

APCWBD 2010

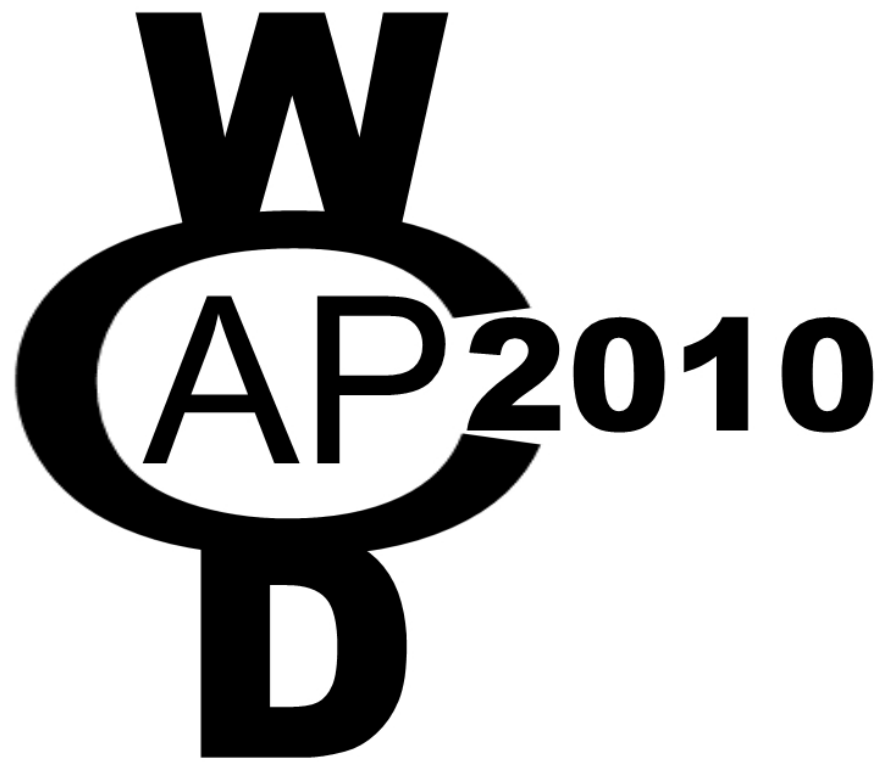
ASIA-PACIFIC CONFERENCE ON WILDLIFE BORNE DISEASES



BEIJING
JULY 19•23

PROGRAM





**Welcome to the Asia-Pacific
Conference on
Wildlife Borne Diseases
2010**

Organizing Agencies

Bureau of Life Sciences and Biotechnology, Chinese Academy of Sciences (BLBT, CAS)

Department of Wildlife Conservation and Nature Reserve Management, State Forestry Administration, China (DWCM, SFA)

Wildlife Services, Animal and Plant Health Inspection Service, United States Department of Agriculture (WS, APHIS, USDA)

Hosting Agencies

Institute of Zoology, Chinese Academy of Sciences (IOZ, CAS)

International Society of Zoological Sciences (ISZS)

China Zoological Society (CZS)

Asia-Pacific Conference on Wildlife Borne Diseases

PROGRAM

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Conference Committee

Co-Chair:

- Zhibin Zhang Director General, Bureau of Life Sciences and Biotechnology, Chinese Academy of Sciences
- Xiwu Zhang Director General, Department of Wildlife Conservation and Nature Reserve Management, State Forestry Administration, China
- William H. Clay Deputy Administrator, Wildlife Service, Animal and Plant Health Inspection Service, United States Department of Agriculture

Vice Chair:

- Fuwen Wei Deputy Director General, Institute of Zoology, Chinese Academy of Sciences
- Thomas Deliberto Coordinator, National Wildlife Disease Program, Animal and Plant Health Inspection Service, United States Department of Agriculture
- Jiansheng Jia Deputy Director General, Department of Wildlife Conservation and Nature Reserve Management, State Forestry Administration, China
- Jinghua Cao Deputy Director General, Bureau of International Cooperation, Chinese Academy of Sciences
- Ronghui Su Deputy Director General, Bureau of Life Sciences and Biotechnology, Chinese Academy of Sciences
- Aiguo Ma Director General, General Station of Forest Pest Management, State Forestry Administration, China
- Dale Nolte Assistant Coordinator, National Wildlife Disease Program, Animal and Plant Health Inspection Service, United States Department of Agriculture

Members (in alphabetical order):

- Dong Chu Director, General Station of Wildlife Pathogen-origins and Epidemic Diseases Monitoring, State Forestry Administration, China
- Ziyuan Duan Director, Office of Agricultural Bases, Bureau of Life Sciences and Biotechnology, Chinese Academy of Sciences
- Hongjie Guo Deputy Director, Division of Science and Biotechnology, Institute of Zoology, Chinese Academy of Sciences

- Hongxuan He Professor, National Research Center for Wildlife Borne Disease, Institute of Zoology, Chinese Academy of Sciences
- Zhipin Lou Director, Division of Integrated Biology, Bureau of Life Sciences and Biotechnology, Chinese Academy of Sciences
- Fuming Lei Professor, Institute of Zoology, Chinese Academy of Sciences
- Ying Luo Director, Division for Wildlife-derived Infectious Disease Management, Department of Wildlife Conservation and Nature Reserve Management, State Forestry Administration, China
- Xiangdong Ruan Deputy Director, Division for Wildlife-derived Infectious Disease Management, Department of Wildlife Conservation and Nature Reserve Management, State Forestry Administration, China
- Hui Sun Chief Program Officer, Division of American and Oceanian Affairs, Bureau of International Cooperation, Chinese Academy of Sciences
- Jianghua Sun Assistant Director, Institute of Zoology, Chinese Academy of Sciences
- Shizhuan Zhang Deputy Director, Division of American and Oceanian Affairs, Bureau of International Cooperation, Chinese Academy of Sciences
- Liping Wang Director, Division of Biomedicine, Bureau of Life Sciences and Biotechnology, Chinese Academy of Sciences
- Zhenyu Wang Director, Division of International Organizations, Bureau of International Cooperation, Chinese Academy of Sciences

Secretariat:

- Hongxuan He Professor, National Research Center for Wildlife Borne Disease, Institute of Zoology, Chinese Academy of Sciences
- Dale Nolte Assistant Coordinator, National Wildlife Disease Program, Animal and Plant Health Inspection Service, United States Department of Agriculture
- Chunxu Han International Society of Zoological Sciences
- Wenhua Xiong International Society of Zoological Sciences
- Chengmin Wang National Research Centre for Wildlife Borne Disease, Institute of Zoology, Chinese Academy of Sciences
- Jing Luo National Research Centre for Wildlife Borne Disease, Institute of Zoology, Chinese Academy of Sciences

Venue Location and Floor Plans

Venue: Beijing Hongxiang Hotel

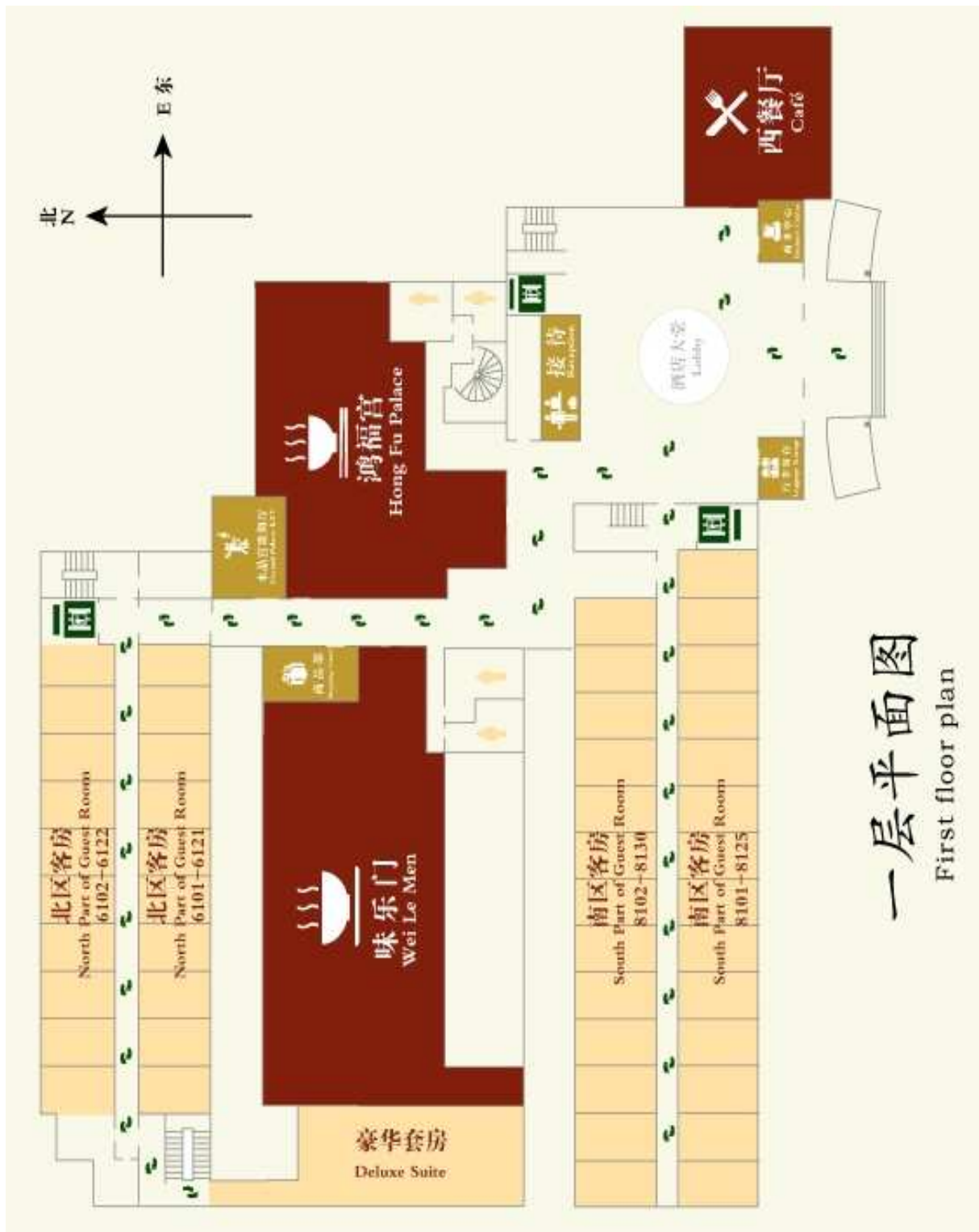
Address: 15 Longxiang Road, Haidian District, Beijing, China

