**JAPAN**

**Besides Fighting Free Radicals, Catechin in Green Tea Combats H1N1 Flu Virus**

Gargling with green tea prevents onset of seasonal flu and can prevent infection by H1N1 flu. The epigallocatechin gallate (EGCg), a kind of catechin in green tea (Camellia sinensis), may be more effective than Amantadine in treating at least three types of flu.

New Japanese research is indicating that EGCg has an inhibitory effect against three types of influenza viruses, including the swine-origin H1N1 virus.

Influenza viruses are highly contagious and susceptible to mutation. This is why flu spreads repeatedly each year. Gargling with green tea has already been shown to prevent the onset of seasonal flu. It is becoming clear that catechin, a type of polyphenol in green tea, plays a major role in the prevention of flu infection, and that, among different types of catechin, EGCg displays the strongest antiviral activity.

The Japanese research demonstrated that EGCg prevented flu virus infections at lower concentrations than Amantadine (a drug used to prevent and treat flu).

A typical concentration of EGCg in green tea infused from a teapot is 5000 to 7000 micromoles per liter. Green tea diluted 1000-fold or more is effective in halving infections by three types of flu viruses, including H1N1.

The 2009 Japanese research follows several earlier Asian studies indicating the health benefits of drinking green tea. In 1994, the Journal of the National Cancer Institute published the results of epidemiological research indicating that drinking green tea reduced the risk of oesophageal cancer in Chinese men and women by nearly 60%.

More recently, University of Purdue researchers concluded that a compound in green tea inhibits the growth of cancer cells. It has also been suggested that drinking green tea lowers total cholesterol levels, as well as improving the ratio of good (HDL) cholesterol to bad (LDL) cholesterol.

Green tea is made from unfermented leaves and contains a high concentration of powerful polyphenol antioxidants. Antioxidants are substances which scavenge free radicals – damaging compounds in the body that alter cells, tamper with DNA and cause cell death. Free radicals occur naturally in the body, but environmental pollutants, including ultraviolet rays from the sun, radiation, cigarette smoke, and air pollution also give rise to these damaging particles.

A consensus view is emerging that free radicals contribute to the aging process and to the development of cancers and heart disease. Antioxidants such as the polyphenols in green tea can neutralize free radicals and may reduce or help prevent some of the damage they cause.

**SINGAPORE**

**Scientists Identify 7 Genes Linked with Leprosy**

In a first-time-ever genome-wide association study (GWAS) of leprosy and the largest GWAS effort on infectious diseases in the world, scientists at the Genome Institute of Singapore (GIS), a biomedical research institute of the Agency for Science, Technology and Research, Singapore and 26 institutes in China found seven genes that can cause people to become susceptible to leprosy. The discovery of these genes – known as CCDC122, C13orf31, NOD2, TNFSF15, HLA-DR, RIPK2 and LRRK2 – highlights the important role of the innate immune response in the development of leprosy.

Led by Dr Jianjun Liu, Human Genetics Group Leader at the GIS, Dr Fu-Ren Zhang at the Shandong Provincial Institute of Dermatology
and Venereology, and Dr Xue-jun Zhang at the Institute of Dermatology and Department of Dermatology at the No.1 Hospital, Anhui Medical University, China, the research involved over 10,000 samples of Chinese leprosy patients and health controls. The study was published on 16 December 2009 in New England Journal of Medicine under the title “Genomewide association study of leprosy”.

Dr Jianjun Liu said, “This is a very significant find, and one that can only be achieved through large-scale genetic studies, with close collaborative efforts among multi-disciplinary research groups, often across different countries. The discovery of these genes is a major breakthrough for research in leprosy and infectious diseases in general, and will be significant in the early diagnosis and development of new treatments.”

“This study represents one of the largest and best organized studies of the host genetics in infectious diseases published. Though leprosy is not common, the discoveries have significant ramifications for chronic infectious disorders and for host-pathogen interactions in other more prevalent mycobacterial diseases such as TB (tuberculosis),” said Prof Edison Liu, Executive Director at the GIS.

