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The FORMOSAT-3/COSMIC Mission

NSC and NSF Collaboration on Pioneering Atmospheric Observation

The FORMOSAT-3/COSMIC mission is a U.S.-Taiwan cooperative project sponsored by the National Science Council (NSC) and National Science Foundation (NSF) to deploy a globe-spanning network of six low-earth-orbiting satellites. Also known as COSMIC (Constellation Observing System for Meteorology, Ionosphere and Climate) in the United States, the FORMOSAT-3/COSMIC mission is based on a system design provided by the University Corporation for Atmospheric Research (UCAR). While Orbital Sciences Corporation designed the spacecraft, the rest of the satellite constellation was built and tested at the National Space Organization (NSPO) in Taiwan.

The goal of the FORMOSAT-3/COSMIC mission is to obtain near real-time global distribution of air pressure, temperature, and water vapor of the atmosphere as well as the ionosphere's electron density. The data collected are used for weather prediction simulations, global climate change analysis, and ionosphere and gravity research. The World Meteorological Organization (WMO) will distribute these data to the weather centers of its member countries.

The FORMOSAT-3 satellites will be the first to provide near real-time global atmospheric data for both research and operation using radio occultation technology, according to NSPO. The satellites will record the bending of radio signals from the U.S. Global Positioning System (GPS) as the signals pass through the Earth's atmosphere and ionosphere. Radio occultation is a technique for determining the property of an inhomogeneous me-

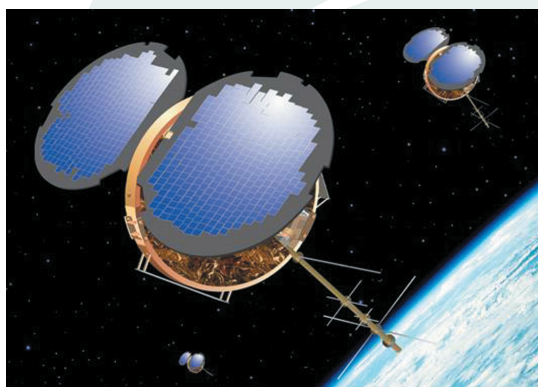
dium by measuring the refractive bending of radio signals passing through the medium. For example, as water molecules in a glass change the path of visible lights from the air into water (or vice versa) so that a pencil appears bent, molecules in the air bend GPS radio signals as they pass through the atmosphere. By measuring the degree of this bending, scientists can then determine the underlying atmospheric conditions, such as air density, temperature and moisture, and electron density in the ionosphere.

The NSPO further stated that the GPS radio occultation technique has been deployed in satellites such as the

oceans and polar region. This is about three times the daily ground-based observation of about 900 measurements, which concentrated mostly on continental regions. The data's high vertical resolution will complement the high horizontal resolution of conventional weather satellite measurements. Temperature, air density and water vapor profiles derived from FORMOSAT-3 GPS data will help meteorologists observe and forecast typhoons, hurricanes, and other storm patterns over the oceans and improve weather prediction. The stability, consistency, and accuracy of the measurements should also help scientists quantify long-term climate changes.

The FORMOSAT-3/COSMIC data will be processed at the Taiwan Analysis Center for COSMIC (TACC) located in the Central Weather Bureau (CWB). Three science teams – the atmospheric science team, ionospheric science team, and geodesy science team – consisting of university faculty, researchers and students in Taiwan will carry out the FORMOSAT-3 mission.

The data collected will be open to scientists from all nations for collaboration on atmospheric and ionospheric research. Centers around the world will have access to this new information for both research and operational forecasting. FORMOSAT-3 data can be accessed through the TACC website or CDAAC (COSMIC Data Analysis and Archive Center) by signing a user agreement with both the NSPO and UCAR. The approved users can access information on global distribution of atmospheric parameters such as refractivity, air pressure, temperature and water vapor, as well as global



GPS-MET, CHAMP and SAC-C and the atmospheric data collected have been highly accurate. However, these have been single-satellite operations without mutual coordination. The FORMOSAT-3 mission satellites use the GPS radio occultation technique on a large scale in near real-time to provide continuous monitoring of worldwide atmospheric conditions. These satellites will take at least 2,500 measurements of vertical profiles of atmospheric air density, temperature and water vapor every 24 hours in a nearly uniform distribution around the globe, filling in current data gaps over the

electron density distribution of the ionosphere. The TACC, led by Mark Cheng, has established the necessary hardware and operating systems and is presently testing the analysis codes. The TACC will be ready for operation when FORMOSAT-3 satellites are launched.

