exposed the rats to a heroin-associated cue, so the extinction session would happen just as the rat's brain would be reconsolidating the emotional memory linking the cue to the heroin. They found that this intervention prevented the rats' heroin-seeking responses from reemerging under conditions that would normally make them reemerge (such as injection of a small "priming" dose of heroin). What's more, this effect persisted even if the rats were tested in a different physical location. This finding strongly suggests that the procedure weakened the emotional memories the rats had previously learned—accomplishing what can't be accomplished with extinction sessions alone. In patients like that, videos showing heroin use and paraphernalia can reliably induce heroin craving, as assessed by questionnaire responses and blood-pressure changes. They found that presenting a heroin-cue videotape 10 minutes before each extinction session (which consisted of exposure to heroin paraphernalia and simulated heroin) attenuated the patients' craving during the extinction session itself, and also prevented cue-induced craving for heroin 1, 30, and 180 days later. Additionally, the memory-maintenance molecule PKM ζ in infralimbic cortex and in basolateral amygdala has been found to implicate in the retrieval-extinction procedure. The potential mechanism of the retrieval-extinction procedure to prevent drug craving and relapse may be the modification of the original drug memories. The superior of the retrieval-extinction procedure is noninvasive and nonpharmacological intervention without any side-effect. Thereby, the retrieval-extinction procedure is a promising method for preventing drug relapse and craving during abstinence.

Series Papers Published in *Energy Policy*: Modeling Energy Use of China's Road Transport and Policy Evaluation

As the travel demand and vehicle population in China are experiencing tremendous growth, China has stepped into the period of rapid motorization. As a result, road transport has become one of the sectors whose energy consumption increases most rapidly in China. This growth trend will continue in the foreseeable future. How to control and reduce the energy use of the road transport sector, meantime ensure the sustainable development of the automotive industry and fulfill the increasing travel demand has become a practical challenge in China. To address this challenge, it is important to understand the growth trends in travel demand, vehicle ownership, as well as vehicle use at different stages of economic development, and to understand the effects of potential policies on vehicle sales, vehicle ownership, vehicle scrappage, vehicle use, and vehicle energy efficiencies.

Dr. Huo Hong, Associate Professor of Institute of Energy, Environment, and Economy of Tsinghua University, has been studying energy issues and associated policies of road transport for years. With the financial support from the National Natural Science Foundation of China, Dr. Huo collaborates with domestic and international research organizations and conducts a series of original research work targeting the scientific issues mentioned above, which has achieved innovative progress.

Dr. Huo's work reveals the intrinsic relationship of vehicle market, vehicle ownership, and vehicle use to economic parameters such as per-capita GDP, per-capita income, income distribution, and vehicle price, models the variation trends of vehicle ownership and vehicle use at different stages of economic development in China, examines the energy and environmental issues of China's road transport based on comprehensive analysis of the impact of future economic development, citizen income distribution, and vehicle scrappage policies on the development of China's automotive industry, simulates quantitatively the energy and environmental effects of potential policies including fuel economy improvement, promoting new energy vehicles and alternative fuels, etc, which provides prospective scientific support for sustainable development of the automotive industry and "Energy Conservation, Emission Reduction" policies in China. The results show that improving fuel economy will offer the best energy and climate benefit in both short and long term; electric vehicles could yield remarkable benefit in energy saving and greenhouse gas emission reduction if the share of renewable power in the generation mix increases and the conversion efficiency of coal-fired power plants improves in the future; alternative fuels are able to save a large amount of petroleum, but may cause an increase in greenhouse gas emissions with the current technologies, and this issue could be addressed as the technologies of carbon capture & storage and second generation bio-ethanol become commercially mature.

Dr. Huo's work improved the understanding of the future variation trend and driving forces of on-road energy demand and greenhouse gas emissions in China. The most recent work was published as four series papers in the 4th issue of *Energy Policy* in 2012. This is the first time for *Energy Policy* since it was founded in the 1970s to publish four series papers written by the same author in one single non-special issue. The four papers discussed vehicle population growth, variation patterns of vehicle use, vehicle technologies and energy efficiencies, and energy and environmental impacts of various policies, respectively. Dr. Huo also has another paper published in the 11th issue of *Energy Policy* in 2011 as a data support for the four papers. This work developed a model named "Fuel Economy and Environmental Impact model (FEEI model)" to simulate the energy use and emissions of China's road transport under

various development pathways and policy scenarios. Now the FEEI model is accessible on-line (www.feeimodel.org), and has been used in several research institutes in the world.

(Department of Management Science, Liexun Yang, Zhonggen Mao, and Yongguang Zhong)

* * * *

Breakthrough in the Ambient Catalytic Destruction of Formaldehyde

Indoor air quality is a major factor influencing the human health. Formaldehyde (HCHO) is a hazardous and dominant common indoor air pollutant in China. How to effectively and economically eliminate the indoor air HCHO is of great interest and challenge to researchers.

The Research Group of Environmental Catalysis, led by Professor Hong He in Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, has been devoted to the development of new methods and technologies for indoor air purification for years. Funded by the National Nature Science Foundation of China, a breakthrough development was achieved in the ambient catalytic destruction of formaldehyde. The research group developed a novel Pt based catalyst after screening a considerable number of various catalytic materials and preparation methods. They discovered that the Pt species on the mentioned catalyst is in an atomically dispersion, with dramatic capacity for activating molecular oxygen in air at room temperature to catalyze HCHO oxidation into H₂O and CO₂ without decrease in activity over long period operation. The related results have been applied for patents and published in the following journals: *Catalysis Communications* 6, 211 (2005); *Applied Catalysis B* 65, 37 (2006); *Catalysis Today* 126, 345 (2007). In addition, with the support from the National 863 Program of China, this group has successfully applied this basic research achievement into practical applications. The new Air Cleaners equipped with novel catalyst have been developed and put into Chinese market; and already become the most selling Air Cleaner in China. Their work is an outstanding contribution in the improvement of indoor air quality and has benefitted the Chinese people.

