

Research on Global Carbon Emission and Sequestration

Prof. Fang Jingyun, member of the Chinese Academy of Science, of Peking University and colleagues published an online article on Science in July, 2011 introducing the findings of an international research group about the global carbon emission and sequestration which will produce significant influence on researches on climate change as well as the international climate change policies. The research project was funded by NSFC and MOST.

As early as in 2007, Prof. Fang initiated the project in collaboration with experts in USDA Forest Service, Princeton University, Duke University and other institutions. In 2009 and 2010, two workshops were held in Peking University and Princeton University successfully which made progress for this project.

The terrestrial ecosystem removes CO₂ from the atmosphere via photosynthesis and plays an important role in balancing the CO₂ density in the atmosphere and slowing down the rise of global temperature. It is an effective approach for us to tackle the global climate change and all countries in the world have attached great importance to researches on ecosystem carbon sequestration.

The research provided with the most comprehensive and systematic evaluation of global forest carbon emission and sequestration so far in the world. Based on forest inventory data and long-term field observations and using ecological models and remote sensing technologies, researchers analyzed the carbon stocks and changes of various factors in forest ecosystems in different terrestrial eco-zones, such as biomass, dead wood, litter, soil and so on. It revealed that in the past 20 years, the world's forest carbon sink was 4 billion tons (about 14.7 billion tons of CO₂) annually, which equals to half of the fossil fuels emission in the corresponding period. However, due to tropical deforestation and degradation caused by human activities, carbon emission added about 2.9 billion tons each year and the net forest carbon sequestration was 1.1 billion tons annually.

The research also showed that factors such as global change notably sped up the growth of tropical forests and thus sequestered more CO₂. With rapid re-growth of tropical forests, tropical forest carbon sink almost compensated the carbon emission caused by deforestation and forest degradation. This result disproved the previous hypothesis that tropical forests were large sources of carbon emission and argued that the net carbon emission of tropical forests had been reversed and tropical forests had achieved "a balance of carbon emission and sequestration". In this sense, the net global forest carbon sink resided mainly in the temperate and boreal forests.

The research showed that China's forest was an important carbon sink. The average Chinese forest carbon sink increased from 130 million tons of the 1990s to the recent 180 million tons. The average carbon stock per area increased from 0.96 (Mg C ha⁻¹ yr⁻¹) to 1.22 (Mg C ha⁻¹ yr⁻¹). These statistics indicated that China's ecological improvement played an important role in slowing down the rise of atmospheric CO₂ density.

Prof. Fang Jingyun has been devoting to the research of terrestrial ecosystem carbon emission and sequestration as well as biodiversity. Many of his articles were published in Science, Nature and PNAS. In 2010, as one of the 12 members appointed by IAC, he jointed the independent evaluation on the IPCC Fourth Assessment Report. The evaluation created extensive influence in the international community and led to the reform of IPCC assessment procedure and organization.

NSFC funded project made significant progress in quantum dynamics

Prof. Zhang Donghui, Prof. Yang Xueming and colleagues in Dalian Institute of Chemical Physics, CAS published on Science in July, 2011 an article “Experimental and Theoretical Differential Cross Sections for a Four-atom Reaction: $\text{HD}+\text{OH}\rightarrow\text{H}_2\text{O}+\text{D}$ ”, summarizing results of a research project funded by NSFC. This is a significant progress made by Chinese scientists in chemical reaction dynamics.