The atmospheric science team, led by Prof. Huang Ching-yuang, National Central University, has been using single satellite GPS radio occultation data to study their effectiveness for improving typhoon predictions. His previous studies, which involved only using the German CHAMP GPS radio occultation data have shown remarkable improvements on 24-hour accumulated rainfall and 48-hour track predictions for typhoons. With at least six times more data collected from the six satellites' continuous monitoring, it is anticipated that typhoon predictions can be greatly improved. On the other hand, Prof. Joseph Chang, Chinese Culture University, has been collaborating with the CWB to assimilate GPS radio occultation data into the global weather model. It is expected that the CWB would be able to improve typhoon track, heavy rainfall area, and rainfall accumulation predictions with FORMOSAT-3/COSMIC data.

The FORMOSAT-3 ionospheric

science team, led by Prof. Chu Yen-hsyang, National Central University, studies the ionosphere's electron density distribution. The measurements of global electron density distribution collected by the satellites are expected to improve analysis and forecasting of space weather – geomagnetic storms that can interrupt sensitive satellite and communication systems and affect power grids on the ground. FORMOSAT-3/COSMIC data allows a global ionospheric electron density model to be established. The ionospheric science team has also established an ionospheric data center at the National Central University for processing electron density data.

The geodesy science team, led by Prof. Tseng Ching-liang of the National Cheng-Kung University, computes the FORMOSAT-3 satellite orbits. To obtain accurate and continuous monitoring of atmospheric data using radio occultation technique, it is necessary to know the satellite orbits in near real-time. Moreover, with precise orbit information on all satellites, one can obtain the Earth's mass distribution that determines the gravity field and satellite orbits. With continuous monitoring of changes in the Earth's mass distribution, studies on global change in ocean circulation, ground water table, and El Nino can

be carried out.

In March 2006, all six satellites of the FORMOSAT-3 mission will be stacked on a Minotaur rocket and launched from the U.S. Vandenberg Air Force Base into initial parking orbits of about 500 km in altitude. It will take 13 months for all satellites to settle in their designed orbital planes with a longitudinal separation of 24 degrees and an altitude of about 700 - 800 km. During the first eight months, the FORMOSAT-3 satellites will stay relatively close to each other in longitude and the GPS radio occultation data points would be very dense. It is an excellent and rare opportunity to perform cross-validation of the radio occultation data with other observations (ground based radiosonde, weather satellite, and balloons). Taking advantage of this tight observation period, Prof. C.Z. Frank Cheng, Chief Scientist of the National Space Organization, is planning an Intense Observation Period (IOP) campaign to conduct data cross-validation as well as perform prediction studies on typhoon track, heavy rainfall area, and rainfall accumulation in the East Asia region. Researchers from East Asia nations as well as the U.S. and Europe will be invited to participate in the IOP campaign.

Know Yourself and Know Your Enemy

Research on Human and Bird Flu Genome Yields Many Discoveries

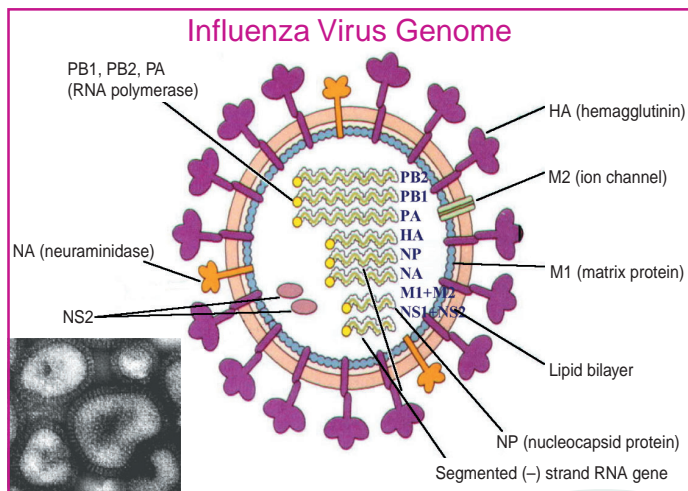
The most deadly disease outbreak in recent history was the 1918 flu pandemic (over 40 million deaths were recorded worldwide during a one-year period), and the flu virus has continuously threatened mankind for almost 90 years. Recently the H5N1 strain of bird flu has been spreading throughout Indonesia, Vietnam, Thailand, and Cambodia; besides causing the death of large numbers of poultry, this strain has infected at least 112 people and killed 57 thus far.