Based on those achievements, Professor Hong He and other partners won the “China National Award for Technological Invention (2nd class)” in 2011.

Novel Findings for High Altitude Adaptation from the Yak Genome

An international consortium, led by Prof. Liu Jianquan in Lanzhou University, comprising researchers from BGI, the world's largest genomics organization, Institute of Kunming Zoology, Chinese Academy of Sciences as well as the other 12 institutes, has completed evolutionary analyses of the genetic bases for yak to survive at high altitude based on the genomic sequence of a female yak. This important research was recently published by an article entitled "The yak genome and adaptation to life at high altitude" on *Nature Genetics* on July 1, 2012. This work was partly funded by National Natural Science Foundation of China (30725004 and 40972018 to Jianquan Liu).

As a standard symbol of the Qinghai-Tibet Plateau (QTP) and high-altitude, yak (*Bos grunniens*) is the most important animal species for Tibetans and other nomadic pastoralists in the QTP and adjacent high-altitude regions. Yaks have provided them not only the basic food resources, i.e., meats and milks, but also transportations, fuels (yak dung), and accommodation tents. 'No domestic yak, no conquest of the QTP by human beings' as suggested by a popular saying. In particular, yak has a very closely related relative, as we all know, cattle. Cattle could not survive at high altitude. Compared with cattle, yak has many anatomical and physiological traits that enable it to live at high altitude, including high energy metabolism, impressive foraging ability, enlarged hearts and lungs, and lack of hypoxic pulmonary vasoconstriction when faced with relatively low oxygen conditions. Therefore, the comparison between yak and cattle has become as a standard model for understanding high-altitude adaptation.

In order to understand genetic bases of the high-altitude adaptation in yak, researchers firstly sequenced the genome of a female domestic yak using whole-genome shotgun strategy based on Illumina HiSeq 2000 platform. The genomic data yielded a high-quality draft assembly, has contig and scaffold N50 size of 20.4 kilobases (Kb) and 1.4 megabases (Mb), respectively. The total length of the assembly is 2,657 Mb, close to 2,649 Mb previously reported for the cattle genome size. Based on the high coverage sequence data, researchers tracked down 2.2 million heterozygous SNPs within the sequenced individual. The researchers also performed whole transcriptome sequencing on RNA samples derived from fresh heart, liver, brain, stomach, and lung tissues collected from the same yak. Based on these RNA-sequence data, combined with homology alignment and gene prediction models, the researchers estimated that the yak genome contains 22,282 protein-coding genes. They also found that the heterozygosity rate is much higher in yak than in cattle. As they suggested that this may result from a longer and more systematic selection in cattle and/or introgression from wild yaks.

Then, researchers conducted the comparative genomic analyses between yak and cattle in order to understand genetic adaptation of yak to the high-altitude. Yak and cattle were estimated to diverge around 4.9 million years ago, around the same time when human and chimpanzee diverged. Therefore, many genes found in yak are similar to those in cattle and 99.5 percent proteins are similar. Despite this, they still found that yak developed its own (yak-endemic) 170 genes belonging to 100 gene families. In yak, genes also became more in the gene families related to sensory perception and energy metabolism. Similarly, in addition, domains also expanded in a few proteins related to the extracellular environment and hypoxic response. For example, the genes with Hig_1_n domain were found to be

highly expressed under hypoxia stress. This domain significantly expanded in yak when compared to cattle and other mammals. The expansions of these gene families and domains in yak may be critical for its high-altitude survival.

Finally, researchers aligned and compared evolutions of the orthologous genes between yak and cattle. They found that those orthologous genes between yak and cattle related to hypoxia and energy metabolism evolved much faster than others. Based on these findings, they further identified the most critical genes during such a high-altitude adaptation, which were assumed to have retained positively selected footprints. Three such genes were identified and these genes should have played important roles in helping yak to regulate hypoxia-response at high-altitudes. Five other such genes may have helped yak to optimize nutritional assimilation and energy production from the limited food resource at high-altitude (Fig. 1).



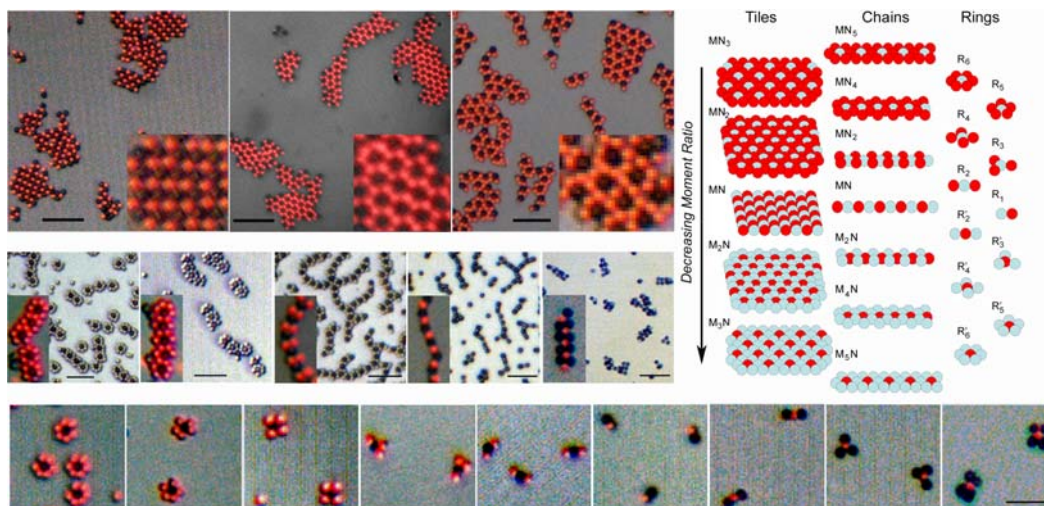
As pointed out by the researchers, the determination of the key genes in the natural high-altitude adaptation in yak will be highly useful to improve current understanding, treatment and prevention of altitude sickness and other hypoxia-related diseases in humans. In addition, the yak genome sequence together with the many SNPs recovered in this study will facilitate genetic dissection of agronomically important traits in the species and accelerate the genetic improvement of milk and meat production of this essential livestock to the Tibetan people and economy.