Prof Edison Liu added, “This is a continuation of a number of deep collaborative studies between the GIS and Chinese scientists in using population sciences to uncover genetic modifiers of human disease. The strength of Chinese clinical sciences and of Singapore’s targeted genomic capabilities makes a powerful scientific combination. The key to this collaboration and one that was recently published on the genetics of Asian migration is that the studies were initiated and executed by Asian partners acting as equals. Hopefully, this will initiate a new phase of cooperation between historically competing Asian countries whose primary links have been with western communities.”

Leprosy is a chronic infectious disease caused by a bacterium known as Mycobacterium leprae (M. leprae). It mainly affects skin and peripheral nerves and may lead to irreversible disabilities. Although it has been largely eliminated in developed countries, leprosy is still a major public health problem in many developing countries, particularly in tropic and sub-tropic regions. As M. leprae cannot be cultured in the laboratory, and it only infects humans and the Armadillo, research and thus the biological understanding of leprosy are very limited.

The discovery of the seven susceptibility genes has not only helped to understand some people’s susceptibility to this disease, but also opened the door for further biological and clinical research to reveal the mechanism of leprosy development.

According to the World Health Organization’s (WHO) report, 254,525 new cases of leprosy were diagnosed in 2007. Although many people are potentially exposed to M. leprae in endemic regions, only a small minority will be infected and develop into clinically overt leprosy, suggesting that only some individuals are susceptible to this disease.

SINGAPORE

Rapid Cardiac Biomarker Testing System Developed By Singapore Scientists

Scientists at Singapore’s Institute of Microelectronics (IME) have developed a rapid and sensitive integrated system to test simultaneously for specific cardiac biomarkers in finger-prick amount of blood.

The silicon-based integrated system’s features could help physicians quickly arrive at the right diagnosis for timely medical intervention in patients suspected of having heart attacks – particularly individuals who do not show obvious signs of chest pains or shortness of breath, according to researchers at IME, one of the research institutes sponsored by Singapore’s A*STAR (Agency for Science, Technology and Research).

The IME-developed cardiac biomarker testing system significantly cuts the time needed for sample preparation and analysis to just 45 minutes from the six hours typically required for the conventional testing platform known as ELISA (Enzyme-linked Immunosorbent Assay).

Because of its multiplexing capability – measuring several cardiac biomarkers simultaneously – the new system contributes to the detail and certainty of diagnosis.

“The key to saving lives in heart attack scenarios is time and the quicker and more accurate the diagnosis can be made, the faster proper care and treatment can be instituted,” said Philip Wong, MD, senior Consultant at the Singapore National Heart Centre, which worked with IME in developing the new system.

“The test kits can be rapidly deployed, and tests to confirm clinical diagnosis can be completed within short time frames,” said Dr Wong. “As the kits are deployed on-site as opposed to a central laboratory, confirmation of condition is rapid without the need to transport patients’ specimens.”
Silicon-based Integrated System: What is it and how does it work?
The IME-developed system is a label-free technology that uses semiconducting silicon nanowires (SiNWs) as biosensors. The working principle behind the nanowire biosensors is the field-effect transistor, which is responsible for generating a measurable electrical response when specific antibody-antigen interactions occur on the nanowire surface.

Specific antibodies that are immobilized onto the nanowire surface will elicit antibody-antigen interactions when allowed to come into contact with the variety of charged cardiac biomarkers. Released into the blood when the heart is injured, cardiac protein biomarkers such as troponin-T and creatinine kinases, are the basis of medical tests of patients in which a heart attack is suspected.

The IME-developed system is a label-free technology – thus eliminating the tagging step, thereby saving time and reagent consumption costs. In classical biochemical methods, the tagging of a fluorescent dye to the targeted analyte is used to detect and quantify the targeted analyte.

The IME-developed system’s parallel detection of several biomarkers is made possible by the integration of the following elements into one single microsystem:

- In-built filtration to extract almost instantaneously the test serum from the whole blood sample
- An array of SiNW chips coated with different antibodies for simultaneous detection of several biomarkers
- A recording microchip for concurrent and immediate signal-readout from multiple SiNW sensors.

The first demonstration of the full system capability revealed impressive sensitivity and speed because it can attain in just under 45 minutes a low detection limit of 1 pg/ml for cardiac biomarkers, troponin-T and creatinine kinases, from 2 μl blood.