The flu virus' life cycle and genetic

characteristics cause it to mutate frequently during replication. The resulting genetic variability of the virus may allow it to infect and cause illness in new and different host species. Many scientists have been attempting to create genetic maps of different types of flu virus over the last few years in order to find out how this virus can mutate into pandemic-causing strains. Prof. Shih Shin-ru, Department of Medical Biotechnology & Laboratory Science, Chang Gung University, has been decoding the genetic sequences of human flu viruses

found in Taiwan over the last decade with funding from the NSC. Prof. Shih's comparative functional analysis of human and bird flu viruses from different periods has yielded many discoveries and some potential applications.

Prof. Shih's laboratory identified enterovirus 71 as the strain responsible for the enterovirus outbreak that occurred in Taiwan during 1998. The laboratory's research on infectious RNA viruses over the last few years has encompassed virus test reagents, anti-viral drugs, and genetic varia-



tions in the flu virus. According to Prof. Shih, all flu viruses, regardless of their strain, possess eight common genes – PB2, PB1, PA, HA, NP, NA, M, and NS. When flu viruses of two different strains simultaneously infect the same host cells, they are very likely to recombine and create an entirely new strain of virus. Human flu virus and bird flu virus can use this mechanism to exchange viral genes. Some of the eight genes in flu viruses vary greatly, while others vary little. After comparing the nucleic acid sequences of pairs of viruses, Prof. Shih's research team calculated that NP is the best suited of the eight genes for

can serve as diagnostic markers allowing researchers studying new types of flu to determine whether the viruses' mutations will increase the likelihood of it jumping to new host species.

After comparing the genomes of the human and bird flu viruses, the research team has been attempting to understand whether the differences between the viruses influence infection. Scientists have developed a "reverse genetics" system for assembling flu viruses in the laboratory. This system can change the nucleic acid or amino acid in a certain position in order to explore how genetic differences affect the virus' ability to infect hosts.

According to Prof. Shih, his team recently used "reverse genetics" to pin down several genetic markers on the flu virus' M gene connected with viral replication ability. This is important because knowledge of genetic markers affecting viral growth will facilitate understanding of how different flu virus strains replicate and cause illness in different hosts, and will also enable the production of easily-cultured, low-toxicity viruses for use in preparing bird flu vaccines.

tracking a virus' source, followed by PB2 and PA. Use of these three genes can clearly distinguish human and bird flu viruses. Beyond allowing scientists to determine whether viruses from humans contain bird flu viral genes, NP sequence analysis can also be used to probe the reasons for viral evolution (such as whether changes are natural or due to exogenous factors such as resistance to vaccines or drugs) and thereby help facilitate the control of flu outbreaks.

Prof. Shih's research team also performed a comparative analysis of the human flu and bird flu genome. The team found that only 19 out of the 4,554 amino acids that comprise the viral genetic sequence are completely different. For instance, the 313th amino acid in the NP protein is a P in the human flu virus and an L in the bird flu virus. These variable amino acid positions

A Powerful New Tool for Genomic Research

NSRRC Inaugurates Protein Crystallography Facility

The sequence of DNA in the genomes of living organisms determines the sequence of amino acids in those organisms' proteins. Hence, identifying the three-dimensional folding and function of a protein molecule can lead to greater understanding of DNA, and help define the characteristics of nucleic acid in scientific and quantitative forms. And having a complete databank of protein structure can give biologists and medical scientists the necessary means and tools to fight diseases. However, this effort has often met with time and technology bottlenecks. Therefore, when the National Syn-

chrotron Radiation Research Center (NSRRC) introduced its Protein Crystallography Facility on November 3, 2005, it marked a special milestone in the genome medicine community. This facility delivers a versatile tool that can produce the necessary structural analysis of protein within a significantly short time frame.