This research has aroused a widespread interest over the world. When the work was published online, *Science Now's* Science-Shot made a timely comment by the title “What gets yaks high” at its homepage (scienceshot-what-gets-yaks-high.html). Since then, numerous institutes, news webs, newspapers and magazines reported this exciting work.

Binary Colloidal Structures Assembled through Ising Interactions

Supported by the NSFC Research Fellowship for International Young Scientists, Professor Benjamin Yellen, together with researchers at University of Michigan – Shanghai Jiaotong University Joint Institute, Shanghai, China, and colleagues at Duke University, Durham, NC, reported an achievement in *Nature Communications* on a versatile colloidal assembly system, in which the design rules can be tuned to yield over 20 different pre-programmed structures, including Kagome, honeycomb, square tiles, and various chain and ring configurations.

The diverse functionality of crystalline materials found in nature has inspired the quest to develop man-made versions with building blocks ranging in size from atoms to bricks. Self-assembly of microscopic particles into macroscopic structures provides a robust pathway for building 2D and 3D crystalline materials that cannot be produced by lithographic methods; however a general pathway for producing a wider variety of structures remains a fundamental challenge.



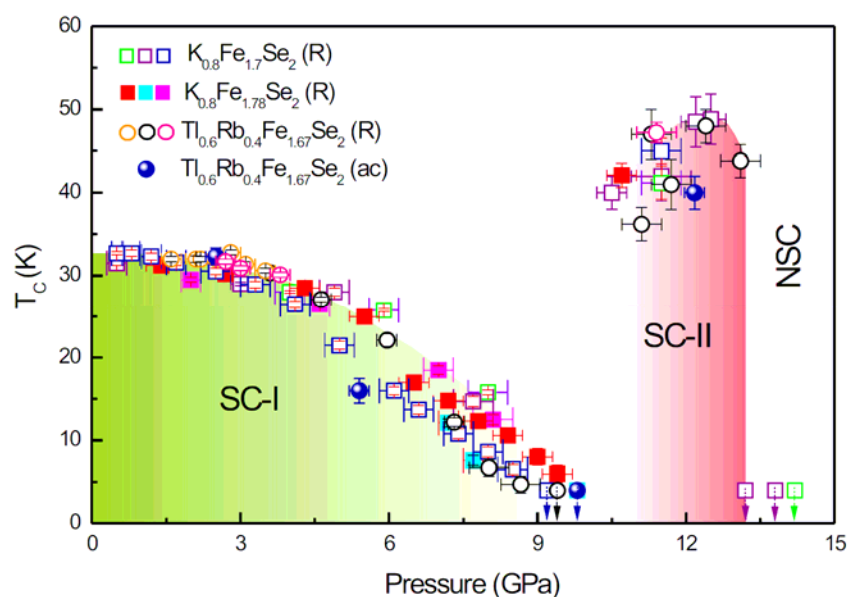
The assembled structures are tuned by controlling the relative concentrations and interaction strengths between spherical magnetic and non-magnetic beads, which behave as paramagnetic or diamagnetic dipoles when immersed in a ferrofluid. When this mixture of beads are immersed in a ferrofluid, the unlike particles attract and the like particles repel in a manner similar to the attraction and repulsion between positive and negative charges. The director of the research, Prof. Yellen, described this process using the analogy, “Conceptually, the role of the ferrofluid is to adjust the effective charges on the different beads, and coax them to form structures that resemble the NaCl lattice as well as others that are not found in nature.” Despite the resemblance to electric charges, the analogy is not exact. Yellen remarks “Compared with ionic systems which are limited to charges of integer number, the magnetic dipoles are not perfectly compensated, and thus we can also produce frustrated lattices, such as various chain and ring states.”

In addition to the experiments, Prof. Yellen and his group developed theoretical models that can predict the assembled structure as a function of the experimental parameters. Yellen explains, “The beauty of this technique is that we can select the type of crystal that forms by choosing the right concentrations of particles and ferrofluid. It turns out that the phase behavior of the assembled structures can be predicted with a simple theory based on two tuning parameters, namely, by the relative particle dipole moments and their relative concentrations. The agreement between theory and experiment is quite remarkable.” Yellen anticipates that by using particles of different sizes, shapes, and types, it is possible to assemble a more diverse set of crystal structures that not only have myriad of applications, but also can provide fundamental insights into how crystals form at the atomic scale.

Reemergence of superconductivity at 48K in Compressed Iron Selenide Based Superconductors

Superconductivity in some materials can be induced or tuned by chemical substitution, external pressure and magnetic field. Among these control parameters, pressure is a “clean” way to produce or manipulate superconductivity of matters without changing their chemistry.