Differential cross sections (DCSs) of chemical reactions characterize the effective target area of the colliding reactants that leads to the scattering of reaction products into a particular angle range. They are the most detailed observables that can be measured experimentally, and also one of the most important physical quantities in chemical reactions. To obtain DCSs theoretically, one needs to solve Schrödinger equations for nuclear motions on a given potential energy surface. In 1976, Schatz of California Institute of Technology and his mentor Kuppermann first converged calculations of state-to-state DCSs for the $\text{H}+\text{H}_2$ reaction, ushering in a new era for accurate calculations for three-atom reactions. In the following thirty years, with the development of more effective quantum scattering methodologies and modern computer technology, researches on three-atom state-to-state quantum dynamics have achieved great progress. Given an accurate potential energy surface for an atom-diatom reaction, quantum scattering theory is now able to provide dynamical quantities that compete in accuracy with state-of-the-art experiments. Close interaction between theory and experiment on three-atom reactions has further clarified many underlying mechanisms. However, extending the success of calculations for three-atom reactions to four-atom reactions is not a trivial task. The number of degrees of freedom increases from three for a three-atom system to six for a four-atom system, which tremendously increases in calculation difficulty and complexity. For this reason, no great progress has been made in the past thirty years for the accurate calculations of four-atom reactions.

With long-term effort, Prof. Zhang and his team developed an effective calculation method and theory for four-atom state-to-state reactions, which provided a possible approach to full-dimensional state-to-state quantum dynamics. With the help of Prof. Xu Xin from Fudan University, the team developed a more accurate energy surface for OH_3 system, and obtained the full-dimensional quantum DCS for $\text{HD}+\text{OH}\rightarrow\text{H}_2\text{O}+\text{D}$ reaction in excellent agreement with those from a high-resolution, crossed-molecular beam experiment by Prof. Yang Xueming’s team. The $\text{H}_2+\text{OH}\rightarrow\text{H}_2\text{O}+\text{H}$ reaction is the easiest four-atom reaction and plays an important role in combustion chemistry. Since it involves three hydrogen atoms, it is an ideal model for accurate quantum dynamics and a benchmark reaction for four-atom reactions. As its isotopic variant, the $\text{HD}+\text{OH}$ reaction has significant meaning for the study of four-atom reactions.

Functional Human Blood Protein Obtained from Rice

Under a research project funded by NSFC, Dr. Yang He of College of Life Sciences, Wuhan University obtained functional human blood protein obtained from rice, and published their research findings in an article "Large-scale production of functional human serum albumin from transgenic rice seeds" on PNAS in November 2011.

The report says that they have devised a way to produce large quantities of the blood protein human serum albumin, or HSA, from rice. HSA is in high demand; it is widely used in drug and vaccine production, in addition to treatments for severe burns, liver cirrhosis, or hemorrhagic shock. However, current HSA supplies are limited by the availability of donor blood from which HSA is traditionally extracted, and carry a high risk of virus contamination.

To overcome these obstacles, Yang He and colleagues engineered rice seeds to produce substantial quantities of HSA, which comprised approximately 10% of the total soluble protein in the seed. The team then developed a method to purify HSA from the rice seeds, and obtained about 2.75 grams of HSA per kilogram of rice. Biochemical tests suggested that the HSA extracted from rice was physically and chemically equivalent to blood-derived HSA. Furthermore, the authors found that rice-derived HSA was as effective as blood-derived HSA in treating liver cirrhosis in rats. The findings suggest that the transgenic rice seeds may be a cost-effective source for HSA and might help satisfy an increasing worldwide demand for the protein, according to the authors.

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How Giant Pandas Thrive on a Bamboo Diet

In a research project funded by NSFC, Dr. Wei Fuwen of Institute of Zoology, Chinese Academy of Sciences, explained how giant pandas thrive on a bamboo diet, and published their research findings in an article "Evidence of cellulose metabolism by the giant panda gut microbiome," on PNAS in October 17, 2011.

The report says that they have identified gut microbes that help giant pandas thrive on a bamboo diet. The dietary habits of giant pandas, whose gastrointestinal tracts are similar to those of carnivores, have long befuddled researchers. The giant panda, an omnivorous bear that consumes up to 12 kg of bamboo every day, lacks enzymes that help herbivores digest cellulose and hemicellulose - the principal components of a fibrous plant diet. Dr. Wei Fuwen and colleagues used gene sequencing techniques to identify the microbes inhabiting the digestive tracts of giant pandas in hopes of finding cellulose-digesting symbionts, which previous attempts have failed to turn up. The authors analyzed more than 5,000 ribosomal RNA sequences that served as genetic barcodes for species of microbes found in the fecal samples of wild and captive giant pandas, and compared the sequences with those found in herbivores.