Commercially available test kits require more than 1 ng/ml of cardiac biomarkers in order for them to be detected, which is 1000 times less sensitive than the IME-developed system. The technology and processes used for fabricating this integrated device have yielded two patents to date.

"IME’s proprietary nanotechnology behind the new silicon-based integrated system can be extended to other protein-based diagnostics from blood and saliva samples to provide fast, sensitive, accurate and portable solutions for protein-based disease screening,” said Kwong Dim-Lee, PhD, IME’s Executive Director.

Significance of Cardiac Biomarkers
Cardiac biomarkers, such as troponin-T and creatinine kinases are proteins used for heart attack diagnosis. Troponin and creatinine are constituents of the cardiac muscle cells that are released into the blood when the cells and tissues are injured after a heart attack. Hence elevated levels of troponin-T or creatinine kinases in the blood alert the doctors that a heart attack has taken place.

Troponin-T is established as a sensitive marker of myocardial injury in the general population. The troponin-T level in the blood increases within 4 to 6 hours after the onset of a heart attack and peaks at about 24 hours. This increase lasts for 10 to 14 days.

Today, the first test performed on a patient who is suspected of having a heart attack would be an electrocardiogram, commonly known as the ECG. However, normal results from an ECG do not rule out the occurrence of a heart attack, because the test is not sensitive enough to detect minute anomalies in the reading, particularly when the anomaly needs to be captured within a narrow time window of 2 to 30 minutes following the onset of a heart attack. When an abnormal
ECG reading cannot be established, the patient has to undergo further blood tests to detect the relevant cardiac biomarkers.

ELISA, which is the current method for detecting cardiac biomarkers, uses fluorescent labeling technology. This biochemical technique is laborious and time-consuming; the entire set-up requires specialized personnel and instruments to implement, thereby contributing to the per analysis cost. Hence, ELISA does not favor prompt diagnosis for critical split-second medical decisions.

**OTHER REGIONS**

**EUROPE**

New Genes for Lung Disease Discovered

Scientists have discovered five genetic variants that are associated with the health of the human lung. The research by an international consortium of 96 scientists from 63 centers in Europe and Australia sheds new light on the molecular basis of lung diseases.

The new findings provide hope for better treatment for lung diseases like Chronic Obstructive Pulmonary Disease (COPD) and asthma. In the past it has been difficult to develop new treatments because the molecular pathways that affect the health of the lung are not completely understood. It is hoped the new pathways discovered could in the future be targeted by drugs.

The ground-breaking research involved a genetic study of 2.5 million sites across the human genome involving samples from 20,000 people across the world. The consortium was led by Dr Martin Tobin from the University of Leicester and Professor Ian Hall from The University of Nottingham. The research, part-funded by the Medical Research Council (MRC) and Asthma UK, is published in *Nature Genetics*. It represents a significant advance because it is the first time that these five common genetic variations have been definitely linked with lung function.

The scientists said, “This work is important because until now we have known very little about the genetic factors that determine an individual’s lung function. By identifying the genes important in determining lung function, we can start to unravel the underlying mechanisms which control both lung development and lung damage. This will lead to a better understanding of diseases such as chronic obstructive pulmonary disease (COPD) and asthma. Crucially, it could open up new opportunities to manage and treat patients with lung conditions”.

The scientists of the SpiroMeta consortium compared genetic variants at each of 2.5 million sites across the human genome in over 20,000 individuals of European ancestry with their lung function measures. In five different locations in the human genome, genetic variants resulted in alterations in lung function. The scientists showed that these were real findings by checking the effects of the same variants in over 33,000 additional individuals.

They also compared their results to those of a second consortium, CHARGE, which has published a paper in the same issue of the journal. The scientists emphasize that they do not expect these findings to lead to immediately to genetic tests to predict who will develop lung disease. What is more important, they say, is that the findings will help understand the underlying causes of lung diseases and thus may indicate new ways of treating the condition.

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**The research sheds new light on the molecular basis of lung diseases. In five different locations in the human genome, genetic variants resulted in alterations in lung function.**