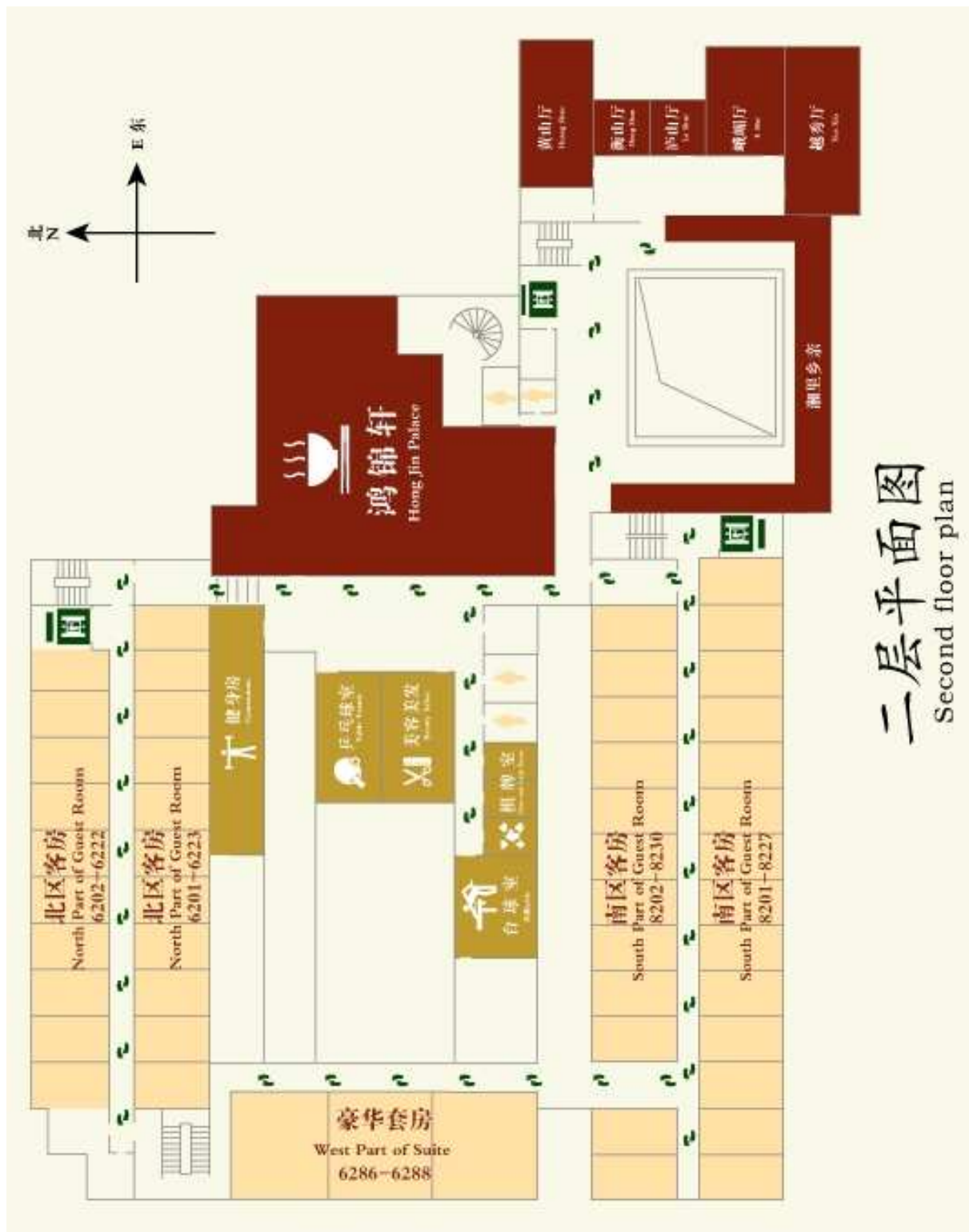
T: +86-10-59838888

F: +86-10-59838860

W: www.hongxianghotel.com.cn/English/index.htm









三层平面图

Third floor plan

Program Overview

Day 1		
MONDAY 19 JULY 2010	0900	Arrival to Beijing Registration from 0900 Hongxiang Hotel, Lobby
Day 2		
TUESDAY 20 JULY 2010	0900	Conference opening
	1025	Keynote talks
	1330	Roundtable discussion
	1620	Signing ceremony
	1640	Poster session
	1800	Reception and dinner
Day 3		
WEDNESDAY 21 JULY 2010	0830	Avian influenza
	1330	Viral diseases
	1515	Wildlife Diseases Issues
	1645	Poster session
Day 4		
THURSDAY 22 JULY 2010	0830	Bacteria, Fungi and Parasites
	1130	Closing remarks
	1400	Free tour of Beijing
Day 5		
FRIDAY 23 JULY 2010	0900	Attendees choose from one of three tours in and around Beijing, fee required
Depart Beijing		

Conference Program

Monday 19 July 2010

	0900	Registration desk open Hongxiang Hotel, lobby
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Tuesday 20 July 2010

	0850	Sign in and copy PowerPoint presentations Conference computer
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0900 Opening Remarks

CHAIR: FUWEN WEI (IOZ)	0900	Introduction Fuwen Wei (IOZ)
	0905	Welcome address Anming Meng (IOZ)
	0915	Welcome address Dale Nolte (USDA)
	0925	Welcome address Xiwu Zhang (SFA)
	0935	Welcome address Zhibin Zhang (CAS)
	0950	Photo
	1010	Tea break

1025 Keynote Talks

CHAIR: JOHN BAROCH	1025	Keynote talk Dale Nolte (USDA)
	1055	Keynote Xiangdong Ruan (SFA)
	1125	Keynote Hongxuan He (IOZ)
	1155	Lunch

1330 Round Table Discussion

CHAIRS ZHIBIN ZHANG (IOZ) DALE NOLTE (USDA) XIWU ZHANG (SFA)	1330	Proposal to establish Asia Pacific Network of Wildlife Diseases Dale Nolte (USDA)
	1350	Representative reports (5 min each) Bangladesh Sunil Chandra Gain Bhutan Karma Rinzin Canada Catherine Soos China Xiangdong Ruan Cambodia Chheang Dany Indonesia Riana Aryani Arief Mongolia Sugir Tsengee Nepal Ram Krishna Khatiwada Philippines Loinda Rugay Baldrias Russia Alexander Malogolovkin Thailand Boripat Siriaroonrat USA John Baroch Vietnam Thanh Long To FAO Fusheng Guo Wildlife Trust Alonso Aguirre Wildlife Conservation Society Yan Xie

		Conservation International Li Zhang
	1540	Tea Break
	1555	Discussion Asia Pacific Network of Wildlife Diseases
	1620	Signing Ceremony Asia Pacific Network of Wildlife Diseases
1630 Poster Display, Hong Xiang Hall		
1630 CAS-USDA High Level Forum, Yong Xiang Hall		
CHAIRS: ZHIBIN ZHANG (CAS) DALE NOLTE (USDA) JINHUA CAO (CAS)	1640	The first meeting for the MOU. Discussing organization of bilateral working group and next work plan.
1800 Conference Reception Opens		
CHAIR: JIANGHUA SUN	1800	Hong Jin Palace
2000 Conference Reception Closes		

Wednesday 21 July 2010

	0820	Sign in and copy PowerPoint presentations Conference computer
0830 Avian Influenza		
CHAIRS: CATHERINE SOOS FUMIN LEI	0830	The viral polymerase mediates adaptation and attenuation of an avian H5N1 influenza virus to mice Jing Li
	0850	Canada's inter-agency wild bird influenza survey: surveillance and research Catherine Soos
	0910	Sialic acid receptor detection in the raptor respiratory tract: evidence for a potential host of avian influenza virus Yuehuan Liu
	0930	Antiviral treatments for avian influenza: siRNA and Retrocyclin2 Kai Zhou
	0950	Tea Break
1015 Avian Influenza		
CHAIRS: ALONSO AGUIRRE HONG ZHANG	1010	The pandemic characteristics and controlling experiences of influenza H1N1 virus one year after the inception in Hangzhou, China Shelan Liu
	1030	Avian influenza virus in domestic ducks in West Java, Indonesia Kristy Pabilonia
	1050	Pathogenic factors and pathogenesis of influenza viruses Hong Zhang

	1110	Migration routes and stop-over sites determined with satellite tracking of bar-headed geese (<i>Anser indicus</i>) breeding at Qinghai Lake, China Jun Lu
	1130	Optional report
	1200	Lunch
1330 Viral Diseases		
CHAIRS: STEPHANIE SHWIFF ZHENGLI SHI	1330	Preliminary observations on primate borne diseases in Bangladesh Mohammad Mostafa Feeroz
	1345	Metagenomic analysis of viruses in bat intestinal tract, implication of important roles played by bats in ecosystem Zhengli Shi
	1400	Japanese encephalitis: wildlife reservoirs Richard A. Bowen
	1415	Wildlife disease surveillance and the West Nile virus response in Canada Ian Barker
	1430	West Nile virus-North American experience Erik K. Hofmeister
	1445	Current epidemiological situation of ASF in Russian Federation Alexander Malogolovkin
	1500	Application of oral vaccination for rabies control in wildlife reservoirs in North America Dennis Slate
	1515	Tea Break
1515 Wildlife Disease Issues		
CHAIRS: RICHARD A. BOWEN YUKUN LI	1530	Wildlife diseases and control strategies in Nepal Kamal P. Gairhe
	1545	Surveillance and monitoring of emerging infectious diseases and viruses in wildlife in Cambodia Chheang Dany
	1600	Developing global capacity to predict and prevent emerging zoonotic diseases from wildlife Alonso Aguirre
	1615	Wildlife health in Indonesia Riana A Arief
	1630	Rapid diagnostic tests Yukun Li
	1645	Economic importance for addressing wildlife diseases Stephanie Shwiff
	1700	Nonzoonotic EIDs as threats to wildlife populations Boripat Siriaroonrat
	1715	Optional report
Sessions End		

Thursday 22 July 2010

	0820	Sign in and copy PowerPoint presentations Conference computer
0830 Bacteria, Fungi and Parasites		
CHAIRS: JOHN BAROCH GUANGYUAN LIU	0830	Coxoella Burnetti antibodies in the sera of animals and man in selected areas in the Philippines Loinda Rugay Baldrias
	0845	Plague surveillance and response John Baroch
	0900	Research on generation and detection to algX gene strain of Pseudomonas aeruginosa in animal Maosheng Yang
	0915	Avian cholera Erik Hofmeister
	0930	Diseases transmitted by mites Guangyuan Liu
	0945	Tea Break
1000 Bacteria, Fungi and Parasites		
CHAIRS: YUNG-FU CHANG JONATHAN SLEEMAN	1000	Binding affinity of ig-like repeat domains of Leptospira Lig proteins to gelatin-binding domain of fibronectin is enhanced through multivalency Yung-Fu Chang
	1015	Huangshan Tibetan monkeys with the visitors access to behavioral and intestinal parasitic infections Huan Ji
	1030	An overview of bat white-nose syndrome in North America Jonathan Sleeman
	1045	Parasite load and genetic variation at MHC loci in the giant panda Lei Zhang
	1100	Surveillance for white-nose syndrome in bats in Ontario, Canada Ian Barker
	1115	Establishment of ELISA and serological investigation on Himalayan marmota toxoplasmosis in Qinghai province Qigang Cai
1130 Closing Remarks		
CHAIR: FUWEN WEI	1130	Remarks Dale Nolte (USDA)
	1140	Remarks Xiwu Zhang (SFA)
	1150	Remarks Fuwen Wei (IOZ)
	1200	Lunch
1400 Free Tour to National Zoological Museum		
	1400	Depart hotel lobby for museum using shuttle bus
	1600	Return to museum using shuttle bus

Friday 23 July 2010

Optional City Tour – Fee Required		
	0900	Depart hotel Three options depending on what you would like to see while in Beijing
	1700	Return to hotel
Saturday 23 July 2010 Depart Beijing		

Background to this Conference

Emerging and re-emerging wildlife borne diseases, such as high pathogenic avian influenza (HPAI), rabies, plague, and SARS, continue to warrant attention because they threaten agriculture, wildlife conservation, and human health. The surveillance and control of wildlife diseases, especially HPAI, is a global concern, not limited to a single country. Research and surveillance conducted to investigate wildlife diseases varies greatly among countries. As a global concern it would be best if activities occurred and information was shared across all countries.