The authors report that seven taxonomically distinct entities closely related to Clostridium bacteria, known to digest cellulose, were unique to the pandas' fecal samples. Further, the authors identified putative gene sequences for enzymes that digest cellulose and hemicellulose. Together with other adaptations such as pseudo-thumbs, strong teeth, chewing muscles, and copious gut mucus, the cellulose-digesting gut bacteria might help sustain pandas' dietary habit, unusual among carnivores, according to the authors.

New evidence of interpersonal violence from 129,000 years ago found in China

The identification of traumatic lesions in human fossils is of special interest because of the underlying behaviors that are involved: accidental or intentional wounding, potential interpersonal violence, and also the social support needed for the care and recovery of impaired individuals. Aside from the Neandertals, secure evidence of healed traumatic lesions is very rare among Pleistocene human remains.

Supported by the National Natural Science Foundation of China, research of the late Middle Pleistocene archaic human cranium from Maba, south China, brings to the new evidence that interhuman aggression and healed blunt force trauma as early as 129,000 years ago in East Asian.

The report published on Monday, 21 November 2011, in the Proceedings of the National Academy of Sciences of the United States of America (PNAS) documents a lunate lesion on the right frontal squamous exocranially concave and ridged lesion with endocranial protrusion. Differential diagnosis indicates that it resulted from localized blunt force trauma, due to an accident or, more probably, interhuman aggression.

The area of the depressed portion of the vault lesion is 14.0 mm in length and 1.5 mm in its deepest point below the frontal external contour. The center of the depression is rough. Several concentric waves within it created rounded edges, none of which is a complete circle. When the lesion is enlarged, healing of the bone can be seen to have taken place surrounding the area of the depressed area. The trauma is very similar to what is observed today when someone is struck forcibly with stones or staves. Its remodeled, healed condition also indicates the survival of a serious brain injury. It is not possible to assess whether the incident was accidental or intentional, or whether it resulted from a short-term disagreement, or premeditated aggression.

Neurocranial abnormalities had been found in Chinese human fossils; however, when evaluated by paleopathological and forensic diagnostic standards, none represents definitely traumatic lesions caused by interpersonal violence. The depressions or damages on the Zhoukoudian *H. erectus* crania were suspected to hominid agency, but they could be more likely made by geological-crushing from the weight of overlying sediment or carnivores. The lesion on the supraorbital of the Lantian (Gongwangling) calvarium, initially thought to be a healed antemortem trauma, were later ascribed to postmortem taphonomic alterations of the bone. The Middle Pleistocene partial cranium from Hulu Cave, Tangshan, Nanjing, exhibits an ecdocranial healed lesion that was caused by either trauma or burning.

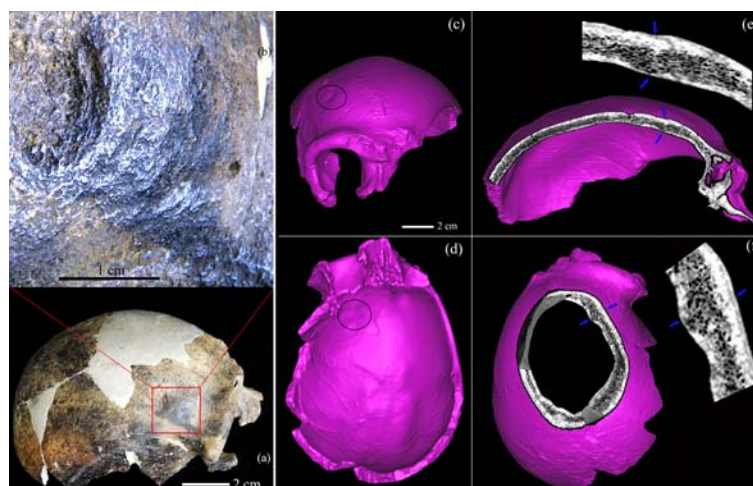


Figure 1. Right superior view of the Maba cranium shows the position and detail of the depressed lesion (Image by IVPP)