Recently, a new finding from Prof. Zhao Zhongxian’s group at Institute of Physics, Chinese Academy of Sciences, demonstrated an unexpected superconducting phenomenon in a newly discovered iron selenide based superconductors under pressure condition. In this investigation, Prof. Sun Liling, a member of this group, and her colleagues in collaboration with Prof. Mao Ho-Kwang and Dr. Chen Xiaojia at Carnegie Institute found that the superconducting transition temperature (T_c) in this kind of superconductor decreases with increasing pressure from the maximum of 31 K to vanishing at around 10 GPa, then reappears at pressure above 11.5 GPa, which was identified by *in-situ* resistance and magnetic measurements in a self-integrated system developed by Zhao’s group. The T_c of the re-emerging superconducting phase reaches 48 K which is considerably higher than the first maximum (31 K), setting a new T_c record in iron selenide based superconductors. Interestingly, the basic structure of these compounds was not changed when the superconductivity reemerged. They believe that further studies can help to determine what is happening on a closer structural level in the pressure-induced superconducting state and shed insight on the underlying mechanism of high- T_c superconductors.



Pressure dependence of the T_c for $Tl_{0.6}Rb_{0.4}Fe_{1.67}Se_2$, $K_{0.8}Fe_{1.7}Se_2$ and $K_{0.8}Fe_{1.78}Se_2$. The symbols represent the pressure–temperature conditions for which T_c values were observed from the resistive and alternating current susceptibility measurements; symbols with downward arrows represent the absence of superconductivity to the lowest temperature (4 K). All samples show two superconducting regions (SC-I and SC-II) separated by a critical pressure at around 10 GPa. NSC, the non-superconducting region above 13.2 GPa. The maximum T_c is found to be 48.7 K in $K_{0.8}Fe_{1.7}Se_2$ at a pressure of 12.5 GPa. At higher pressures above 13.2 GPa, the samples are non-superconducting. Error bars are one standard deviation.

The work is the first observation on the pressure-induced reemergence of superconductivity among the high-T_c superconductors. It is also demonstrated that high pressure is an effective tool in manipulating quantum state of matters. This work is published by *Nature* on March 1, 2012 [*Nature* 483, 67 (2012)] and highlighted by *Nature's* news online.

The samples studied were provided by Prof. Chen Xiaolong and Prof. Chen Genfu from Institute of Physics, Prof. Fang Minghu from Zhejiang University. High-pressure x-ray diffraction measurements were performed at Shanghai Synchrotron Source and Advanced Photon Source. This project was supported by the NSFC, 973 projects, and Chinese Academy of Sciences.

<http://www.nature.com/nature/journal/v483/n7387/full/nature10813.html>

<http://www.nature.com/news/superconductor-breaks-high-temperature-record-1.10081>

* * * *

Nucleosomes Suppress Spontaneous Mutations Base-Specifically in Eukaryotes

A research team led by Professor He Xionglei at the College of Life Sciences, Sun Yat-sen (Zhongshan) University made a breakthrough in understanding how chromatin structure regulates spontaneous mutations, with a discovery that nucleosomes, the structural units of chromatin, suppress mutations from cytosine (C) to thymine (T) in eukaryotic cells. This research appears as a Report in the March 9th issue of *Science*.

Mutations not only provide new materials for evolution, but also are the primary cause of diseases. Among the four bases that constitute DNA, cytosine is unique because it is subject to a high rate of hydrolytic deamination, a major source of C→T mutations that account for up to ~40% human Mendelian inheritance disorders. Prof. He and colleagues examined how C→T mutations are regulated in eukaryotic cells, by using comparative genomic analyses and a mutation accumulation experiment. What they found was that nucleosomes nearly eliminate deamination-derived C→T mutations, presumably by preventing the cytosines from the attack of water via suppressing DNA breathing. Further analysis shows that nucleosome occupancy suppresses ~50% G→T and A→T mutations, possibly by protecting the DNA from reactive oxygen species.

This work reveals how chromatin structure, the major player in epigenetics, regulates a central genetic process. It suggests that nucleosomes can serve as a GC-content modulator through adjusting mutation direction, shedding light on the unique features of eukaryotic genome structure and evolution. It also has important implications in understanding the origin of somatic mutations in cancers and in induced pluripotent stem cells, both of which are associated with chromatin re-modelling.

Single-Chain Fragmented Antibodies Guided SiRNA Delivery in Breast Cancer

Over the past ten years, the enthusiasm to harness small RNA molecules, mainly small interfering RNAs (siRNAs) and microRNA mimics, into therapeutic weapons has never been quenched. However, a major obstacle hindering the clinical application of these small molecules is how to efficiently and precisely deliver siRNAs *in vivo* into target cells to silence target genes. An international collaborative study led by Song Erwei from the Memorial Hospital of Sun-Yat-Sen University and Wang Jun from Hefei National Laboratory for Physical Sciences at Microscale and School of Life Sciences of University of Science and Technology of China has now shed light on the possibility of targeting anti-cancer siRNAs directly to the tumor cells using single-chain fragmented antibodies (ScFvs).

This study was funded by two NSFC grants of Talent-Training Program for Song Erwei and Wang Jun respectively, as well as other funding from the NSFC and the Ministry of Science and Technology, and lasted for a period of six years. In this study, the authors exploited a fusion protein of ScFv specific to Her2 and a positively charged protamine to deliver siRNA for Polo-like kinase 1 (PLK1), a master regulator to promote cell division, to Her2⁺ breast cancer cells. The delivery is efficient and specific not only in cell cultures but also *in vivo* in xenografted mice. Only breast cancer cells overexpressing Her2 took up the siRNAs efficiently. More importantly, intravenous injection of siRNAs complexed with the fusion protein suppressed tumor growth, reduced metastasis and prolonged survival with no observed toxicity in immuno-compromised mice xenografted with Her2⁺ breast cancers. This research appears as a research article in the April 18th issue of *Science Translational Medicine*.

