ASIA BIOTECHNOLOGY FORUM

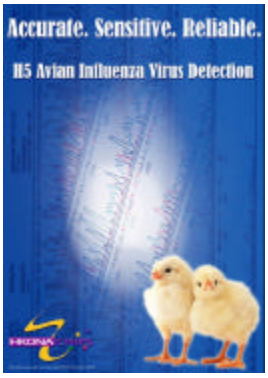
HKDNA CHIPS

Issue 6 **December, 2000**

New product launch

On 24 October 2000, Hong Kong DNA Chips Ltd (HKDNA), Asia's leading biotechnology company, launched the *H5 Avian Influenza Virus Detection Kit*. Details of the new kit were revealed at a well-attended press conference. The kit was developed in a collaborative effort between several groups, including Organon Teknika China Ltd, the Hong Kong University of Science and Technology (HKUST) and the Agriculture, Fisheries and Conservation Department (AFCD).

Project Manager, Dr Richard Collins, explained that avian influenza virus H5 has the potential to occur anywhere where intensive poultry farming is conducted and has led to several economically serious outbreaks in various countries around the world. In 1997, an outbreak of H5N1 influenza led to the deaths of six people in Hong Kong. The virus was contained by the destruction of 1.4 million chickens and other poultry across the territory. The release of the kit came almost immediately after another influenza scare, when antibodies to the H5 virus were detected in chickens on several farms in the New Territories. Sale and movement of poultry from the affected areas were immediately prohibited until the AFCD had completed further tests, some involving use of the new kit.



The H5 kit allows the virus genetic material to be amplified, or increased, making it easier to detect. This new method of detection is much more sensitive than the previous method of analysing blood and serum for antibodies to the virus. Antibodies take some time to develop in an infected animal and their presence merely indicates that a subject has been exposed to virus at some time in the past. It does not indicate the current viral load. By identifying viral genetic material, the new kit accurately and reliably indicates how much virus is actually present in the subject. This increases the sensitivity of the test and allows decisions to be made more rapidly on what course of action to take, for example flock eradication or quarantine. This could result in great savings in manpower, flock replacement and lost earnings.

Dr Albert CH Yu (Department of Biology, HKUST), who helped develop the kit, said, "The accuracy of this technique is 100% — every positive case of H5 infection in poultry can be identified."

Mr John Ford (General Manager Greater China/ASEAN) from Organon Teknika China Ltd praised the new kit and its application to solving problems faced by society. The *H5 Avian Influenza Virus Detection Kit* is based on Organon's proprietary nucleic acid sequence-based amplification (NASBA) system — specially designed to amplify small quantities of genetic material from a variety of biological samples. It is the first product to be developed during a 2-year collaboration with the company. Many other products based on this technique are currently in development by HKDNA.

Mr Terence Lau (General Manager, HKDNA) said, "The *H5 Avian Influenza Virus Detection Kit* marks a new era in viral diagnosis. Infectious agents can now be detected readily at the molecular level in a simple and cost-effective manner."

The kit is mainly aimed at government health departments, food monitoring inspectorates and large poultry producers worldwide. The new kit received a great deal of coverage in the local press and TV and several organisations expressed an interest in acquiring it.

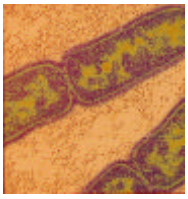
From the Editor

Welcome to the sixth edition of ***Asia Biotechnology Forum***, a monthly online newsletter providing news and information on the events affecting biotechnology in Hong Kong and Asia. This newsletter is provided with the compliments of Hong Kong DNA Chips Limited.

In this issue we focus on our new product, the H5 Avian Influenza Virus Detection Kit. We also look at the potential benefits of sequencing the genome of microbes, investigate a new genetic marker system for transgenic crops, and examine the future of GM crops.

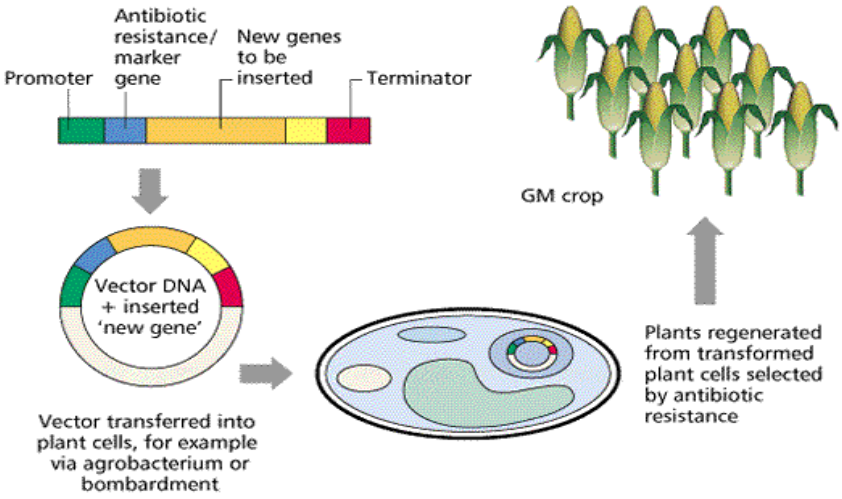
Genome sequencing offers potential cures