Maba cranium was discovered in 1958, in a karst cave at Lion Rock, Maba town, Qujiang district, Shaoguan city, [Guangdong](#) province. The Maba cranium and a large quantity of mammal fossils were found in a deep and narrow crevice inside the cave. Maba has a thick, prominent and projecting supraorbital torus that arches over the circular profile orbits. The nasal bones are narrow, pinched and strongly projecting. Since its unique morphology in the middle stage of Early Homo Sapiens from mainland northern eastern Asia, Maba has been described extensively from a comparative morphological perspective. Although lots of researchers studied the Maba partial cranium, no one pay more attention and analysis the special lesion. Using a high-resolution industrial CT scanner and stereomicroscopy, Dr Xiu-jie WU and her co-author suggested that the Maba individual survived from serious injury and post-traumatic disabilities, and that it obviously did not kill the person. Maba would have needed social support and help in terms of care and feeding to recover from this injury long before death.

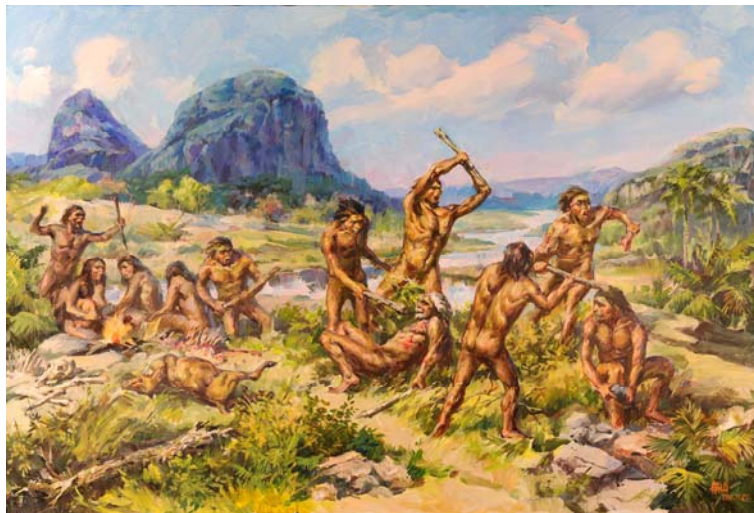


Figure 2. The living scene of the Maba human (Image by IVPP)

The Maba 1 lesion joins a series of other craniofacial traumatic lesions of Pleistocene humans which provide evidence of both apparently elevated levels of risk to injury and the ability to survive both major and minor conditions.

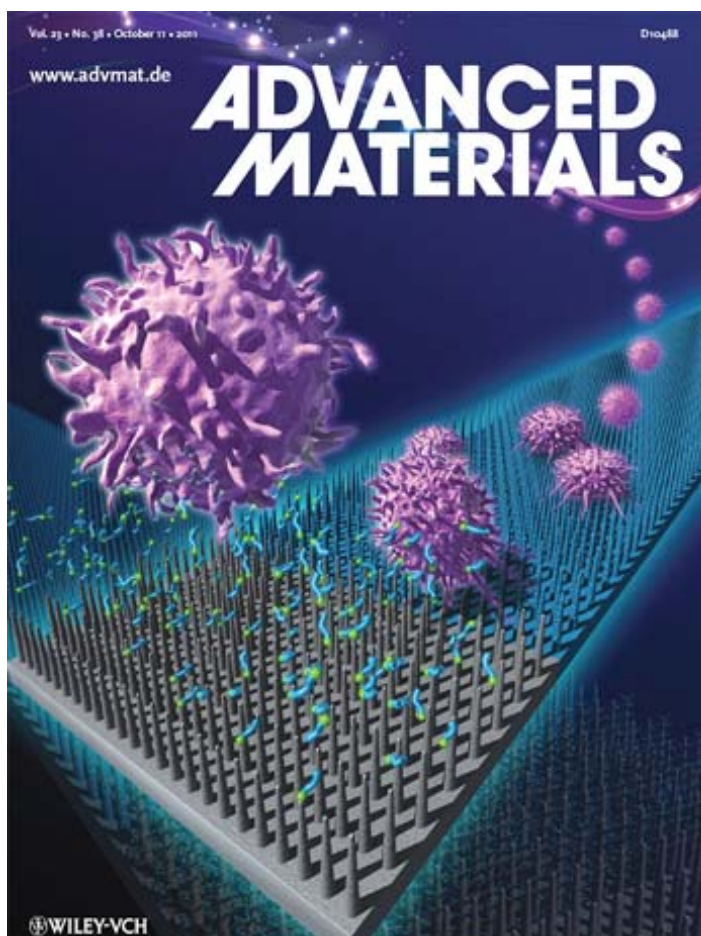
Aptamer Mediated Efficient Capture and Release of T Lymphocytes on Nanostructured Surfaces