Wildlife Services, Animal and Plant Health Inspection Service, United States Department of Agriculture (USDA, APHIS, WS) and Institute of Zoology, Chinese Academy of Sciences (CAS, IOZ) have cooperated for the past several years to conduct surveillance activities and to develop workshops to bring countries together, in their efforts to monitor for and respond to wildlife disease outbreaks and obtain a better overall understanding of wildlife borne diseases.

The objectives of this conference are: (1) to promote collaboration in the field of wildlife diseases among countries and districts in the Asia-Pacific region; (2) to share activities related to investigation, surveillance, and research on wildlife diseases; and (3) to coordinate the cooperation and communication of specialists in multiple fields and areas such as wildlife conservation and management, veterinary, ecology, and biology.

The workshop “Asia-Pacific Conference on Wildlife Borne Diseases” is being held to further understanding of wildlife diseases through the communication and cooperation among multi-countries and multi-fields. This workshop is convened by Bureau of Life Science and Biotechnology, Chinese Academy of Sciences, Wildlife Services, Animal and Plant Health Inspection Service, United States Department of Agriculture, and Department of Wildlife Conservation and Nature Reserve Management, State Forestry Administration, China.

Overarching theme: Research, prevention and control of important wildlife borne diseases in Asia-Pacific

The theme of the conference is: Research, prevention and control of important wildlife borne diseases in Asia-Pacific. The intent of the theme is to enhance further discussion, and consolidate and develop approaches for the prevention and control of wildlife diseases.

The conference gives special emphasis to high pathogenic avian influenza, rabies west Nile virus, Japanese encephalitis, diseases associated with feral swine, and plague, along with other wildlife borne diseases.

Instructions for Participants

All events and sessions will take place at **Beijing Hongxiang Hotel** located between the North 3rd ring road and North 4th ring road, adjacent to Olympic Park, ZhongGuanCun and the Badaling Express Way. From the hotel it is only a 30 min drive to Badaling section of the Great Wall, 20 min to the Summer Palace, 10 min drive to Olympic Park, and 30 min to Beijing's airport and major train stations.

In English:

Beijing Hongxiang Hotel

Address: No.15 Longxiang Road, Haidian District, Beijing, China

Tel: 86-10-59838888

Fax: 86-10-59838860

Website: www.hongxianghotel.com.cn/English/index.htm

In Chinese:

北京鸿翔大厦

地址：北京市海淀区龙翔路15号

电话：86-10-59838888

传真：86-10-59838860

网站： www.hongxianghotel.com.cn

Transport to and from Beijing Capital International Airport

Beijing Hongxiang Hotel is not conveniently serviced by a subway or direct bus from the Beijing Capital International Airport. Therefore **Taxi is recommended transport** means to travel to the hotel from the airport. Taxi service is available at the Beijing Capital International Airport (<http://en.bcia.com.cn/ecotraffic/taxi.shtml>) 24 hours a day. There are signs to follow to the Taxi Bay. You should not follow anybody advertising or offering you an unofficial taxi. The airport is well managed and **English-speaking information attendants** are available to assist you if you have questions.

Taxi drivers do not speak English well. Therefore, you need to be prepared to show the name of your hotel in Chinese. The Chinese name and address are provided above. If you have any problems, the taxi driver will call the hotel and get directions from them. Chinese taxi drivers are very patient with visitors and **will use the taxi meter without being asked**.

Using the taxi meter is the law and you should insist on the meter.

Your **fare should be around 110 Chinese Yuan** (please exchange or withdraw cash at the airport) to get to the hotel. **Tipping is not practiced in China**, so pay the fare as shown on the meter plus any tolls your driver may have gone through. Taxi drivers usually offer a receipt but in case they do not, remember to ask for it. The English translation for the Chinese expression meaning receipt is 'Fa piao'.

Weather in Beijing

The climate in Beijing is continental. Weather during the summer months, June to August, is generally hot and wet. Approximately 40% of the annual falls during these months.

Average Data	May	Jun	July	Aug	Sep
Average High (°F)	78/82	86/89	87/90	84/88	77/81
Average High (°C)	26/28	30/32	30/32	29/31	25/27
Average Low (°F)	54/58	63/67	69/73	67/72	56/60
Average Low (°C)	12/14	17/19	21/23	20/22	13/15
Max (°F)	99	104	104	107	92
Max (°C)	37.2	40.0	40.0	41.7	33.3
Min (°F)	39	48	63	54	36
Min (°C)	3.9	8.9	17.2	12.2	2.2
Rain (in)	1.4/1.5	2.9/3	8.0/8.1	7.1/7.2	<0.1
Rain (mm)	35/40	75/80	205/210	180/185	<5

Currency Exchange, Credit Cards and ATM

The Chinese currency is the Chinese Yuan, or Ren Min Bi (said: Wren-min-bee). The international standard abbreviation for the Yuan is CNY. Chinese Yuan bank notes are 1, 2, 5, 10, 50 and 100 CNY. Participants **can use their ATM cards** anywhere in China, or exchange currencies at airports, major hotels and banks in China. Currently, 1 USD is equivalent to 6.75 CNY. All **currency exchange receipts should be saved** in case participants want to exchange RMB back to their own currency. Banks may demand to see the original exchange receipt. Please **have your passport available** when exchanging money.

Visa, MasterCard, American Express, Diners Club, and JCB are accepted in many department stores and hotels. ATMs are available to obtain RMB with your credit or debit card. The amount deducted from your account will vary due to fluctuations in the exchange rate.

There is normally a 4% additional bank charge.

Smoking Policy

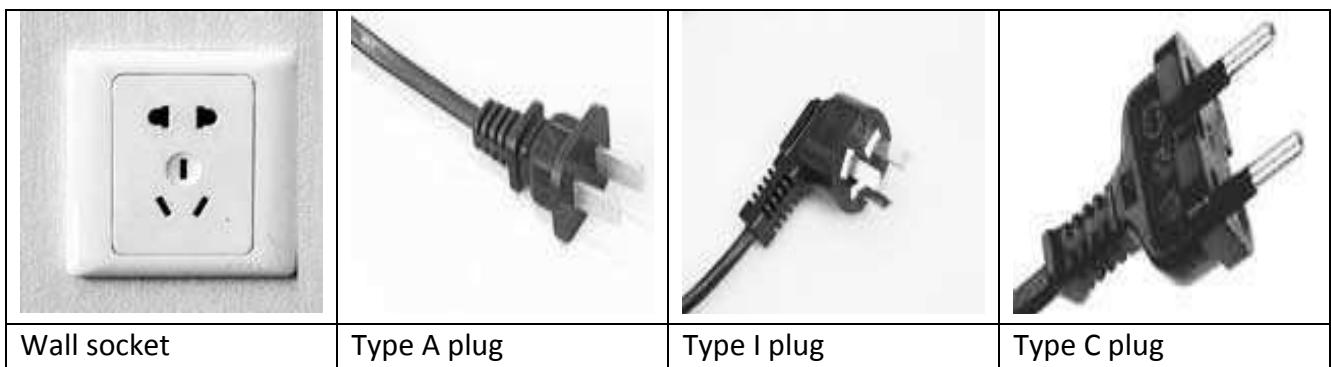
Please remember that smoking is prohibited within the conference premises.

Water

It is recommended that you do not drink water directly from the tap in your hotel room. If you want to drink cold water, it is best to order or buy bottled water, mineral or distilled. Hotels will also provide a kettle to boil water from the tap in your room. The boiled water can then be stored in a thermos for drinking. Some hotels also provide a special tap in the lavatory that delivers a flow of purified water for drinking or taking medication.

Voltage, Socket and Plugs

The electrical current in China is 220-volts, 50Hz A/C. Hotels generally provide **universal wall sockets in every room**, accommodating both the standard “Flat blade attachment plug (Type A)” and common “Oblique flat blades with ground (inverted V) plug (Type I)”, as well as the not-so-common “Round pin attachment plug (Type C)” as shown:



Recording and photography

Taking photographs, audio-taping, video-recording, digital taping and any other form of duplication are strictly prohibited in the session rooms and poster areas without first obtaining permission from the appropriate author.

Cell Phones

Participants are kindly requested to turn off their cell phones or turn their cell phones to vibration mode when entering the meeting rooms and in the poster areas.

Hotlines and Emergency Numbers

Dial:

110 Police

114 Local Telephone Number Inquiry

116 Domestic Long Distance Inquiry

117 Time Inquiry

119 Fire

120 Ambulance

121 Weather Forecast

122 Traffic Police

Registration

Participants should check-in to the Beijing Hongxiang Hotel on 19 July 2010. When you sign in at registration you receive assigned house arrangements and conference documents. You also need to sign up for any city tours you want to take after the conference.

Language

English will be used for communication at the conference.

Accommodation

(1) Please do not damage articles in the room. If any articles are damaged, you will be required to compensate the hotel. Participants will be required to pay for any expenses charged to their rooms. If you need any item for personal consumption, please contact the Service Desk in the Hall.

(2) During the meeting, participants shall take care of all personal items and never leave them unattended.

(3) Please refer to the room service guide or contact the Hotel Advisory Desk for any other issues or questions you may have regarding accommodation or hotel services.

Dining during the Conference

	19 July	20 July	21 July	22 July	23 July
Breakfast	X	Hong Fu Palace (provided with your accommodation)			
Morning tea	X	Hong Xiang Hall			X
Lunch	Hotel	Hong Fu Palace (Buffet)			Hotel
Afternoon tea	X	Hong Xiang Hall		X	X
Dinner	Hotel	Hong Jin Palace (Reception)	Hong Fu Palace (Buffet)		Hotel

- 1) Please present your dining ticket issued at registration when dining.
- 2) Breakfast should be included with your accommodation and available at Hong Xiang Palace by presenting your dining ticket.
- 3) Morning tea on 20 to 22 July, and afternoon tea on 20 and 21 July, will be provided and available between lectures outside Hong Xiang Hall.
- 4) Lunch from 20 to 22 July, and dinner on 21 and 22 July, will be available as buffet at Hong Fu Palace by presenting your dining ticket.
- 5) Dinner on 20 July will be available as Reception Banquet at Hong Jin Palace.
- 6) Lunch and dinner on 19 and 23 July will be available by presenting your dining ticket at the hotel. Dining ticket for lunch is valued at 65 RMB, and dining ticket for dinner is valued at 60 RMB. Dining tickets can be used on any food or drink up to this value. Additional costs must be covered by you.