The incidence of breast cancer is increasing rapidly in China (by 3% annually), and 25-30% of these patients have Her2⁺ tumors. This subtype of breast cancer behaves aggressive and is apt to develop distal metastasis and post-treatment recurrence. Although trastuzumab (Herceptin), a humanized monoclonal anti-Her2 antibody, is effective to prolong survival of patients with Her2-overexpressing breast cancers, about 60% of metastatic Her2⁺ breast cancers do not respond to the treatment. Song's study, herein, presents a novel strategy to combat Her2⁺ breast cancers by linking the technology of RNA interference and single chain antibodies. Dr. Song has already been authorized to hold the patent of using the fusion protein for siRNA delivery. The present study is another success after his landmark study at Judy Lieberman's lab at Harvard Medical School in the field of RNA interference, which employed antibody for gp120 to delivery anti-HIV siRNAs into HIV infected cells and was published in 2005 in *Nature Biotechnology* as one of the cover stories.

(By Hong Wei, Li Cui, Dong Erdan)

Does Yeast Suicide?

There has been much controversy on whether the single-cell eukaryote yeast undergoes programmed cell death (PCD), or so-called apoptosis. The only caspase-related gene, *YCAI*, also termed *MCAI* (encoded by Yor197w), identified in the yeast genome so far, suggests that apoptosis does occur in the unicellular organism *Saccharomyces cerevisiae*.

Yca1 belongs to the metacaspase subfamily of caspase family in clan CD protease family. **Caspase** is a family of Cysteine proteases that specifically hydrolyzes *asp*artyl bonds. Metacaspases, on the other hand, were suggested to cleave after positively charged residues like lysine or arginine. Although caspases have been intensively studied and are proven to be key players in apoptosis in metazoans, little information on the structure and functional mechanism of metacaspases limited our knowledge of Yca1 to a positive regulator of apoptosis in yeast.

Supported by the National Natural Science Foundation of China, the research group led by Professor Shi Yigong of Tsinghua University solved the crystal structure of the yeast metacaspase Yca1 at 1.7 angstrom resolution. The structure of Yca1 represents an overall caspase fold. This supports the notion that metacaspase is a distant relative of caspases and, probably, the evolutionary conservation of apoptosis in yeast.

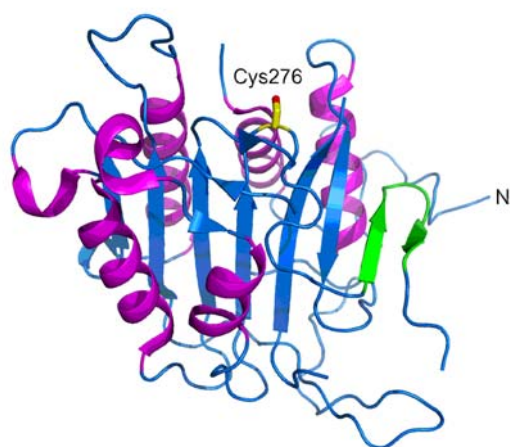


Figure. Structure of Yca1. The structure of the yeast metacaspase Yca1 (PDB code 4F60) represents an overall caspase fold but contains an extra pair of anti-parallel β -strands (highlighted in green) that disrupts potential caspase-like homo-dimerization. The catalytic residue Cys276 is shown in yellow.

However, unlike canonical caspases and the paracaspase MALT1, which belongs to another caspase subfamily, the yeast metacaspase Yca1 contains an extra pair of anti-parallel β -strands that disrupts potential caspase-like homo-dimerization. Indeed, our researchers observed that Yca1 exists as a monomer in the crystals and in solution. Moreover, Yca1 was indicated to be a calcium-activated protease. These results suggest that the mechanism of Yca1 activation is distinct from canonical caspases and paracaspases.

On the other hand, researchers found out that Yca1 cleaves a truncated fragment of the yeast Bir1 protein *in vitro*. This is the first direct substrate protein of Yca1 reported up to date. This finding opens new doors to future studies of the molecular mechanism of apoptosis in yeast.

Caspases are important proteases that play pivotal roles in apoptosis. Crystal structures of various canonical caspases and the paracaspase MALT1 have been solved by researchers led

by Professor Yigong Shi over the past decade. Solving the crystal structure of the metacaspase Yca1 provides the last piece of puzzle and gives insight to functional mechanism of this huge caspase family.

For details of this research, please refer to the article published by Wong A.H., C. Yan and Shi Y. in *Journal of Biological Chemistry*.

China Scientists Developed Important Methodologies for Spatiotemporal Detecting and Manipulating of Cellular Activities

Recently, technologies that enable spatiotemporal detecting and manipulating of cellular activities have become one of the most important frontiers of life science research, providing powerful tools to tackle complex biological questions. However, most of the original research of these technologies and methodologies had occurred in the developed countries.