The cells-substrate interaction is one of the most important scientific issues in biointerface, materials, medicine and other related fields. Considering the more similar environment with that in real biological body, three dimensional (3D) structural surfaces have attracted more attention than two dimensional (2D) surfaces. In previous work, researchers of the CAS Key Laboratory of Organic Solids revealed that the special 3D nano-structural surface could provide an excellent enhancement of the circulating tumor cells capture efficiency. (*Angew. Chem. Int. Ed.* 2011, 50, 3084).

Recently, under the supports of the National Natural Science Foundation of China, the Ministry of Science and Technology of China, the Chinese Academy of Sciences, and the Institute of Chemistry of CAS, the Research group in the Key Laboratory of Organic Solids developed a specifically adhesive nanoplatform targeting to T lymphocytes. This nanostructured platform has high efficiency of T lymphocytes capture and release. As described by S.T. Wang and co-workers in their communication, they successfully modified the cell affinitive DNA aptamers, which could specifically recognize T lymphocytes, onto the silicon nanowire arrays (SiNW). As the co-effect of molecular identification and size match at nanoscale, the capture efficiency on this substrate increased up to two orders more than that of planar surfaces and the release efficiency was $97\% \pm 2\%$ after treatment with exonuclease. The results have been published in *Advanced Materials* (*Adv. Mater.* 2011, 23, 4376).

The paper is highlighted at the front cover of the journal. This method of capture and release provides an artful strategy to fulfill the demands of isolation and analysis of many kinds of cells, such as other leukocytes, circulating tumor cells, and stem cells. This study will have an important impact on rare cell detection and cell-based disease diagnosis.

These achievements have also been affirmed and highlighted by other organizations. Material view of China (Wiley) has reported this work at their homepage, and the authors also received an invitation from Science Publishers for writing a chapter named Emerging Nanotechnology for Efficient Capture of Circulating Tumor Cells in the nano-medical book *Nanomedicine in Diagnostics*. (*Nanomedicine in Diagnostics*, Chap 8, 172-190)



BGI Study Results on Resequencing 50 Accessions of Rice Cast New Light on Molecular Breeding

According to a report in *Nature Biotechnology* (online), supported by the National Natural Science Foundation of China, on December 12, 2011, Shenzhen, China - BGI, the world's largest genomics organization, announced that a study on resequencing 50 accessions of cultivated and wild rice was published online today in *Nature Biotechnology*. The study provides one of the largest genome variation data sets for wild and cultivated rice, which is valuable for breeding and for identifying agronomically important genes in rice. This data also yields new insights for geneticists and biologists to deeply explore the domestication history of cultivated rice.

Rice feeds more than half the world's population, and accounts for over 20 percent of the world's total calorie intake. At various times and places in history, some wild rice species formed particularly close relationships with human populations resulting in a range of biological and genetic changes owing to a process known as domestication, a special artificial selection. This process has played an important role in rice cultivation with divergence of many genes controlling important agronomic traits.