As has been well reported, the human genome has finally been sequenced (see ABF 2, August 2000). What is less well known is that the entire genome sequence of numerous pathogenic organisms has also been determined. Thirty microbes have been sequenced in the past five years, and another 100 are expected to be completed in the coming 2-4 years. The first bacterium for which the complete sequence was deduced was *Haemophilus influenzae* — an important cause of pneumonia and meningitis. Recently, the sequences of *Vibrio cholera* and *Mycobacterium tuberculosis* — the organisms causing cholera and tuberculosis (TB) — have been added to the list. These diseases still cause millions of new infections and deaths every year around the world, despite effective vaccines being available. *M. tuberculosis* has around 4,000 genes, only about half of which have a known function. The sequence information allows the identification of the components of internal metabolic pathways, some unique to each organism, which will allow effective inhibitors to be produced. In this way the bacterium can be inhibited without significant adverse effects to the patient. This approach is essential to combat the spread of disease. No new TB drugs have been developed in 30 years and multidrug resistant strains are on the increase. An important enzyme allowing the TB bacterium to lie dormant inside its host for many years has been identified following sequence analysis. The enzyme, isocitrate lyase, allows the bacteria to obtain energy and build carbohydrates from fatty acids in the absence of oxygen. This enzyme is likely to be the focus of intensive research for effective therapeutic agents.



New GM marker unveiled

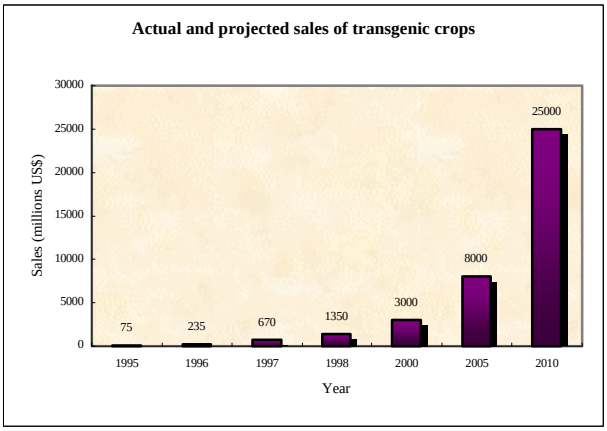
One of the biggest concerns about genetically modified organisms (GMOs) being released into the environment is the possibility of the cross-species spread of foreign genes. One gene considered particularly hazardous in this regard is that conferring antibiotic resistance. Foreign genes are inserted into new species for many reasons, e.g. to make them more resistant to herbicides or insects. The process of integrating a gene into a plant is a complex process. First, the gene is assembled into a DNA carrier molecule, or vector, containing other genetic elements ensuring efficient production of the desired characteristic. The vector is then injected into the plant cell. Transgenic cells are then selected by their ability to grow in the presence of antibiotic, which kills normal non-GM cells. The gene for antibiotic resistance is present in the DNA vector. The most commonly used antibiotic resistance gene is NPTII (neomycin phosphotransferase), which breaks down the antibiotic neomycin. There are fears



that such introduced genes could "jump" from transgenic plants to microorganisms, such as gut bacteria, increasing antibiotic resistance in humans. An alternative marker system is now available. Scientists at Novartis Seeds have launched their Positech system utilising the gene encoding the enzyme phosphomannose isomerase (PMI). Cells having the introduced gene are able to grow using only mannose, a simple sugar, as the carbon source. Non-GM cells cannot use this sugar and die. The system has been successfully tested with transgenic maize and wheat. Researchers hope that the use of less controversial markers, such as PMI, will improve the acceptance of GM foods and reduce the public debate.

GM crops – a bright future?

By now almost everyone has heard about genetically modified (GM) crops — but what is the global extent of the phenomenon? The situation can be examined in a number of ways. In terms of the area under GM crops, a steady increase has occurred. In 1997, transgenic crops were grown on 11 million hectares (ha). This increased to 27.8 million ha in 1998 and 40 million ha in 1999. However, it seems that public concern over GM food has had an effect and there is little difference between 1999 and 2000 in terms of area farmed. Three countries dominate the transgenic crop market with the USA (74%), Argentina (15%) and Canada (10%) contributing by far the most to the total area under GM crop cultivation. Five other minor producers account for the remainder — Australia, Spain, France, South Africa and Mexico. China currently grows GM tobacco and cotton in small quantities but this may well increase significantly in the coming years. The most important GM crops in 1998 in terms of area farmed were corn (51%), soybean (30%), cotton (9%), rapeseed (9%) and potato (1%). Generally, only a single trait is introduced into each GM plant. This reflects the difficulty of the transgenic process and the nature of the major threat to the production of each crop. For example, corn and soybean farmers are mainly concerned with weeds competing with their crops. Hence, the introduction of herbicide-resistant crops allowing extensive use of weed-killers on their fields. In other areas, cotton and corn crops are prone to insect infestation. The use of insect-resistant strains prevents potentially huge reductions in yield due to pest damage. In contrast, multiple or stacked traits are far less common, as are quality traits that improve flavour, texture, nutritional content, or ease of processing after harvest. The potential for rapid growth in GM crop usage seemed almost infinite and gave rise to phenomenal sales projections. In the light of recent GM scares however, these projections now seem optimistic. Biotech and agricultural companies now hope that the second-generation GM foods — those that have enhanced nutritional qualities, e.g. vitamin A-enriched rice and tomatoes — may stem the tide of public disquiet and allow GM agriculture to proceed unabated.



Corporate information

We hope you enjoyed this edition of ***Asian Biotechnology Forum***. If you have any news or topics you would like to see featured in upcoming editions, or you have any comments or queries we would be pleased to hear from you.

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- Cloning endangered species
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- DNA screening & insurance
- ISO 9002