Venue

The **meeting venue will be Hong Xiang Hall** located in the Beijing Hongxiang Hotel

Internet

The Hotel has both wireless and cable connections in each room. The meeting room also has wireless internet available.

Secretariat Room

The Secretariat Room will be located near the Hong Xiang Hall. Feel free to approach the following members of the Secretariat if you require any help during the conference:

- Chengmin Wang T: 13552962162
- Jing Luo T: 13810808273

Notes for Conference

(1) Admittance only with your Participant Card. Persons without a Participant Card will not be permitted entrance.

(2) Casual dress attire will be appropriate for the meeting.

(3) Please turn off your cell phone or switch it to vibrate mode.

(3) The organizer has the right to temporarily change the schedule or activities if a Force Majeure occurs during the conference.

(4) Presenters should check in at least 10 minutes before the starting of their session. Please copy your PowerPoint presentations to the Conference Computer before your scheduled presentation. The Operating system of the conference computer is Windows XP. Please transform your documents ahead of time to a file type that can be recognized by the windows XP system.

(5) Air conditioning for Hong Xiang Hall will be set at 26°C (78°F) and you are encouraged to dress casually and comfortably.

City Tour I on 22 July (Free for participants)

National Zoological Museum

The National Zoological Museum is located inside the Institute of Zoology, Chinese Academy of Science in eastern Beijing's Chaoyang district. The ticket price is normally 40 Yuan or approximately 6 USD for adults, but free for conference participants. There is also a discount for students and group visits. The museum is open from 0900-1600 on Tuesday through Sunday, closed on Mondays. As the largest zoological museum in China, the complex has attracted many visitors to experience the mystery of the animal kingdom.

City Tour II on 23 July (optional, fee to be covered individually)

Packages include: admission fee, air-condition coach, lunch, English speaking guide. The

price is based on the number of travelers, if the number is less than 5, the price will be raised.

Cell Phone: +86-013146319209 Email: Millerliu444@gmail.com

Plan I—The Summer Palace

The Summer Palace landscape is dominated by Longevity Hill and Kunming Lake. The Palace grounds extend across an area of 2.9 square kilometers. Kunming Lake covers about three quarters of the grounds. A variety of palaces, gardens and other ancient-style architectural structures provide approximately 70,000 square meters of building space. The Summer Palace is well known for its large and priceless collection of cultural relics. It was among the first group of historical and cultural heritage sites in China to be placed under special state protection. The Summer Palace, originally named Qingyi Yuan or the Garden of Clear Ripples, was first constructed in 1750. Anglo-French Allied Forces razed it to the ground during 1860. The Government of the Qing Dynasty started to rebuild it in 1886 with funds that it had misappropriated from the Imperial Navy and other sources. Renamed two years later as Yihe Yuan or the Garden of Health and Harmony, it was supposed to serve as a summer resort for the Empress Dowager Cixi. Known also as the Summer Palace, it was ravaged by the Allied Forces of the Eight Powers that invaded China during 1900.

Plan II—The Palace Museum (the Forbidden City) and Tiananmen Square

Established in 1925, the Palace Museum was installed within the imperial palace of two consecutive dynasties – the Ming (1368 to 1644) and the Qing (1644 to 1911). The magnificent architecture, also is known as the Forbidden City. The Palace Museum contains the vast holding of the imperial collections of paintings, calligraphy, ceramics, and decorative objects, making it one of the most prestigious museums in China and the world at large. In 1961, the imperial palace was designated by the State Council as one of China's foremost-protected cultural heritage sites, and in 1987 was made a UNESCO World Heritage site. Located at the center of Beijing City (next to the Forbidden City) is Tiananmen Square. At Tiananmen Square you can visit Tiananmen Tower, Monument to the People's Heroes, Great Hall of the People, Mao Zedong Memorial Hall and see the national flag raising ceremony. Thousands of people come to the Square every day. It is a must place to visit in Beijing City.

Plan III—The Great Wall

“He who does not reach the Great Wall is not a true man.”The majestic Great Wall touches

the billows of the Bohai Sea in the east, and traverses the vast expanse of the Gobi desert in the west. It crosses prairies and deserts, nestles up to the Yellow River, surmounts high mountains, stretches 10,000 li (approximately 5,000 km) and, like a soaring dragon, leaps over the boundless land of China. The Great Wall was built with the blood and sweat of laboring people of ancient China. It is a symbol of the brilliance of China's ancient culture and a pride of the Chinese nation. The Great Wall of China possesses thousands of famous passes. Badaling, located in the outer town of Juyong Pass, is recognized as one of the top nine passes in the world. It boasts a strategically important position, long history, rich culture, spectacular architecture, inspiring sight, and great fame. For these reasons, it is considered one of the best places to see the Great Wall. Badaling Great Wall is an outstanding representative of the Great Wall of China. It is the best section of the Great Wall constructed during the Ming Dynasty. It is a precious part of human cultural heritages and a center of attention for world tourists. Badaling Great Wall embodies the wisdom and civilization of the Chinese nation. It is laid with historical heritages covering thousands of years. Badaling Great Wall, a place contested by all strategists since ancient times, is endowed with new historical missions these days. Its reputation strides across high mountains, straddles deep oceans, crosses time and space, and serves as a bridge of friendship for all people of the world. The seeds of friendship are sown here. The songs of peace are sung here.

Departure

The conference departure date is 24 July 2010. After this date accommodation support will stop.

Introduction of Key Sponsors and Organizations



Bureau of Life Sciences and Biotechnology, Chinese Academy of Sciences

The main functions of the Bureau of Life Sciences and Biotechnology, Chinese Academy of Sciences are: to analyze world tendencies in the disciplinary development of the life sciences and biotechnology; to formulate research planning and strategies for major disciplines in coordination with relevant bureaus; to organize and coordinate institutes in a bid to apply for national major programs concerning the life sciences and biotechnology; and to undertake the planning, initiation, public bidding, supervision, appraisal and official acceptance of major research projects and bases in these fields of the CAS. The Bureau of Life Sciences & Biotechnology provides advice and guidance on the readjustment and reorientation of the development directions of CAS institutes in these fields. Website: www.english.cas.cn



Department of Wildlife Conservation and Nature Reserve Management, State Forestry Administration, China

The Department of Wildlife Conservation and Nature Reserve Management is an internal institution of the State Forestry Administration (SFA), and at the same time, the Department also functions as the SFA Wildlife Conservation and Nature Reserve Construction Program Office and SFA Wetland Convention Implementation Office. It is responsible for guiding the management of the nationwide management of wildlife and Nature Reserve, and for coordinating the programs in the nationwide wetland conservation. Website: <http://www.wildlife-plant.gov.cn/en/aboutus.htm>

Introduction of Key Sponsors and Organizations



National Wildlife Diseases Program, Wildlife Services, Animal and Plant Health Inspection Services, United States Department of Agriculture

Wildlife Services (WS), a program within the U.S. Department of Agriculture's Animal and Plant Health Inspection Service, provides Federal leadership and expertise to resolve wildlife conflicts that threaten U.S. agricultural and natural resources, as well as human health and safety, and property. Wildlife Services' National Wildlife

Disease Program (NWDP) promotes safe agricultural trade by protecting the health of humans, animals, plants and ecosystems to reduce the levels of incurred losses to agricultural and natural resources.

NWDP participates in wildlife disease monitoring and surveillance in all regions of the United States. The program's Wildlife Disease Biologists act as WS' first responders through NWDP's Surveillance and Emergency Response System. Additionally, NWDP collaborates with non-governmental organizations and officials from other countries to promote and assist in the development of wildlife disease monitoring programs worldwide. Website:

http://www.aphis.usda.gov/wildlife_damage/nwdp/index.shtml



Institute of Zoology, Chinese Academy of Sciences

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Abstracts

Viral polymerase mediates adaptation and attenuation of an avian H5N1 influenza virus to Mice

Jing Li, Yongqiang Li, Yi Hu, Guohui Chang and Qingyu Zhu

Beijing institute of microbiology and epidemiology, Beijing, 100071

H5N1 avian influenza virus from its natural bird hosts could infect human beings and other mammalian hosts, showing high pathogenicity and lethality. Of more concern is what kind of mutation or selection happened to the virus during its infection in the mammalian host. Here, we determined several variants, isolated from the lung of mice infected intranasally with an avian H5N1 strain isolated from a fatal human case in 2004. A single mutation in those variants PB1 contributed to higher polymerase activity and replication efficiency in mammalian cells, and another mutation in PB2 resulted in non-lethality to mice. These two adaptive and attenuated mutations of the polymerase complex demonstrate a mutual-beneficial evolution or selection for both H5N1 virus and mammalian hosts.

Canada's inter-agency wild bird influenza survey: surveillance and research

C. Soos^{1,14}, E.J. Parmley², I.K. Barker², A. Breault³, P.A. Buck⁴, P-Y. Daoust⁵, J. C. Davies⁶, M. Fortin⁷, T. Hisanaga⁸, E. Jenkins^{1, 14}, H. Kehler⁸, F. Kibenge⁹, R. King¹⁰, S. Lair¹¹, J. Leafloor¹², K. McAloney¹³, R. Nallar¹⁴, D. Ojkic¹⁵, J. Pasick⁸, J. Robinson¹⁶, J. Rodrigue¹⁷,
H. Whitney¹⁸ and F.A. Leighton^{14,19}

¹Environment Canada - Science & Technology Branch, Saskatoon, SK; ²Canadian Cooperative Wildlife Health Centre, Guelph, ON; ³Environment Canada - Canadian Wildlife Service, Delta, BC; ⁴Public Health Agency of Canada - Foodborne, Waterborne and Zoonotics Infections Division, Ottawa, ON; ⁵Canadian Cooperative Wildlife Health Centre, Charlottetown, PE; ⁶Ontario Ministry of Natural Resources, Peterborough, ON; ⁷Laboratoire d'épidémiosurveillance animale du Québec, Saint-Hyacinthe, QC; ⁸National Centre for Foreign Animal Disease - Canadian Food Inspection Agency, Winnipeg, MB; ⁹University of Prince Edward Island, Charlottetown, PE; ¹⁰Agri-Foods Laboratories Branch, Edmonton, Alberta; ¹¹Le Centre québécois sur la santé des animaux sauvages, St-Hyacinthe, QC; ¹²Environment Canada-Canadian Wildlife Service, Winnipeg, MB; ¹³Environment Canada - Canadian Wildlife Service, Sackville, NB; ¹⁴University of Saskatchewan, Saskatchewan, SK; ¹⁵University of Guelph, Guelph, ON; ¹⁶Animal Health Centre, British Columbian Ministry of Agriculture and Lands, Abbotsford, BC; ¹⁷Environment Canada - Canadian Wildlife Service, Sainte-Foy, QC; ¹⁸Newfoundland and Labrador Department of Natural Resources, St John's, NL; ¹⁹Canadian Cooperative Wildlife Health Centre, Saskatoon, SK

Canada's Inter-agency Wild Bird Influenza Survey is a collaboration between federal, provincial and territorial government agencies, academic institutions and non-governmental organizations involved in wildlife, domestic animal, and human health. The objectives of the Survey are to achieve vigilance for highly pathogenic avian influenza viruses (HPAIV) that threaten animal or human health, to determine and characterize avian influenza viruses circulating among wild bird populations, and to establish and maintain an integrated national laboratory and surveillance capacity for avian influenza viruses. To meet these objectives, the Survey is composed of: (i) a live wild bird survey, focusing on the sampling of waterfowl and other wild bird species across Canada, and (ii) a dead bird surveillance program to enhance Canada's ability to detect highly pathogenic avian influenza strains or other emerging diseases of concern. Since its inception in 2005, >17 200 live dabbling ducks, >8,500 birds of other species, and >12 000 dead birds have been tested for the presence of avian influenza virus, and overall, 25%, 4%, and 2% have tested positive, respectively. All strains have been of North American lineage, and no highly pathogenic avian influenza viruses have been detected.