Asian cultivated rice (*Oryza sativa*) is thought to have been domesticated from divergent populations of Asian wild rice, *O. rufipogon* and *O. nivara*, about 10,000 years ago. For decades, geneticists have tried various ways to identify the major causative genes responsible for the significant phenotypic traits changed during the domestication, such as grain size, color, shattering, seed dormancy, among others.

"If we want to clearly understand the genome variation between cultivated and wild rice, it's better to know the comprehensive catalog of genome variation in both cultivated and wild rice," said Xu Xun, Vice President of Research and Development Department at BGI, and the leading author of the paper. "The high-quality variation data will greatly facilitate the identification of functional variations and be useful for marker-assisted breeding and gene mapping of rice."

In this study, researchers sequenced 40 cultivated accessions selected from the major groups of Asian cultivated rice and 10 accessions of their wild progenitors. They next investigated genome-wide variation patterns in rice and obtained 6.5 million high-quality single nucleotide polymorphisms (SNPs).

"This is one of the largest high-quality SNP data sets obtained in rice," said Liu Xin, Senior Bioinformatician of BGI and the co-leading author of this paper. "It could provide molecular markers for designing rice SNP arrays and for breeding to identify important rice genes that could potentially improve the quality and yield of rice."

Because of the low levels of variation and skewed allele frequency spectra, some favorable alleles associated with important biological features tend to be rare and are difficult to detect. Using these population SNP data, researchers successfully identified thousands of genes with significantly lower diversity in cultivated but not in wild rice, which indicated the candidate regions were selected during domestication. The validity of this approach was further evidenced by the successful identification of the two well-known rice domestication genes, *prog1* and *sh4*. In addition, the results also support the view that japonica and indica, two major subspecies of cultivated rice, were independently domesticated, and further suggest japonica was domesticated from the Chinese strain of *O. rufipogon*.

"The millions of SNP data generated in this study not only provide tremendous opportunity to unravel the domestication history of rice, but they also could serve as a valuable source for researchers to rapidly identify agronomically important genes in rice," said Xu. "We hope that this new data accelerates the global effort to improve the quality and yield of rice in order to better address the challenges of a growing world population and food shortages."

BGI Reports Study Results on Frequent Mutation of Genes Encoding UMPP Components in Kidney Cancer

According to a report in *Nature Biotechnology* (online), supported by the National Natural Science Foundation of China, on December 4th, 2011, Cambridge, MA and Shenzhen, China - BGI, the world's largest genomics organization, announced that a study on frequent mutation of genes encoding ubiquitin-mediated proteolysis pathway (UMPP) components in clear cell renal cell carcinoma (ccRCC) is published online today in *Nature Genetics*. In addition to BGI, co-leaders of the study included Peking University Shenzhen Hospital, Shenzhen Second People's Hospital, among others. The study reveals that alteration of UMPP may contribute to ccRCC by activation of the hypoxia regulatory network, providing new clues to trace the key molecular mechanisms and pathways that underlie the tumorigenesis and progression of ccRCC.

Clear cell renal cell carcinoma (ccRCC) is the most common and aggressive type of kidney cancer, with 102,000 deaths worldwide each year. It is characterized by high metastatic potential and poor prognosis. Up to 40% of patients have disease recurrence after nephrectomy. In this study, the research team specifically looked at alterations in ubiquitin-mediated proteolysis pathway and studied its potential impacts linked to ccRCC tumorigenesis. The UMPP has been reported to be associated with many diseases including cancer and plays a critical role in the protein metabolism as a major pathway for protein degradation in cells.

"Adding to the previous research effort of transitional cell carcinoma in bladder cancer published in *Nature Genetics* earlier this year, we and our partners continued our study of strongly aggressive ccRCC tumors to identify the mutated genes associated with the process of tumorigenesis," said Guo Guangwu, one of the co-leading authors of the study and PI of this project at BGI. "The new discoveries in this study led us to a remarkable step in our understanding of the genetic landscape of ccRCCs and toward potential treatment against this aggressive tumor."