Over the past few years, Dr. Yang Yi, a biochemist and a chemical biologist based on East China University of Science and Technology, Shanghai, has devoted himself to the studies looking for solutions that can image or control intracellular biological activities in situ, in vivo and in real time. He and his team members have established in situ labeling and imaging methods for various oxidative modifications of protein thiols such as S-nitrosothiols, disulfides and vicinal dithiols, and discovered the prominent role of mitochondria played in the function and regulation of cellular thiol proteome, not only as the producer but also as the target of reactive oxygen species. These studies offered methods and insights into identifying mechanisms of cellular redox signaling and associated diseases such as cardiovascular diseases and inflammation (*PNAS*, 2007, 104, 10813; *Angew. Chem.* 2011, 123, 7693). He also developed a series of genetically encoded fluorescent sensors for one of the most important metabolite NADH (*Cell Metab.* 2011, 14, 555). These sensors, termed as Frex, manifest a large change in fluorescence upon NADH binding, and can be targeted to different subcellular compartments, allowing monitoring and imaging cellular metabolism with high spatial resolutions and in real time. Owing to their superior sensitivity and specificity, these sensors can be used to investigate the effect of various stimuli on living cell metabolism in the research of cell biology and developmental biology, in the mechanism studies of metabolic disorders and cancer, and in the innovative drug discovery, as many enzymes that make and use NAD⁺ and NADH are important in pharmacology and disease pathobiology.

Most recently, Dr. Yang developed an easy to use and robust light switchable gene expression system by combining strategies of synthetic biology and chemical biology (*Nature Methods*, 2012, 9, 266). This transactivator–promoter transgene system, named LightOn, was based on a synthetic, genetically encoded light-switchable transactivator. The transactivator binds promoters upon blue light exposure, and rapidly initiates transcription of target transgenes. Not only does the LightOn system have fast kinetics, high transcriptional activity and reversibility, but also it has the capability to be spatially and precisely controlled. Spatiotemporal control of red fluorescent protein gene expression by light was also achieved in living mice transfected with the LightOn system. In type I diabetic mice, light induced expression of insulin was able to decrease blood glucose. These advanced characteristics of LightOn system provides a convenient way to control gene function in mammalian cells with unprecedented temporal and spatial accuracy, and can be used to manipulate an extremely broad range of biological processes in living systems with minimal perturbation. The system will find its applications for tackling complex biological questions in developmental biology and neuroscience, three dimensional stem cell differentiation and even artificial organ construction, and for dosage titrated spatiotemporal control of gene therapy. The technique was highlighted by *Nature Reviews Molecular Cell Biology* and *China Science Daily*. The background story of the invention was also published in the Author File of the same issue of *Nature Methods*.

(Department of Chemical Sciences)

Scorpions Inspire Chinese Scientists in Making Bionic Non-eroding Surfaces for Machinery

Erosion exists diffusely in machinery, metallurgy, energy, building materials, aviation, spaceflight, and many other industrial fields. It has become one of the important reasons of material damage and equipment failure. A series of issues caused by erosion have been paid more and more extensive attentions by academic researchers and applied engineers.

Recently, Prof. Han Zhiwu and his colleagues from Jilin University in China published an article in *Langmuir* (2012, 28, 2914-2921), titled "Erosion Resistance of Bionic Functional Surfaces Inspired from Desert Scorpions", in which they reported their latest research results of erosion resistance of the bionic functional surfaces. It has attracted enormous attentions from the fields of international academics, industry, aviation and commerce, etc. The highlight of comments about their latest achievements were released in "ACS News Service Weekly PressPac", the full-length feature reports and high evaluation were also carried out by other famous news magazines, such as "Scientific American", "The Economist", "Science Daily", "EurekAlert", and "AirspaceMag", etc. They said that Prof. Zhiwu Han and his research group sought the secrets of the yellow fat-tailed desert scorpion (*Androctonus Australis*) body surface of erosion resistance for the first time, and the special structure on its back surface could resist the erosion of the wind sand. Hence, they found a new method in bionics to solve the mechanical moving parts of the erosion resistance. Subsequently, their research results were reported and reshopped by more than 60 international science and technology news magazines and websites.

In order to adapt to the harsh natural environment and meet the survival needs, the living creature evolved and optimized specific structures under the law of natural selection for millions of years. Prof. Han Zhiwu and his research group, supported by the National Natural Science Foundation of China, studied the erosion resistance characteristics of the yellow fat-tailed desert scorpion further. They found the erosion resistance mechanism and characteristics rule of the desert scorpion body surface under gas-solid two-phase flow, and revealed the multi-element mechanism of comprehensive influences of the desert scorpion back morphology, microstructure and flexibility. They established the computing model and the bionic model of erosion resistance of the desert scorpion body surface.

Based on the characteristics of the scorpion body surface dissemination of fluorescence under UV irradiation, the desert scorpion back was observed by combination of methods such as 3D laser scanning and stereo microscope with UV. The longitudinal and transverse contours of the desert scorpion back were obtained. They found that the scorpion back is composed of a very tough chitin membrane, and covered with many round granules. The particle size on the tergums front-end is larger than that on the back-end. Both sides of tergum and breastplate are connected with flexible lateral membrane, and the tergums are connected with flexible intersegment membrane. The intersegment membrane has elasticity, and is formed grooves in the junction. The flexible connection of intersegment membrane and lateral membrane contribute to release the energy of erosion, but the round convex granules and the grooves can change the state of two-phase flow boundary layer. Hence, the scorpion evolved to survive the abrasive power of harsh sandstorms.

The bionic design and manufacture of the functional surfaces is a new interdisciplinary field of mechanical engineering and life science. The core scientific problems are the forming mechanism and the action law of the excellent functional surfaces of living creature, as well as the design principles and the manufacturing techniques of the bionic functional surfaces. Taking inspiration from the yellow fat-tailed scorpion, which uses a shield to protect itself against scratches from desert sandstorms, Prof. Zhiwu Han and his research group presented multi-element bionic comprehensive design principles of erosion resistance for the functional surfaces.