Sialic acid receptor detection in the raptor respiratory tract: evidence for a potential host of avian influenza virus

Chun-Hua Han¹, Jian Lin¹, Jing-Wen Han¹, Ying-Li², Xiu-qing Wang³, Hui-Juan Duan¹, Jie Pan¹
and Yue-Huan Liu¹

¹Institute of Animal and Husbandry Medicine, Beijing Academy of Agriculture and Forestry Sciences, Beijing, 100097, China; ²Biology Garden, Beijing Normal University, IFAW Beijing Raptor Rescue Center, No.19 Xijiekou Wai street, Beijing, 100875, China; ³Department of Biology and Microbiology, South Dakota State University

Influenza viruses initiate infection via the binding of hemagglutinin to sialic acid on the host cell surface in $\alpha 2, 3$ or $\alpha 2, 6$ linkages to galactose. To understand the pathologic basis of the susceptibility of eight species of raptors to avian influenza virus, we examined the presence of sialic acid (SA) and galactose(Gal) linkage in eight species of raptors. Our data showed that there was abundance of SA $\alpha 2, 3$ -Gal in tracheal and pharynx epithelium of *Accipiter gularis*, *Buteo buteo*, *Falco tinnunculus*, *Accipiter nisus* and *Falco peregrinus*. No SA $\alpha 2, 6$ -Gal was found in *Accipiter nisus*, *Falco tinnunculus* and *Falco peregrinus*. The epithelial surfaces of the pharynx and trachea of *Accipiter gularis* similarly expressed SA $\alpha 2, 3$ -Gal and SA $\alpha 2, 6$ -Gal. Strong positive staining for SA $\alpha 2, 3$ -Gal receptors and mild positive staining for SA $\alpha 2, 6$ -Gal receptors were visible in the trachea and pharynx epithelium of *Buteo buteo*. Both SA $\alpha 2, 3$ -Gal and SA $\alpha 2, 6$ -Gal were found in the alveolus of *Buteo buteo* and *Falco peregrinus*, while only SA $\alpha 2, 3$ -Gal in *Accipiter nisus*, *Accipiter gularis* and *Falco tinnunculus*. As for the tested *Strigiformes raptor*, there were both SA $\alpha 2, 3$ -Gal and SA $\alpha 2, 6$ -Gal in the tracheal and throat epithelium of *Otus sunia* and *Asio otus*, the same as in *Otus sunia*, *Bubo bubo* alveoli. The extensive presence of SA $\alpha 2, 3$ -Gal receptor in the upper and lower respiratory of eight species of raptors suggests that these raptors may be permissive to influenza virus entry or infection. In conclusion, raptors could be a potential host of avian influenza virus.

Antiviral treatments for avian influenza: siRNA and Retrocyclin2

Kai Zhou^{1,2}, Qinglong Liang^{1,2} and Hongxuan He¹

¹Institute of Zoology, Chinese Academy of Sciences; ²Graduate School of Chinese Academy of Sciences

Avian influenza virus H5N1 causes widespread respiratory tract infections in birds and humans, and existing vaccines and drug therapy are of limited value. Here, we show that small interfering RNAs (siRNAs) specific for conserved regions of the viral genome can potently inhibit influenza virus production in cell lines, embryonated chicken eggs and BALB/c mice. This inhibition is dependent on the presence of a functional antisense strand in the small interfering RNA duplex, suggesting that viral mRNA is the target of RNA interference. For the three small interfering RNA expression plasmids we designed, we found that small interfering RNA for nucleocapsid protein (NP) had a specific effect in inhibiting the accumulation of RNA in infected cells. This is because of a critical requirement for newly synthesized nucleocapsid proteins in avian influenza viral RNA transcription and replication. Our findings reveal that newly synthesized nucleocapsid, polymerase A (PA) and polymerase B1 (PB1) proteins are required for avian influenza virus transcription and replication. They also provide a basis for the development of small interfering RNAs as forms of prophylaxis and therapy for avian influenza infection in birds and humans. We also tested the ability of retrocyclin 2 to protect cells and chicken embryos from highly pathogenic H5N1 avian influenza virus infection. The gene fragment of retrocyclin 2 was designed based on the protein sequence, and was cloned into the eukaryotic expression vector pcDNA4.01 (HismaxA). pcDNA4-RC2 protected MDCK cells and chicken embryos from infection by the H5N1 virus, through inhibition of virus replication and viral mRNA transcription.

Pandemic characteristics and controlling experiences of influenza H1N1 virus one year after inception in Hangzhou, China

Shelan Liu¹, Zhiruo Zhang², Ying Dong³, Lunbiao Cui⁴, Xuhui Yang¹, Zhou Sun¹, Jing Wang¹, Jin Chen¹, Renjie Huang¹, Fan Liao¹, Hongxuan He⁵, Bing Ruan⁶,
Li Xie¹ and Jing Deng¹

¹Department of Infectious Diseases, Hangzhou Center for Disease Control and Prevention, Zhejiang province, China; ²Shanghai Institute of Hematology, Rui-Jin Hospital affiliated to Shanghai Jiao Tong University School of Medicine, Shanghai, China; ³Department of Oncology, the Second Affiliated Hospital of Zhejiang University School of Medicine, Zhejiang province, China; ⁴Department of Acute Infectious Disease, Jiangsu Province Center for Disease Control and Prevention, Jiangsu province, China; ⁵National Research Center for Wildlife Born Diseases, Key Lab of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences, Beijing, China; ⁶National Key Laboratory for Diagnosis and Treatment of Infectious Diseases in China, The First Affiliated Hospital, College of Medicine, Zhejiang University, Hangzhou, China.

Here, we summarize the characteristics and experiences of the influenza A/H1N1 pandemic one year after the first confirmed case. On 31 March 2010, 2078 influenza A/H1N1 cases were downloaded from the China information system for disease control and prevention and analyzed by DNASTAR. Our results showed an infection prevalence of 2.77/10 000 individuals (2078/7 510 844), with an age range of one month to 89 years. 52.99% (1435/2708) were in the 10–29 year age group, and this percentage was even greater in downtown areas compared to suburban areas. The first epidemic peaked in September, and the second in November. The first severe case was reported five month after inception, and the case-severity rate was 10.44% (217/2078) and the case-fatality rate 0.48% (10/2078). Fifty percent of serious cases had severe underlying diseases including cardiovascular disease (13.66%), chronic lung disease (2.02%), and pregnancy (7.1%). The asymptomatic carrier rate was 9.52% and secondary attack rate was 8.66%. The hemagglutinin gene remained stable, with 98.5% homology to the North American strain, but only 70% to the 1947–2008 Chinese H1N1 strains. Methods such as blocking admitting patients, health education, outbreak control, vaccination, treatment of severe cases and surveillance after admission, took place post-epidemic, along with community outbreaks, pandemic, and severe cases. In conclusion, the influenza/H1N1 strain was identical to that found elsewhere in the world, and resulted in low pathogenicity in Hangzhou.

Avian influenza virus in domestic ducks in West Java, Indonesia

Kristy Pabilonia¹, Surachmi Setyaningsih², Albert Mulyono³, Winda Digna³, Riana Arief³,
Erianto Nugroho³ and Richard Bowen¹

¹Colorado State University, Fort Collins, CO, USA; ²Bogor Agricultural University, Bogor, Indonesia;

³Center for Indonesian Veterinary Analytical Studies, Bogor, Indonesia

H5N1 avian influenza virus is endemic in domestic poultry in Indonesia. Village poultry flocks are common in West Java and numerous H5N1 outbreaks have been documented in this area. Domestic duck flocks, used for egg, meat and feather production, are also common. Outbreaks of avian influenza virus in domestic ducks likely go undetected, as waterfowl are the reservoir of avian influenza virus and infections are often subclinical or mild. The aim of this study was to determine if domestic ducks play an important role in the spread and transmission of avian influenza virus to chicken populations and are important to the maintenance of avian influenza virus in West Java. Duck flocks were characterized into one of three categories, fully free-ranging, partially free-ranging and confined, based on movement patterns and production type. For a cross-sectional study, ten flocks from each category were selected from each district, totaling 90 flocks. Flock owners were interviewed to collect information on flock size, movement, purpose and interaction with wild birds and mammals. Thirty ducks from each flock were sampled. Positive samples were tested for H5 avian influenza virus by rRT-PCR. In addition, serum samples were collected to determine antibody levels to avian influenza virus in the duck flocks. For the longitudinal study, two flocks from each category were selected from each district, totaling 18 flocks. Thirty ducks from each flock were selected as sentinels. Results to date show a high prevalence of avian influenza virus infection in domestic ducks, as well as the detection of H5 positive avian influenza flocks. Isolation and characterization of viruses is ongoing.

Pathogenic factors and pathogenesis of influenza viruses

Hong Zhang

Z-BioMed, Inc., Rockville, MD 20855, USA; Department of Respiratory Medicine, Affiliated Hospital of Zunyi Medical College, Zunyi 563003, China

The first transmission of the highly pathogenic H5N1 avian influenza A virus directly from chickens to humans in Hong Kong was reported in 1997 and more than 400 laboratory-confirmed human cases (~60% fatal) of avian H5N1 infection have been reported to the World Health Organization (WHO) since then. The swine-origin H1N1 influenza A virus caused the first pandemic of this century and less than 2% of the cases were fatal. The continued circulation of avian and swine influenza viruses in Asia and the world reminds us of the real threat of future pandemics from non-human influenza viruses. It is poorly understood why highly pathogenic H5N1 virus caused approximately 60% mortality and swine-origin H1N1 virus caused less than 2% mortality. It is therefore important to identify pathogenic factors of different influenza viruses and understand why and how certain factors, either viral or host, contribute to the virulence of some influenza viruses. In this presentation, I will discuss pathogenic factors of different influenza viruses and future studies to develop treatment for severe influenza virus infection through regulations of pathogenic factors.

