NOVEL AND RE-EMERGING RESPIRATORY VIRAL DISEASES
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Towards the end of 2006, the Novartis Company undertook a review of the Foundation as a consequence of which the Foundation’s Trustees were informed that Company support for the Foundation would cease with effect from the end of February 2008.

The Foundation’s Trustees have considered various options for the future, the favoured of which is a merger with another, cognate, organization whereupon the Foundation will then formally be dissolved. Any future activities at 41 Portland Place will then be determined by the new organization.

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Funded primarily by Biomedical Research Council (BMRC) of A*STAR, IMCB has about 35 core research labs and 8 core facility units consisting of over 400 research scientists. IMCB’s research activities focus on five major fields: Cell Biology, Developmental Biology, Structural Biology, Infectious Diseases and Cancer Biology. IMCB continues to publish in renowned international journals, with more than a 1000 publications since 1987.

IMCB is currently based at The Biopolis @ One North. It is envisioned to be the biggest Biomedical Sciences R&D hub in Asia. IMCB continues to strive for excellence in biomedical R&D and the vision of Singapore as a world class hub for the Biomedical Sciences in Asia and beyond.
NOVEL AND RE-EMERGING RESPIRATORY VIRAL DISEASES
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Editors: Gregory Bock (Organizer) and Jamie Goode

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Emerging and re-emerging infectious diseases are part of the natural history of humankind, for there has always been a struggle between microbes and humans. A considerable part of the human genome is concerned directly or indirectly with strategies to combat infectious diseases. Humans have continued their global dominance and in the past century have used scientific knowledge to reduce the impact of novel disease agents. The ever-increasing human population expansion and factors such as land use, water use and energy use needed to support the burgeoning human population, has resulted in production of animals on megafarms in close proximity to wild animals and birds. The export of intensive farming practices to the developing world, for example chicken and pig raising, has not always been accompanied by the best practices for ensuring bio-security and disease prevention in those operations. Thus intensive poultry and pig raising, without adequate separation from free-flying birds and water treatment, is a recipe for disaster. The increasing number of outbreaks of lethal H5 and H7 influenza, in domestic poultry, globally attests to these assertions.

The emergence of novel infectious diseases is a continuing process with multiple novel agents emerging in the past decade. While many of these agents caused transitory disease outbreaks—Nepah virus from bats to pigs and people in Malaysia, and Hendra virus from bats to horses and people in Australia—that were rapidly identified and stamped out, others became endemic in humans and in domestic animal species. Notable examples are human immunodeficiency virus (HIV) (African primates to humans) and West Nile virus (introduction to the Americas from Europe and spread through mosquitoes to wild birds, domestic mammals and humans).

Two recent examples of emerging infectious disease agents are severe acute respiratory syndrome (SARS) and highly pathogenic H5N1 avian influenza (‘bird flu’). These two disease agents are the main topics for this meeting. Both of these diseases are caused by RNA viruses of zoonotic origin; SARS by a novel coronavirus from bats via civet cats in live animal markets (‘wet markets’) to humans, and H5N1 bird flu by a type A orthomyxovirus from wild aquatic birds via
domestic poultry to humans. Both of these emerging infectious diseases were ‘man made’ in the sense that increased affluence of humans in the region increased the demand for protein in the diet. Intensified animal raising and the demand for exotic wild animal meat permitted these viruses to initially spread to humans in Hong Kong and Southern China through wet markets. The actual precursor viruses of neither SARS nor H5N1 bird influenza have been identified, but their closest genetic relatives were detected in animals and poultry in wet markets at the time they initially spread to humans.

Southeast Asia has been described as the epicentre for the emergence of pandemic influenza viruses, including the Asian H2N2 influenza of 1957, the Hong Kong H3N2 virus of 1968, as well as the re-emerging H1N1 Russian influenza virus of 1977. Both the H5N1 highly pathogenic avian influenza virus and the SARS coronavirus emerged in this region of the world. While culling of all domestic poultry in Hong Kong in 1997 successfully stamped out the initial genotype of H5N1, the virus re-emerged from apparently healthy ducks and geese in the region and spread to multiple countries in Southeast Asia including Vietnam, Cambodia, Laos, Indonesia, Japan and South Korea. The virus was largely restricted to the Southeast Asia region until 2005. The dramatic spread of the virus in mid-2005 occurred after H5N1 infected Bar-headed geese and other wild water fowl in Qinghai Lake in Western China. After that event, the virus spread rapidly through the Indian subcontinent, the African continent and Europe. The role of migratory birds seems probable. While the highly pathogenic H5N1 virus continues to spread throughout Eurasia it has, to date, not spread to the Americas despite the overlap of migrating birds in Alaska.

Both SARS and H5N1 bird flu are similar in being poorly transmissible in humans. During the SARS outbreak, this virus infected 8096 persons globally with 774 deaths (9.6%), while H5N1 bird flu has infected over 300 humans with 60% lethality. The poor transmissibility of SARS led to the control of this virus by conventional biosecurity and quarantine. While SARS is under control, H5N1 bird flu is not. H5N1 appeared in Hong Kong a decade ago: it has now spread to over 60 countries in Eurasia and has evolved into at least four antigenically distinct clades. Although H5N1 has not acquired consistent human-to-human transmission the possibility exists that we may be witnessing the evolution of a human influenza pandemic in real time.

Dr Yee-Joo Tan from The Institute of Molecular and Cell Biology, Proteos, Singapore, who participated in the battle against SARS in Singapore, proposed the topic of emerging and re-emerging respiratory viruses as the subject for the present meeting. Both the topic and the site for the meeting were most appropriate. Although the economic impact of SARS turned out to be relatively short term (due to rapid acquisition of scientific knowledge and control strategies) the initial impact on service exports in Singapore and Hong Kong, especially on tourism, was par-
particularly severe. If SARS had not been controlled so expediently, the economic impact would have been much worse.

The lessons from SARS are certainly applicable to the expanding problem of H5N1 bird flu and to future emerging infectious diseases. The successful containment of SARS and the lessons learned from that successful programme are important to be considered in the face of a possibly emerging influenza pandemic in humans. However, we must keep in mind that the transmissibility of influenza is likely to be very different from that of the SARS coronavirus.