These findings not only are expected to develop a new way to protect the helicopter rotor, the rocket engine nozzles, turbine blades, pipes and other mechanical parts from wear and tear damage, but also bring some new development opportunities in the materials science field.

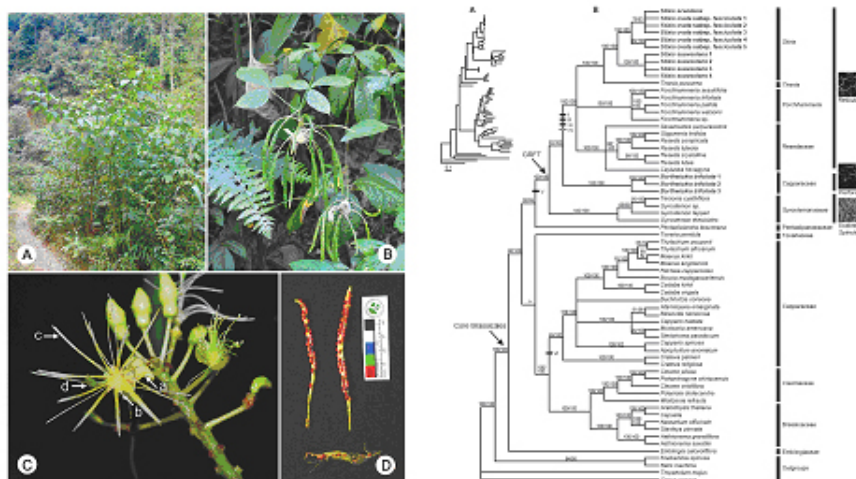
Research on Phylogenetic Placement of *Borthwickia* and Description of a New Family of Angiosperms, Borthwickiaceae

Under a research project funded by NSFC, Dr. Chen Zhiduan's group from State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, CAS published on *Taxon* in June, 2012 an article "Phylogenetic placement of two enigmatic genera, *Borthwickia* and *Stixis*, based on molecular and pollen data, and the description of a new family of Brassicales, Borthwickiaceae", establishing a new family of angiosperms. This is a significant achievement made by Chinese scientists in plant phylogenetics.

In the past two decades, tremendous progress has been made in understanding relationships within angiosperms. The order- and family-level tree of life of angiosperms has been reconstructed. However, due to relatively limited taxon sampling within families, those higher-level phylogenetic analyses of angiosperms did not clarify the circumscriptions of some heterogeneous families.

Capparaceae (Brassicales) as traditionally circumscribed is heterogeneous, and several genera have been segregated from it based on molecular and/or morphological data. *Borthwickia*, one Southeast Asian endemic genus of Capparaceae with controversial position and taxonomic rank, has not previously been evaluated in a molecular phylogenetic study. The authors used four plastid DNA regions (*matK*, *ndhF*, *rbcL*, and *trnL-trnF*) and pollen data to determine its phylogenetic relationship within core Brassicales.

Their results show that *Borthwickia* is not a member of Capparaceae, which is also supported by leaf, placentation, sepal, and carpel characters. Instead *Borthwickia* is sister to the *Forchhammeria*-Resedaceae-*Stixis*-*Tirania* clade with moderate to strong support. However, *Borthwickia* differs markedly from its sister group in having opposite leaves, one indistinct stigma, more than four carpels and locules, a linear ovary with ridges, and pollen grains with perforate exine sculpturing. Thus, a new family, Borthwickiaceae, for the genus, was established. This paper was just published in *Taxon* (2012, 61(3): 601-611), which has been cited by AP-Web (<http://www.mobot.org/MOBOT/research/APweb/>).



Borthwickiaceae Plant and its systematic position

Among angiosperms, there are so far only four families established by the Chinese scientists: Torricelliaceae Hu (1934), Barclayaceae H.L. Li (1955), Acanthochlamydeaceae P.C. Kao (1989), and Borthwickiaceae J.X. Su, Wei Wang, Li Bing, Zhang & Z.D. Chen (2012). However, both Barclayaceae and Acanthochlamydeaceae were not accepted by APG classification system. Therefore, the new established family by Chen Zhiduan's group is the second family named by the Chinese and accepted by APG system.

Borthwickiaceae is placed Brassicales and contains one species, *B. trifoliata*, which is restricted to wet valleys, forests and ravines in southern to southeastern Yunnan (China) and eastern to northern Myanmar. The study on Borthwickiaceae will be helpful to understanding the phylogeny and biogeography of Brassicales. This work also indicates that future direction of plant phylogenetics will be to expand comprehensive comparisons beyond the level of orders and families, to that of genera and species.

* * * *

Plasmoid Ejection and Secondary Current Sheet Generation from Magnetic Reconnection in Laser-plasma Interaction

Funded by NSFC, MOST and CAS, the teams led by Prof. Li Yutong of Beijing National Laboratory of Condensed Matter Physics, Institute of Physics, CAS, Prof. Zhang Jie of Key Laboratory for Laser Plasmas and Department of Physics, Shanghai Jiaotong University and Prof. Zhao Gang of Key Laboratory of Optical Astronomy, National Astronomical Observatories, CAS, obtained important breakthrough in their research, and the findings is published on *Phys. Rev. Lett.* recently.

Reconnection of the self-generated magnetic fields in laser-plasma interaction was first investigated experimentally by Nilson *et al.* [*Phys. Rev. Lett.* 97, 255001 (2006)] by shining two laser pulses a distance apart on a solid target layer. An elongated current sheet (CS) was observed in the plasma between the two laser spots. In order to more closely model magnetotail reconnection, here two side-by-side thin target layers, instead of a single one, are used. It is found that at one end of the elongated CS a fan-like electron outflow region including three well-collimated electron jets appears. The (>1 MeV) tail of the jet energy distribution exhibits a power-law scaling. The enhanced electron acceleration is attributed to the intense inductive electric field in the narrow electron dominated reconnection region, as well as additional acceleration as they are trapped inside the rapidly moving plasmoid formed in and ejected from the CS. The ejection also induces a secondary CS.