Structural genomics seeks to identify the structures of all proteins corresponding to a complete genome, and uses the resulting structural information to deduce the functions of all proteins. Since such a huge number of

proteins must be subjected to structural analysis (approximately 25,000 proteins in the case of the human genome), the time required for this task would be indefinitely long using conventional technology. So far, only



roughly 10,000 proteins have been identified with such information using conventional technology during the last decade. The fusion of synchrotron radiation and protein crystallography, however, holds out the hope that the great undertaking of structural genomics can be completed at a much earlier date. The intensity of synchrotron radiation can shorten data collection time (in some cases from weeks to days) and yield high-quality data, and the tunability of this radiation can provide the phase information needed to identify protein structures. The goals of structural genomics can be realized in the very near future if the effectiveness of synchrotron radiation beamlines continues to improve.

The “National Research Program for Genomic Medicine” (NRPGM) of the NSC expressed the need for a synchrotron-based protein crystallography facility (SPXF) in September 2001. According to SPXF principal investigator Dr. Andrew H.J. Wang, it was a perfect match between NRPGM and NSRRC to build the SPXF together. The three-year project included construction of two high-performance protein crystallography beamlines, a multi-wavelength anomalous dispersion (MAD) beamline for analyzing unknown protein structures, and a Mono beamline used for crystal selection, drug design, and high-resolution analysis of protein structures. Thanks to the mature, reliable beamline technology available today, the MAD beamline can obtain approximately 800 sets of MAD data in one year, and the Mono beamline can obtain approximately 1,200 sets of high resolution data annually. It is conservatively estimated that the 2,000 sets of data will allow the identification of 500 new protein

structures each year – a performance several dozen times better than traditional analysis.

The NT\$300 million SPXF instrument has been proven to meet international standards. More importantly, a dedicated NSRRC support team with research knowledge and capable of maintaining superior standards of operation has been essential to the success of this project. The opening of the facility will create many research opportunities and greatly enhance the country’s biotechnology advantages. At the opening ceremony on November 3, Taiwan Premier Frank Hsieh, Academia Sinica president and NSRRC chairman of the board Dr. Lee Yuan-tseh, NSC Minister Wu Maw-kuen, government officials, and distinguished researchers jointly pressed buttons to start up the world-class SPXF and begin a new chapter in Taiwan’s structural genomics research.

After the ceremony, Premier Hsieh and all guests were briefed by NSRRC director and Academician Dr. Chen Chien-te on the planning of a new-generation “Taiwan Photon Source” (TPS) synchrotron accelerator. Chen noted current plans for an additional synchrotron light source to be constructed at the existing NSRRC site within seven years. According to Dr. Chen, the TPS will have a circumference of 518 meters, a rated energy of 30 ~ 33 eV, and ultra-low beam dispersion. When completed, it will provide the world’s brightest synchrotron X-ray illumination. This facility will also ensure that Taiwan’s scientific facilities and research community remain competitive to worldwide standards. The facility will not only open the door to new experimental technologies in biomedicine and nanotech-

nology, but also inspire young domestic researchers to undertake careers in advanced scientific research. The “Taiwan Photon Source Synchrotron Accelerator Construction Feasibility Study” was submitted to the NSC in July 2005, and a construction proposal and formal application are expected to be submitted by the end of the year.

Prior to departing NSRRC, Premier Hsieh toured the NSRRC’s synchrotron accelerator designed and built by domestic engineers and scientists 12 years ago. The current accelerator has been upgraded several times over the years, and now offers performance comparable with that of the best accelerators overseas. Its stability and reliability have won praise from the international scientific community. The accelerator recently jumped ahead of many of its peers with the adoption of superconducting technology and currently supports annual usage of approximately 4,200 person-times for basic and applied scientific research.

Premier Hsieh’s visit to the NSRRC is a token of government’s support for scientific research as well as the synchrotron-based research. To wrap up the program, a closing presentation was given by Dr. Hwu Yeu-kuang, research fellow of Academia Sinica Institute of Physics, on “nanometer high-speed X-ray microscopy.” This combination of high resolution microscopy and powerful synchrotron X-ray is used to perform deep, rapid microscopic observations of macroscopic objects without destroying their natural state, producing images 10,000 times faster with 10,000 times higher resolution than that of standard X-ray machines. This instrument is also a powerful research tool for life science and materials science.

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