Migration routes and stop-over sites determined with satellite tracking of bar-headed geese (*Anser Indicus*) breeding at Qinghai Lake, China

Guo-Gang Zhang¹, Dong-Ping Liu¹, Yun-Qiu Hou¹, Hong-Xing Jiang¹, Ming Dai¹, Fa-Wen Qian¹, Jun Lu¹ and Zhi Xing²

¹Research Institute of Forest Ecology and Environment Protection, Key Laboratory of Forest Protection of State Forestry Administration, Chinese Academy of Forestry, National Bird Banding Center of China, Beijing 100091, China; ²Qinghai Lake National Nature Reserve, Xining, Qinghai 25700, China

A large outbreak of avian H5N1 occurred in Qinghai Lake (historically known as Koko Nor) from late April to June of 2005, in which about 6000 waterbirds died, mostly bar-headed Geese (*Anser indicus*), brown-headed Gulls (*Larus brunnicephalus*), great black-headed gulls (*Larus ichthyaetus*), and great cormorants (*Phalacrocorax carbo*). In 2006 and 2007 we used satellite telemetry at Qinghai Lake to study the migration of bar-headed geese. The goals of this study were to: 1) determine migration routes and stop-over sites of bar-headed geese breeding at Qinghai Lake; and 2) assess movement and habitat use at major stopover and wintering sites by this species. Ten Bar-headed Geese were banded with satellite transmitters at Qinghai Lake in western China in the July of 2006 and 2007 to determine their migration routes. Of the ten tagged geese, eight left Qinghai Lake and began autumn migration. Of the eight geese, four completed their autumn migration, lasting 50 to 90 days, using one of two migration routes to their wintering grounds near Caohai Lake in Guizhou Province, Yarlung Zangbo valley in Tibet, and Kohima in India. The tagged geese each stopped at three to four sites and traveled 1270 to 1470 km from their breeding to wintering grounds. Wetlands at Muli Marsh, Zhaling, Eling and Galalacuo Lakes in Qinghai Province, Nagqu and Damxung in Tibet, and Ruorgai Marsh in Gansu and Sichuan Provinces were used as major stop-over sites.

Preliminary observations on primate borne diseases in Bangladesh

Mohammad M. Feeroz, G. A Engel, A. Escalante, N. Lerche, M. Linial, S. Oberste and
L. Jones-Engel

Human interaction with nonhuman primates (NHPs) is common in Asia and particularly in Bangladesh, where they have lived sympatrically for centuries. Among the ten species of NHPs found in Bangladesh, rhesus macaques (*Macaca mulatta*) and Hanuman langur (*Simnopithecus entellus*) are the only species living in and around human settlement. They have adapted well to human altered environments and can thrive in both urban settings and at religious sites (monkey temples). This expanding urban niche frequently and increasingly brings NHPs into close contact with humans, facilitating the potential for cross-species transmission of infectious agents. Whether cross-species transmission occurs depends on a number of factors, including the types and prevalence of infectious agents present in the human and NHP reservoirs, the contexts of interspecies contact, and the frequency and type of contact that occurs. In Bangladesh we are characterizing the zoonotic transmission of two enzootic simian viruses: Simian Foamy Virus and Simian Retrovirus from NHPs in different regions and contexts of contact. We are also characterizing the Enterovirus pathogen landscape for NHPs in Bangladesh. Human and NHP population densities and sanitation conditions in Bangladesh favor efficient fecal-oral transmission of Enteroviruses. Host-switches within these shared ecological contexts appear to be common. The implications for primate conservation and human health are discussed.

Metagenomic analysis of viruses in bat intestinal tracts: the important role of bats in ecosystems

Xing-yi Ge¹, Yan Li¹, Hua-jun Zhang¹, Peng Zhou¹, Yun-zhi Zhang^{1,2} and Zheng-li Shi¹

¹State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; ²Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China

Bats are the second most diverse mammals on Earth. Increasing data indicate that bats harbor diverse viruses and some of them cause severe human diseases. Here, random-polymerase chain reaction (rPCR) and high throughput sequencing technology (Solexa) was applied for metagenomic analysis of viruses harbored in bat intestinal tracts. Bat feces were collected from six different locations and used for virus concentration and purification. The nucleic acid of purified viruses was extracted and used for Solexa sequencing. A total of 8 746 417 reads with a length of 306 124 595 bp, were obtained. Among them, 13 541 reads have homologies to phages, 9170 reads to other viruses. A total of 105 assembled contigs (>75 nt) have been constructed and compared with GenBank, 22 contigs showed identities of 68–99% to known virus genomic sequences, 83 showed identities of 20–95% to viral protein sequences. The most frequent reads and contigs are homologous to densoviruses, dicistroviruses, coronaviruses, paroviruses and tobamoviruses, covering invertebrate viruses, vertebrate viruses and plant viruses. This study provides a more comprehensive understanding of virome in bat intestinal tracts.

Wildlife disease surveillance and the west Nile virus response in Canada

Ian Barker

Ontario/Nunavut Region, Canadian Cooperative Wildlife Health Centre, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada N1G 2W1.

Surveillance of dead corvids began in Canada in 2000 to detect West Nile virus (WNV) activity across space and time. By 2003 a system of rapid decentralized specimen accession/testing/electronic reporting (usually same day), based on the VecTest[®] immunochromatographic strip had been validated and implemented. Over 11,000 specimens were tested that year. WNV was first detected in Canada in a dead corvid from southwestern Ontario in August 2001. Subsequent distribution of WNV in Canada over time followed the general pattern in the USA to the south, but extended into boreal ecosystems; it was finally detected in British Columbia, west of the Rocky Mountains in August 2009. Major human WNV epidemics have occurred in southern Ontario (2002), and Manitoba and Saskatchewan (2003, 2007). Quebec ceased all WNV testing and mitigation activity (including mosquito larvaciding) in 2006, based on an assessment of low risk due to climatic factors, and Ontario has terminated systematic dead bird testing effective 2009. Ontario, Manitoba and Saskatchewan prefer to use mosquito surveillance. Manitoba is the only jurisdiction in Canada where control of adult mosquitoes has been routine, primarily to reduce the burden of nuisance species in Winnipeg, and where adulticiding has been used for WNV mitigation. While general correlations between WNV activity in dead corvids and risk of human infection have been established over a large geographic scale in southern Ontario, sophisticated models of WNV monitoring, such as DYCAST, which incorporate dead bird surveillance, have not been applied in Canada, in part probably because large high-risk areas with dense human populations are rare.

Current epidemiological situation of African swine fever in Russian Federation

A.S. Malogolovkin, D.V. Kolbasov, V.V. Kurinnov and V.M. Balyshev

National Research Institute for Veterinary Virology and Microbiology, Russian Academy of Agriculture Science, 601120, Vladimir region, Pokrov, Russia,

During the first half of 2010, 21 outbreaks (15 outbreaks within domestic pig and six wild boar populations) of African swine fever (ASF) were detected across Russia. In summary, from 2007–2010 in South –Russian and Northern Caucasus regions 122 cases of the disease were found. The last outbreak was reported from Rostov region on 27 June 2010 at a domestic pig farm. The outbreaks continue to appear on the territory of Caucasus republics in spite of long outbreak-free periods up to 6–7 mo, and this confirms that endemic foci are developing in given region. The investigations carried out with ASF viruses, collected from outbreaks of the disease in 2007–2010 allowed to deposit seven isolates of the virus in the NRIVVaM collection. All these isolates belong to the II genotype according to gene encoding major structural protein p72 partial sequencing. In setting up HADIT using ASF reference serum of serotype I to VIII, the examined isolates were found to be typed with VIII serotype. Our findings suggest that only one genotype of the virus is circulating in Russia, in spite of different methods of virus transmission. The role of vectors such as ticks and other blood-feeding species of the insect inhabiting South-Russia and Northern Caucasus requires further investigation.

Application of oral vaccination for rabies control in wildlife reservoirs in North America

Dennis Slate¹, Richard B. Chipman², Timothy P. Algeo¹, Kathleen M. Nelson¹, Dennis Donovan³, Ernest H. Oertli⁴ and Charles E. Rupprecht⁵

¹USDA, APHIS, Wildlife Services, National Rabies Management Program, Concord, New Hampshire, USA; ²USDA, APHIS, Wildlife Services, National Rabies Management Program, Castleton, New York, USA; ³Ontario Ministry of Natural Resources, Wildlife Research and Development Section, Rabies Research and Development Unit, Peterborough, Ontario, Canada; ⁴Texas Department of State Health Services, Zoonosis Control Branch, Austin, Texas, USA; ⁵Centers for Disease Control and Prevention, National Center for Zoonotic, Vector-Borne, and Enteric Diseases, Division of Vector-Borne Infectious Diseases, Pox Virus and Rabies Section, Atlanta, Georgia, USA

Oral rabies vaccination (ORV) has demonstrated success in controlling rabies in specific wildlife meso-carnivores at the landscape scale. ORV has been applied to free several countries in Europe from fox rabies. Ontario, Canada is on the verge of eliminating an arctic fox (*Vulpes lagopus*) variant of rabies virus adapted to red foxes (*Vulpes vulpes*) that was formerly widespread throughout the province prior to intervention with ORV. In the USA, integration of ORV into conventional rabies prevention and control in south Texas led to the elimination of a canine rabies virus variant that had spilled over into coyotes (*Canis latrans*) from sources in Mexico. Other ORV accomplishments in the USA include preventing raccoon (*Procyon lotor*) rabies from gaining a broader geographic foothold beyond the eastern USA and Canada, and reducing by 50% the amount of area occupied by a unique variant of rabies in gray foxes (*Urocyon cinereoargenteus*) in west Texas. The signing of the North American Rabies Management Plan in 2008 extended that collaborative framework for coordination of surveillance, control and research in border areas among Canada, Mexico and the USA advances in enhanced surveillance have facilitated sampling of greater scope and intensity ($N > 40\ 000$ since 2005) near ORV zones for improved rabies management decision making in real time. Among the many challenges associated with ORV in North America is the need for inexpensive, improved or new vaccines and baits with demonstrated enhanced performance in the current target species, as well as other important rabies reservoirs such as the striped skunk (*Mephitis mephitis*).