Cotton Bollworm Adapts to Bt Cotton via Diverse Mutations

Resistance of cotton bollworm to Bt cotton plants involves more diverse genetic changes than expected, a research team led by Prof. Wu Yidong in Nanjing Agricultural University reports in the journal *PNAS* (109:10275-10280, June 26 of 2012). This work was funded by an NSFC project (grant no. 31071983).

To reduce reliance on insecticide sprays, cotton and corn have been genetically engineered to produce insect-killing proteins derived from the bacterium *Bacillus thuringiensis* (Bt). In 2011, farmers worldwide grew 160 million acres of Bt cotton and Bt corn. The percentage of cotton acreage planted with Bt cotton has exceeded 90% since 2004 in northern China. Although Bt cotton has helped to suppress pests, decrease insecticide sprays, and promote biological control, evolution of resistance to Bt toxins by pests can diminish these benefits.

Monitoring data from China have provided an early warning of resistance to Bt cotton in the cotton bollworm, *Helicoverpa armigera*, a major lepidopteran pest of cotton that also attacks many other crops including corn, soybeans, peanuts, and sorghum. Bioassays show that the frequency of cotton bollworm resistance to Cry1Ac is higher in northern China, where Bt cotton has been grown intensively, than in areas of northwestern China where Bt cotton planting has been limited. The frequency of mutations conferring resistance to Cry1Ac was three times higher in northern China than in northwestern China.

We discovered that in this early stage of field-evolved resistance, diverse mutations confer resistance to Cry1Ac in cotton bollworm populations from northern China. To proactively develop strategies to delay resistance and sustain the efficacy of Bt crops, researchers have used various indirect methods to try to better understand resistance to Bt toxins. In particular, to evaluate the genetic basis of resistance, researchers have selected for resistance in cotton bollworm and other pests by exposing them to Bt toxins in controlled laboratory experiments. The assumption implicit in this approach is that the genetic basis of resistance in the field will be similar to that found in lab-selected strains. Primarily because of limited data on the genetic basis of resistance to Bt crops in field populations, this assumption had not been tested before for Bt crops.

We found that the most common mutation in field-selected populations of cotton bollworm from northern China was the same as a mutation that was detected with lab selection. This recessively inherited mutation disrupts a cadherin protein that binds Cry1Ac in the larval gut of susceptible insects. Because binding to cadherin is required for toxicity, this mutation confers resistance. We also found other recessive mutations in the cadherin gene that confer resistance to Cry1Ac. All of these mutations are similar to recessive mutations conferring resistance to Cry1Ac that were characterized previously in several species of lepidopteran pests.

Unexpectedly, we found two dominant mutations, one in the cadherin gene and the other in a different gene that is not yet identified. The discovery of dominantly inherited resistance is important, because dominant resistance is more difficult to manage than recessive resistance. In particular, the most widely adopted strategy for delaying pest resistance to Bt crops, the refuge strategy, works best when inheritance of resistance is recessive.

One practical option for responding to the early warning of bollworm resistance to Cry1Ac in China would be switching to transgenic cotton that produces two Bt toxins, Cry1Ac and Cry2Ab. Bt cotton producing these two toxins is grown extensively in the United States and Australia. It would be better to switch to Bt cotton that produces Cry2Ab and one or more additional toxins unrelated to Cry1Ac, such as Vip3A (a vegetative insecticidal protein from Bt), so that the increased frequency of resistance to Cry1Ac already seen in some populations would not reduce efficacy of the new Bt cotton. This option would probably require more time to develop. Three-toxin Bt cotton producing Cry1Ac, Cry2Ab and Vip3A may be available by 2016 in the United States and Australia. Planting more cotton that produces no Bt toxins would increase refuge abundance and could help immediately to delay resistance.

In general, we advocate incorporating Bt crops as one tool in integrated pest management (IPM). IPM uses the best available combination of pest control tactics, including transgenic and conventionally bred host plant resistance, biological control, crop rotation, and judicious application of insecticide sprays. IPM can extend the efficacy of Bt crops while promoting sustainable agriculture that limits pest damage, optimizes returns to growers, and preserves environmental quality.

* * * *

A Histone Acetyltransferase Regulates Active DNA Demethylation in Arabidopsis

Under a research project funded by NSFC, Prof. Zhu Jiankang and his team of Shanghai Center for Plant Stress Biology and Shanghai Institute of Plant Physiology and Ecology, Shanghai Institutes of Biological Sciences, CAS, achieved remarkable progress and their latest findings is published on *Science* online recently.

Active DNA demethylation is an important part of epigenetic regulation in plants and animals. How active DNA demethylation is regulated and its relationship with histone modification patterns is unclear. Here, we report the discovery of IDM1, a regulator of DNA demethylation in Arabidopsis. IDM1 is required for preventing DNA hypermethylation of highly homologous multicopy genes and other repetitive sequences that are normally targeted for active DNA demethylation by Repressor of Silencing 1 and related 5-methylcytosine DNA glycosylases. IDM1 binds methylated DNA at chromatin sites lacking histone H3K4 di- or trimethylation and acetylates H3 to create a chromatin environment permissible for 5-methylcytosine DNA glycosylases to function. Our study reveals how some genes are indicated by multiple epigenetic marks for active DNA demethylation and protection from silencing.