To gain a deep insight into the genetic basis of ccRCC, researchers analyzed ten primary tumors with matched morphologically normal renal tissues utilizing the whole exome sequencing approach on BGI's sequencing platform. The mutation prevalence was estimated by screen of ~1,100 genes with somatic mutations or that have been causally implicated in cancers in 88 additional ccRCCs for prevalence screen.

There were 23 significantly mutated genes identified in the 98 ccRCCs, including the five well-known renal cancer genes such as VHL and TP53, and genes involved in chromatin modification such as PBRM1, JARID1C and SETD2. "We have identified 12 genes which were previously unknown to be involved in ccRCC, including two tumor suppressor genes, BAP1 and TSC1. Integration of previous studies and our findings suggest that some of the genes may play important roles in ccRCC genesis," said Guo.

In addition to the attempt to identify all mutated genes associated with ccRCC, researchers also focused on specific genes, pathways and mechanisms that potentially play a key role in ccRCC tumorigenesis and warrant exploration as potential targets for treatments. One of the targets was mutations in VHL gene that were commonly suggested to be involved in ccRCC genesis in many previous genetic studies with reported prevalence ranging between 50% and 80%. Interestingly, researchers have found a much lower prevalence of 27% in this study. VHL promoter hypermethylation was only found in 6% of the tumors relative to their matched normal samples, also suggesting a lower prevalence of epigenetic VHL alternation, according to the researchers.

Although the alteration of VHL gene is widely known for its association with kidney cancer, researchers also revealed the frequent mutation of UMPP linked to ccRCC in this study and have sequenced all 135 genes in UMPP in the prevalence screen. A significantly high mutation frequency of UMPP was found in the 98 carcinoma samples. The pathway analysis suggested that alternation of UMPP could potentially play an important role in

ccRCC tumorigenesis, and it may contribute by activating the hypoxia regulatory network.

"This study has enhanced our knowledge and laid an important foundation for future research of ccRCC. The new discovery on the potential contribution of UMPP to ccRCC justifies more comprehensive investigation of this pathway, including proteomics research of the protein network to fully elucidate its role in ccRCC genesis," said Professor Wang Jun, Executive Director of BGI.

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Research on Habitat Shift Promoting Species Diversification

PNAS published on August 15, 2011 the article "Eocene habitat shift from saline to freshwater promoted Tethyan amphipod diversification" by Professor Shuqiang Li of Institute of Zoology, CAS, together with Slovenian cooperators.

Current theory predicts that a shift to a new habitat would increase the rate of diversification; while as lineages evolve into multiple species, intensified competition would decrease the rate of diversification. Darwin's finches on the Galapagos Islands and the drosophilid flies of the Hawaiian Islands are the best known cases. However, there are few reports in aquatic systems.

The research used Holarctic aquatic amphipods of the genus *Gammarus* to test the hypothesis that speciation are facilitated by ecological opportunity. Researches sequenced four genes (5,088 base pairs) for 289 samples representing 115 *Gammarus* species. It revealed that *Gammarus* originated from the Tethyan region with a saline ancestry in the Paleocene, and later colonized the freshwater habitat in the Middle Eocene. The research also showed that habitat shift from saline to freshwater led to an increased diversification rate. The saline lineage of *Gammarus* dispersed to both sides of the Atlantic at 55 million years ago (Ma) because of the few barriers between the Tethys and the Atlantic, and diversified throughout its evolutionary history with a constant diversification rate (0.04 species per million years (sp/My)). The freshwater *Gammarus*, however, underwent a rapid diversification phase (0.11 sp/My) until the Middle Miocene, and lineages successively diversified across Eurasia via vicariance process likely driven by changes of the Tethys and landmass. In particular, the freshwater *G. lacustris* and *G. balcanicus* lineages had a relatively high diversification shift, corresponding to the regression of the Paratethys Sea and the continentalization of Eurasian lands during the Miocene period. Subsequently (14 Ma), the diversification rate of the freshwater *Gammarus* decreased to 0.05 and again to 0.01 sp/My. The genus *Gammarus* provides an excellent aquatic case supporting the hypothesis that ecological opportunities promote diversification.

The above-mentioned project has been funded by NSFC.