Wildlife diseases and control strategies in Nepal

Kamal P. Gairhe¹, Jacques R. B. Flamand² and Sarad Paudel³

¹Chitwan National Park, Nepal; ²GPO Box 25, Mtubatuba 3935, South Africa; ³Veterinary Officer, Biodiversity Conservation Center, Sauraha, Nepal

Nepal is rich in faunal and floral diversity due to its geographical variation in altitude and climate. It hosts many endangered animals such as the greater one horned rhinoceros, royal bengal tiger, gaur, snow leopard and several threatened birds. Interventions to create newer populations or foster suitable habitats for wildlife are ongoing. Action plans for conservation of flagship species have been prepared and launched to establish their good population. However, very little attention is currently paid to the future consequences of diseases, except the recent tuberculosis control strategy in captive elephants and a nationwide avian influenza control program. Foot and mouth disease, rabies, pasteurellosis, leptospirosis, hog cholera, tuberculosis are recorded infectious diseases in Nepalese wildlife. The only sero-surveillance work in wild buffalo carried out in 2001 showed positive titers to salmonella (27.2%) and infectious bovine rhinotracheitis (36.3%). Rhino sera tested against salmonella, brucella and leptospira did not indicate a serious threat. Tiger sera tested against toxoplasma, feline immunodeficiency virus, feline panleucopenia virus, feline herpes virus, feline calici virus, canine distemper virus, corona virus and feline leukemia virus also did not show a threat to the population. Tests in elephants showed tuberculosis infection in 23% of captive elephants in Nepal. Recent foot and mouth disease outbreaks in Barasingha and Black buck population warrants an effective control strategy for Nepal. A strategic plan to monitor and control diseases in Nepalese wildlife is emphasized along with adequate resources and trained manpower.

Surveillance and monitoring of emerging infectious diseases and viruses in wildlife in Cambodia

Chheang Dany¹ and Lim Sopheap²

¹Wildlife Protection Office, Forestry Administration Cambodia; ²Forest and Wildlife Research Institute, Forestry Administration Cambodia

The periodic appearance of emerging infectious diseases (EIDs), including the pandemic swine flu (H1N1) and highly pathogenic avian influenza H5N1 bird flu in Southeast Asia, over the past few years continues to raise concern. These concerns are primarily related to the potentially serious impacts on human lives as the result of potential flu pandemics, and also animal production industries, wildlife conservation, economic growth, and food security. The role of wildlife in carrying and ultimately transmitting EIDs viruses is under-researched, controversial, and largely speculative. A comprehensive disease surveillance and monitoring program regarding the link between EIDs and wildlife has been lacking in Southeast Asia, especially Cambodia. In response to the uncertainty of role of wildlife in the spread and re-emergence of EID viruses, Wildlife Protection of Cambodia is proposing a program titled 'Surveillance and Monitoring of Emerging Infectious Diseases and Viruses in Wildlife in Cambodia'. The objective of this project is to enhance early detection and characterization of EIDs in wildlife, and to coordinate surveillance and monitor networks in neighboring countries and at the regional level. Information on the prevalence of EIDs in wildlife, especially swine flu and avian influenza, their regional movements, and the incidence of contact between wildlife, domestic animals, and humans is of critical concern in establishing baseline levels and understanding the risks of the transmission of these virulent viruses.

Developing global capacity to predict and prevent emerging zoonotic diseases from wildlife

A. Alonso Aguirre¹, Peter Daszak¹, William Karesh² and Jonna Mazet³

¹Wildlife Trust, Conservation Medicine Program, 460 W. 34th St., 17th Fl., New York, New York, USA; ²Wildlife Conservation Society, Global Health Program, 2300 Southern Boulevard, Bronx, New York, USA; ³Wildlife Health Center, One Health Institute, School of Veterinary Medicine, One Shields Avenue, University of California, Davis, California, USA

Emerging zoonotic diseases are a major threat to public health globally, and include HIV/AIDS, SARS, Ebola, Nipah and H5N1 avian influenza. Rather than respond to the disastrous effects after they have emerged, we attempted to prevent these diseases from ‘spilling over’ from animals to humans by understanding what factors induce emergence and identifying ways of prevention, control, and mitigation. Our One Health approach that we call the practice of Conservation Medicine, brings together an understanding of human and wildlife health and the environmental changes that cause diseases to emerge and spread. We are fostering the growth of a collaborative initiative across Bangladesh and India among both ministry officials and scientists. The intent is to respond to outbreaks while they are still within the animal community or to rapidly identify spillover to humans in the early stages of emergence. The geographic scope of this expanded effort is directed to those zoonotic “hotspots” of wildlife and domestic animal origins. A One Health/Conservation Medicine approach involving many parties including human and animal health professionals, scientists, ecologists, and others would help provide comprehensive, coordinated, and cohesive strategies in addressing this immense threat.

Wildlife health in Indonesia

Riana A. Arief, Albertus T. Muljono and M. D. Winda Widyastuti

Center for Indonesian Veterinary Analytical Studies

Wildlife health is commonly a supportive component in wildlife programs in Indonesia, hence not much is known about diseases in wild populations. Only recently has there been active surveillance after the discovery of wildlife-borne zoonoses, such as Henipavirus and AI. Studies conducted on animal health and disease are mostly on primates, with few studies on non-primates as the flagship species. By national law, wildlife health is under the authority of two ministries; the Ministry of Forestry for nature conservation and the Ministry of Agriculture for animal health. This division has made it difficult for wildlife health components in the government to develop, as regulations for both ministries have never recognized animal health in conservation. It has only been recently defined in Act 18 for 2009 on Livestock and Animal Health. Currently, there are very few wildlife veterinarians in the government and medical cases are mostly handled by veterinarians from NGOs and private zoos. Medical attention is mainly required for animals rescued from conflict incidents or confiscated from illegal trade. Unfortunately, not all cases could be reached in time due to limitations in rescue facilities and medical personnel. Similar restrictions are also found in animal rescue and rehabilitation centers. In zoos and safari parks, health incidents are mostly related to animal management practices. In conclusion, to improve wildlife health in Indonesia, communication and understanding in both the Ministry of Forestry and Ministry of Agriculture should be improved. Disease surveillance and studies should also be conducted more actively to detect potential disease and health risks for both animals and human. And lastly, animal rescue and rehabilitation facilities should be improved and more medical personnel should be trained to overcome the shortage of wildlife veterinarians and paramedics in Indonesia.

Rapid diagnostic tests

Yukun Li

Microbiology Division, Thermo Fisher Scientific

Rapid diagnostics and point-of-care for infectious diseases is a fast growing market, which is important not only for human health but for animal health as well. Rapid detection methods at the time of field sampling make it possible to effectively prevent infectious disease outbreaks, especially for global pandemics. This presentation will highlight two technologies used for rapid tests: Lateral flow assays and PCR-based tests.

Economic importance for addressing wildlife diseases

Stephanie Shwiff

USDA, APHIS, Wildlife Services, National Wildlife Research Center, 4101 LaPorte Avenue, Ft. Collins, CO 80521 USA

Wildlife can serve as a vector for many economically important diseases (foot and mouth disease, various form of influenza, brucellosis) that can affect humans, livestock, companion animals and wildlife species. Wildlife transmitted diseases in livestock can decrease productivity and cause death, resulting in a regional job and revenue losses. Additionally, a national loss of disease-free status in livestock can impact trade and result in bans on the import or export of livestock, causing billions of dollars in loss, as evidenced by the economic destruction wrought by FMD in the UK (\$11–12 billion) and Taiwan (\$1.6 billion) (FAO, 2009; Yang et al., 1999). It has been estimated that if FMD were to enter the US, the economic losses would be \$14 billion (Paarlberg et al. 2002). The livestock sector can be directly impacted by the introduction of wildlife transmitted diseases, which can multiply throughout the rest of the economy. In order to mitigate the impacts associated with wildlife transmitted diseases, the Wildlife Services (WS) branch of the U.S. Department of Agriculture (USDA) has established a wildlife surveillance network to test feral swine for a myriad of diseases; this surveillance network can easily be adapted to test for the presence of foreign animal diseases, thus alerting domestic producers and minimizing the impact of disease spread throughout the U.S. Wildlife disease surveillance, especially in feral swine, has the potential to reduce the impact of wildlife transmitted diseases by either preventing the spread of disease to domestic animals or reducing the duration of the outbreak once introduced to livestock, potentially saving millions of dollars.

Non-zoonotic EIDs as threats to wildlife population in Southeast Asia

Boripat Siriaroonrat

Conservation, Research & Education Division, The Zoological Park Organization, 71 Rama 5 Road,
Dusit, Bangkok 10300, Thailand

When public awareness on threats to human health and food security from zoonotic EID (such as H5N1 HPAI and various encephalitis viruses) is raised by local and international organizations, the veterinary community has a tendency to pay less attention or receive limited resources to manage non-zoonotic diseases. Although 60% of EIDs are zoonotic, and 70% have a wildlife component, non-zoonotic EIDs still needs continuous surveillance programs for better management of animal populations because non-zoonotic diseases will likely be endemic in many countries around the world. For livestock health, veterinarians are still being challenged by the classical diseases (e.g. parasitic infestations such as liver flukes, blood and intestinal parasites), swine fever, hemorrhagic septicemia, and FMD. Wildlife species (in the wild, in captivity) continue to be a reservoir of unfamiliar pathogens that are previously unknown. Rapid and continued emergence of EIDs in wildlife has been observed in Asia in the past decade. However, wildlife can be a victim of spilled-over infection from human and livestock in many interfaces. In captivity it has been hypothesized that mahout and people with direct contact with Asian elephant potentially cause tuberculosis in this large herbivore. In the wild habitat, many endangered species are facing extinction by threats from hunting, habitat destruction and fragmented population. However, diseases are the risk factor that is difficult to assess in protected areas and interface areas that wildlife shared with human and livestock. Recently (2009), Chytridiomycosis fungal infection had been discovered in Thailand in imported poison dart frog with no reports in native frogs at present. Ecology of disease of interested must be studied and drivers that resulted in the spread of diseases into wildlife population has to be carefully assessed. Human activity is likely to be the most important factor that break bio-security and transport pathogens from one place to another. The magnitude of the problem may not be clear at present but scientists, veterinarians and wildlife conservationists must be working together to address problems and try to design the preventive measures for the protection of endangered wildlife populations.

Coxiella Burnetti antibodies in the sera of animals and humans in selected areas of the Philippines

Loinda R. Baldrias and Fernando C. Cardona

Department of Veterinary Paraclinical Sciences, College of Veterinary Medicine, University of the Philippines Los Baños

Sixty serum samples from human donors and 180 serum samples from cattle, goats and water buffaloes, obtained from selected areas in the Philippines, were examined for the presence of *Coxiella burnetti* antibodies using the micromethod complement fixation test. Of the 180 animals sampled, 42.77% (77/180) were positive for *C. burnetti* antibodies, with 70% (42/60) of goats serologically positive, by at 53% (32/60) of carabaos, and 40% (24/60) of cattle. Seropositivity rate for Q-fever antibodies among animals by location was found highly significant ($p < 0.01$), with animals from General Santos City, Cotabato having the highest seropositivity at 61.67% (37/60) Los Baños, Laguna 50% (30/60), and Catarman, Northern Samar 23% (14/60). Of the 60 human sera examined, 36.66% (22/60) were positive for antibodies to *C. burnetti*. The percentage of positive human samples by location was found to be highly significant ($p < 0.01$), with human donors from Los Baños, Laguna at 20% (12/60), those from General Santos City, Cotabato at 16.7% (10/60), while those from Catarman, Northern Samar were negative for antibodies to *C. burnetti*. The percentage of sero-positivity among human donors according to age was also significant ($p < 0.05$), with the 31-40 year old age group having the highest age-specific rate at 50% (14/28), the >40 year old group at 33.33% (5/15) and the 21-30 year old group at 17.64% (3/17). Animal owners had the highest occurrence of Q-fever antibodies at 50% (4/8), followed by animal caretakers with 47.37% (9/19), butchers/slaughterhouse workers with 41.67% (5/12) and veterinarians at 33.33% (4/12). Results indicate the occurrence of antibodies for *C. burnetti* in the Philippines among humans, cattle, goats and buffaloes sampled and highlight the probable zoonotic nature of Q-fever infection by exposure to infected animals.

