

Two special topics on the avian influenza virus and on epigenetics, have drawn much attention

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Several excellent well-organized reviews and research papers on two special topics, “The challenges of avian influenza virus: mechanism, epidemiology, and control” and “Molecular epigenetics: dawn of a new era of biomedical research”, published in the 2009 edition of *Science in China Series C: Life Sciences*, have drawn much attention.

An editorial by Gao & Shaw [1] and nine papers dedicated to the study of H5N1 avian influenza were published in the May issue. The outbreak of human cases of the highly pathogenic avian influenza H5N1 in Hong Kong in 1997 and its subsequent recurrences in Hong Kong, mainland China, and other regions reminded us that deadly pandemic influenza, similar to the 1918 Spanish Flu (estimated to have killed 50–100 million people worldwide), remains a threat to public health in an ever more globalized world. The outbreak of H5N1 was especially alarming because the virus has an expansive range of avian hosts and is known to infect many mammalian species. Human infection is highly lethal (with mortality at 62%), and human-to-human infection is widely viewed as the last barrier before a global pandemic. At the epicenter of the H5N1 outbreak and leading the fight against it, scientists from mainland China and the Hong Kong Special Administrative Region contributed greatly to our understanding of this virus. A review by Shu YueLong and colleagues at the national Center for Disease Control (China CDC) [2] summarizes the epidemiological, clinical, and virological characteristics of human infections of this virus in China. Chan Paul K S from the Chinese

University of Hong Kong reviewed the first human case of H5N1 infection and presented a detailed timeline of related events in Hong Kong [3]. These two reviews provide valuable lessons for the future monitoring of the infection. Chen HuaLan reviewed the H5N1 outbreaks in poultry flocks and in migratory birds in China and discussed the vaccination efforts by the Chinese government [4]. Liu Di *et al.* [5] focused on the adaptation of the H5N1 virus, inter-species transmissions, and the likely molecular mechanisms of virus-host interactions. They especially considered the likely host receptor molecules used by the H5N1 virus for entry into and fusion with host cells. Two reviews of structural biology studies of the proteins from influenza virus are also in this issue. In the first review, Ng *et al.* [6] reviewed the structural and sequence analysis of the nucleoprotein (NP) of influenza virus. NP together with viral RNA and RNA polymerase form the ribonucleoprotein (RNP) which is uniquely organized for transcription and replication of the viral genome. In the second one, Liu YingFang *et al.* reviewed studies on the PA subunit of influenza virus RNA polymerase [7]. The PA subunit is essential to the viability of the influenza virus and has been a target for antiviral drug development. The last review in this series is by Wang and Jiang. It focuses on the molecular pathogenesis of H5N1 infection [8]. A research article by the same authors reveals that H5N1 virus entry into host cells is through clathrin-dependent endocytosis [9]. Because a virus must enter the host cell to initiate its life cycle, this finding may provide a new target in antiviral drug development. A paper that summarizes the extensive academic information that is

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available on the Internet about H5N1 and other influenza viruses concludes this series [10]. This final paper also discusses the bioinformatic tools commonly used by researchers worldwide.

In the April issue of the Series, an editorial and three review papers are dedicated to epigenetic studies. Epigenetics, the study of inherited changes in phenotype (appearance) or gene expression caused by mechanisms other than changes in the underlying DNA sequence, has witnessed a “gold rush” in the past decade. The background information and phenomenal growth in this field have been nicely summarized in the editorial by Xu RuiMing [11]. The three reviews cover three different research areas. Lan Fei & Shi Yang reviewed recent progress in studies of histone methylations, especially the dynamic nature of histone methylation regulation on four sites of histone H4 and H4 tails (H3K4, H3K9, H3K27, and H3K36) and its relationship with epigenetic control of gene regulation. The authors also discussed non-histone proteins that are regulated by methylation such as p53 and DNMT1, and a DNA methylase [12]. Ma *et al.* [13] reviewed recent progress in the studies of microRNAs, focusing on the biogenesis and target recognition of microRNAs and the mechanisms by which they mediate gene silencing. Chinnusamy V. & Zhu JianKang reviewed research on DNA methylation, another important area of epigenetic research, with special emphasis on RNA-directed DNA methylation and demethylation in plants [14].

In addition to the two special topics, two interesting articles in other issues of the series provide an overview of the PP2A and APOBEC proteins [15,16].

In the February issue, Shi YiGong reviewed recent research on protein phosphatase 2A (PP2A) [15]. PP2A is a member of a conserved serine/threonine phosphatase family. It is ubiquitously expressed and highly enriched in tissues and organs such as the brain. This protein plays critical roles in many cellular physiology functions such as cell cycle regulation, cell proliferation and death, development, cytoskeleton dynamics, and cell mobility. Shi's review focuses on the assembly and structure of the PP2A core enzyme, substrate targeting, and the methylation and demethylation of PP2A.

Research on the apolipoprotein B mRNA-editing enzyme

catalytic polypeptide (APOBEC) family of cytidine deaminases was reviewed by Prochnow *et al.* [16], with emphasis on the activation induced cytidine deaminase (AID) and APOBEC3G. Members of the APOBEC family play important roles in adaptive and innate immune systems. APOBEC3G, for example, is active against HIV-1 and other retroviruses. This review provides an overview of recent structural and functional studies of these molecules, especially of their role in immune defense and of the structural basis of their biochemical functions.

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- 6 Ng A K L, Wang J H, Shaw P C. Structure and sequence analysis of influenza A virus nucleoprotein. *Sci China Ser C-Life Sci*, 2009, 52: 439–449
- 7 Liu Y F, Lou Z Y, Bartlam M, *et al.* Structure-function studies of the influenza virus RNA polymerase PA subunit. *Sci China Ser C-Life Sci*, 2009, 52: 450–458
- 8 Wang H L, Jiang C Y. Avian influenza H5V1: an update on molecular pathogenesis. *Sci China Ser C-Life Sci*, 2009, 52: 459–463
- 9 Wang H L, Jiang C Y. Influenza A virus H5N1 entry into host cells is through clathrin-dependent endocytosis. *Sci China Ser C-Life Sci*, 2009, 52: 464–469
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- 11 Xu R M. Molecular epigenetics: dawn of a new era of biomedical research. *Sci China Ser C-Life Sci*, 2009, 52: 309–310
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- 13 Ma C, Liu Y F, He L. microRNAs – powerful repression comes from small RNAs. *Sci China Ser C-Life Sci*, 2009, 52: 323–330
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- 15 Shi Y G. Assembly and structure of protein phosphatase 2A. *Sci China Ser C-Life Sci*, 2009, 52: 135–146
- 16 Prochnow C, Bransteitter R, Chen X J S. APOBEC deaminases-mutases with defensive roles for immunity. *Sci China Ser C-Life Sci*, 2009, 52: 893–902