3	Clinician-Scientists in Singapore	
8	10 th MASEAN Mid-Term Meeting	
10	6 th SMA Annual Ethics Convention	
12	Medical Malpractice in Singapore	
	13	A Beautiful Mind
	14	The Sleep Factor

VOLUME 34 NO.11 NOVEMBER 2002 MITA (P) 209/02/2002



SMA Lecture 2002: "Genomics and Medicine in Singapore"

Delivered by Professor Edison T. Liu, Executive Director, Genome Institute of Singapore

Editorial Note:

The SMA Lecture 2002 was held on Saturday, 9 November 2002, at the Grand Copthorne Waterfront Hotel. We reproduce here an abstract of Professor Edison Liu's lecture. The full text will be published in the Singapore Medical Journal at a later date. For the Citation of the SMA Lecturer 2002, delivered by Professor John Wong from the National University of Singapore, please see page 2.

he fundamental goal of genomics is to uncover the structure and sequence of the genetic material that defines an organism. Therefore the operational tasks are to map the position of the genes to each other, and to sequence every unit of genetic information in that genome. It is a remarkable thought that in the 3 billion nucleotides that make up the human genome resides all the information necessary to reconstruct our species. Equally astounding is that the complete human sequence will be deciphered within the next few years. This realization has had a profound effect on our thinking of biological knowledge.

In cosmology, the Big Bang theory not only scientifically explained observed events but it also reshaped our collective psyche by confirming a beginning of the Universe. In biology, our Big Bang equivalent may be the sequencing of the human genome. In that act, we will face the reality that everything that needs to be known about a human being can be read as a decipherable code of finite length. This may be viewed as the inherent limitations of man. However, we also know that the complexity of man resides in how the encoded genes are expressed, in what patterns, and at what intensities. Moreover, this complexity is heightened by the sequence diversity in human populations. Thus, though our building blocks are finite, the combinatorial possibilities are staggering.

The power of this knowledge will be made apparent in how we investigate human cancer. Potential targets for new therapeutics will be discovered through computer searches in the database of the genome sequence; and through the identification of uniquely expressed genes. New classifications of cancers are appearing that are based on the profiles from thousands of genes. The number of genes induced or repressed can be used as a measure of the effectiveness of a therapeutic agent. The fundamental change, however, is not the technology, but the complete knowledge of the genome sequence.

What do we hope to learn? By comparing sequence data, we can precisely define the differences between normal and diseased states; we can uncover the location of genes predisposing to human illnesses, and we can begin to fathom the complex interplay between different gene products, or between different forms of the same gene leading to specific phenotypes. Not only is the human genome important, but knowing the sequence of genomes from a variety of organisms important in research, medicine, or industry will permit the development of novel antibiotics, of industrial scale production of useful biologics, and of sensitive diagnostics. Virtually all aspects of biotechnology will use some by-product of genome sequences. Therefore, public health and public wealth will benefit from this genomic revolution.

The Genome Institute of Singapore (GIS) was first launched on 24 June 2000 by Minister of Trade and Industry BG(NS) George Yeo as the Singapore Genomics Programme. It is a national flagship programme that will serve as a vehicle to drive the life sciences enterprise in Singapore. Its strategic goals are:

Page 7 🕨



Prof Edison Liu, SMA Lecturer 2002.





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- ◄ Page 1 SMA Lecture 2002
- To promote genetic research and to establish a genomics infrastructure in Singapore;
- To provide international visibility for Singapore life sciences through initiatives that have scientific impact;
- To support the training of manpower in life sciences for Singapore, and to attract scientific talent to Singapore;
- To be the academic genomics

partner for the industry in Singapore, in order to attract investments and create jobs; and

• To be a nucleating force in the Singaporean biological research enterprise.

We have three main areas of scientific concentration:

 We will focus on transcriptional mapping and studying the transcriptome.
We will explore the genetic architecture of Asian populations and apply this knowledge to the understanding of human disease.

3. We will concentrate on the integration of genomics and medicine. For each focus area, we describe several representative research programmes.

We will also describe some of the findings from the investigators of the Genome Institute of Singapore.

SMA News November 2002 Vol 34(11)