Plague surveillance and response

John Baroch

USDA, APHIS, Wildlife Services, National Wildlife Disease Program, 4101 LaPorte Ave, Fort Collins, CO 80521

Plague is a zoonotic disease caused by infection with the bacterium (*Yersinia pestis*), which is maintained by a complex cycle involving small mammals and fleas. The disease has had a profound effect on human and animal populations over many centuries. Currently, human cases are limited to a few thousand per year. However, plague is endemic in many parts of the world and remains a serious threat to human and wildlife health because of its potential to spread rapidly, its swift clinical course, and high mortality rate if untreated. Additional concerns include the emergence of multi-drug resistant strains, and the potential use of plague as a bio-weapon. While the ecology of plague outbreaks is still not fully understood, advances are being made in modeling risk factors and developing rapid diagnostic methods. In the United States the risk of plague is increasing as the endemic plague zone is spreading. Wildlife Services monitors plague distribution through sero-surveillance of carnivores, in addition to surveillance of susceptible rodent populations and operational responses to outbreaks with a variety of risk mitigation measures.

Isolation, detection and characterization to algX of alginate-producing *Pseudomonas aeruginosa* by using PCR based techniques and colony hybridization *aeruginosa* in animals

Maosheng Yang

Guizhou Institute of Animal Husbandry and Veterinary Medicine, Guiyang 550005,China

The best-characterized alginate producing organism is *Pseudomonas aeruginosa*, an opportunistic human and animal pathogen. The alginate producing strain was generated and its algX gene was detected by PCR, gene cloning, strain conjugation and alginate production purification in order to investigate the functional role of AlgX in alginate biosynthesis and to determine the specific role of algX in susceptibility towards the mucoid phenotype. Our experimental results indicated that the algX gene from *Pseudomonas aeruginosa* was part of the alginate biosynthesis gene cluster.

Binding affinity of Ig-like repeat domains of *Leptospira* Lig proteins to gelatin-binding domain of fibronectin is enhanced through multivalency

Yi-Pin Lin¹, Sean P, Mcdonough², Yogendra Sharma³ and Yung-Fu Chang^{1*}

¹Department of Population Medicine and Diagnostic Sciences¹, Department of Biomedical Science, ²College of Veterinary Medicine, and ³Center for Cellular and Molecular Biology, Uppal Road, Hyderabad 500 007, India.

Leptospira spp. are pathogenic spirochetes that cause the zoonotic disease leptospirosis. Leptospiral immunoglobulin (Ig)-like protein B (LigB) contributes to the binding of *Leptospira* to extracellular matrix (ECM) proteins such as fibronectin (Fn), fibrinogen, laminin, elastin, tropoelastin and collagen. A high-affinity Fn-binding region of LigB has been localized to LigBCen2, which contains the partial 11th and full 12th Ig-like repeats (LigBCen2R) and 47 amino acids of the non-repeat region (LigBCen2NR) of LigB. In this study, the gelatin binding domain (GBD) of Fn was shown to interact with LigBCen2R (KD = 1.91±0.40 μM). Ig-like domains of Lig proteins other than LigBCen2R including LigAVar7'-8, LigAVar10, LigAVar11, LigAVar12, LigAVar13, LigBCen7'-8, and LigBCen9 also bind to GBD. Interestingly, the GBD of Fn interacts with different Ig-like domains. A large increase in affinity was achieved through an avidity effect, with the terminal domains, 13th (LigA) or 12th (LigB) Ig-like repeat of Lig protein (LigAVar7'-13 and LigBCen7'-12) enhancing binding affinity approximately 50 and 30 fold respectively, compared to recombinant proteins without this terminal repeat. The inhibited effect on MDCKs cells can also be promoted by Lig proteins with terminal domains, but these two domains are not required for GBD binding and cell adhesion. Lig proteins with the terminal domains could form compact structures with a round shape mediated by multidomain interaction. This is the first report about the interaction of GBD of Fn and Lig proteins and provides an example of multivalency mediated bacterial-host interaction.

Macaque-tourist interactions and intestinal parasites of Tibetan macaques (*Macaca tibetana*) at Mt Huangshan, China

Huan Ji¹⁻³ and Jin-hua Li^{1,-3}

¹School of Life Science, Anhui University, Hefei, China; ²Anhui Key Laboratory of Eco-engineering and Bio-technique, Hefei, China; ³Anhui Research Center of Ecological Economy, Hefei, China

Although humans and non-human primates (NHPs) are spatially separated, indirect ecological contact exists through vectors and environmental media including soil and water, which can lead to infections. NHPs, especially wild macaques, come into frequent contact with humans as a result of tourism. Here, we assessed the disease risk related to macaque-tourist interactions, and examined the intestinal parasites commonly found in wild Tibetan macaques (*Macaca thibetana*) at Mt Huangshan, China. By using all-occurrence sampling and continuous recording, we evaluated macaque-tourist interactions over two periods (November–December 2008 and April–May 2009), and collected 83 fecal samples during the first period to identify the species prevalence of intestinal parasites using the precipitation-washed and saturated saline flotation method. We found that Tibetan macaques were infected with *Oesophagostomum apiostomum*, *Ancylostoma duodenale*, *Strongyloides stercoralis*, *Rhabditis spp.*, *Trichuris trichura*, *Gongylonema spp.*, *Trichostrongylus spp.*, *Copillaria hepatica*, and *Ascaris lumbricoides*. *Gongylonema spp.* had the highest infection rate (31.58%), and *Rhabditis spp.* and *Ascaris lumbricoides* had the lowest (1.31%). Oral infection made up 57.78% of infection routes. Contact interactions made up only 6.80% of macaque-tourist interactions, and the adult male monkeys participated in significantly more interaction behaviors than females ($P < 0.01$). Our results indicate that (1) Tibetan macaques had a historically high infection rate (2) the adult male monkeys should be monitored because of their high participation in interactions; (3) The interactions observed between tourists and macaques are not responsible for transmission of parasites.

An overview of bat white-nose syndrome in North America

David Blehert, Carol Meteyer, Anne Ballmann, Jeff Lorch and Jonathan Sleeman

USGS, National Wildlife Health Center, Madison, Wisconsin

White-nose syndrome (WNS) is a disease associated with unprecedented bat mortalities in the eastern United States and Canada. Since the winter of 2006–2007, bat population declines approaching 100% have been documented at some surveyed hibernacula. Total estimated losses have exceeded one million bats over the past three years. Affected hibernating bats often present with visually striking white fungal growth on their muzzles, ears, and/or wing membranes. Histopathological and microbiological analyses demonstrated that WNS is characterized by a hallmark fungal skin lesion caused by a recently discovered species of psychrophilic (cold-loving) fungus, *Geomyces destructans*. The fungus was initially cultured at 3°C and grows optimally between 5°C and 14°C, temperatures consistent with the body temperatures of hibernating cave bat species from temperate regions of North America. Laboratory infection trials indicated that *G. destructans* is transmissible bat-to-bat, and a genetic signature of the fungus has been identified in environmental samples collected from several bat hibernation caves within WNS-infested states. There is a growing body of evidence supporting an association between WNS and cutaneous fungal infection by *G. destructans*, and this disease represents an unprecedented threat to bats of temperate regions of North America and beyond. Worldwide, bats play critical ecological roles in insect control, plant pollination, and seed dissemination, and the decline of North American bat populations may have far-reaching ecological consequences.

Parasite load and genetic variation at MHC loci in the giant panda

Lei Zhang^{1,2} Qi Wu¹ and Fuwen Wei¹

¹Key Laboratory for Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences, 1-5 Beichenxi Road, Beijing 100101, China; ²Graduate School of the Chinese Academy of Sciences, Beijing 100039, China

We investigated the importance of the major histocompatibility complex (MHC) constitution on the parasite load of free-living giant pandas (*Ailuropoda melanoleuca*) in six mountains areas. Ninety-six individuals were genetically examined and the endoparasite load was quantified by counting fecal helminth eggs using a modified McMaster technique. Fifty-three animals (55.2%) were infected by five helminth species with *Baylisascaris shroederi* as the dominant parasite. We indentified 6 MHC class II DRB-exon2 alleles and 14 MHC class II DQA-exon2 alleles in these samples. Heterozygosity in general was uncorrelated with the infection measures (prevalence and intensity). However, a positive relationship was found between specific alleles and parasite load. The alleles associated with parasite burden had unique amino acid motifs in the antigen binding sites. Our results support the hypotheses that MHC polymorphism in giant pandas is maintained through pathogen-driven selection acting by frequency-dependent selection. Other datasets are required to test whether the associations vary in time and to confirm these results for applications in the conservation of giant pandas.

Surveillance for white-nose syndrome in bats in Ontario, Canada

Ian K. Barker, G. Douglas Campbell, Claire M. Jardine, Cheryl A. Massey, Leonard J. Shirose
and Melanie Whalen

Canadian Cooperative Wildlife Health Centre, University of Guelph, Guelph, Ontario, Canada
N1G 2W1 Durda Slavic; Animal Health Laboratory, University of Guelph, Guelph, Ontario,
Canada N1G 2W1 David S. Blehert; USGS-National Wildlife Health Center, 6006 Schroeder
Road, Madison, WI 53711, USA

White-nose Syndrome (WNS) is characterized by cutaneous infection by the fungus *Geomyces destructans* and causes devastating mortality in cave bats in the northeastern United States. We investigated 12 Ontario hibernacula between March and May, 2009. Muzzle and wing lesions resembling WNS were observed on ~10/80 live *Myotis spp.* bats at one cave, and on ~100/15,000 at one abandoned mine. Seventeen bats from the two affected sites were suitable for histopathology and mycology. Spores characteristic of *G. destructans* were not seen histologically or on fungal tape lifts, nor was *G. destructans* isolated. PCR and fungal culture for *G. destructans* in tissue from WNS-suspect bats also failed to detect *G. destructans*. Conclusive evidence of WNS, in the form of the putative etiological agent, was not confirmed in Ontario in 2009. *G. destructans* was isolated in 23/52 cases in a subsequent study, and it was demonstrated by PCR in 21/21 cases. In the course of one year, WNS became widespread in *Myotis* hibernacula known in eastern Ontario, and it affected up to half the bats observed in several hibernacula, although major mortalities were only registered among bats day-flying in winter/early spring before the availability of prey insects. It was detected over 560km from the nearest known affected hibernaculum in New York State, in bats using a hibernaculum from which people were physically excluded, suggesting that it was disseminated considerable distances by affected bats. The rapid spread and high prevalence of the syndrome north of its former range in the USA are cause for marked concern about *Myotis* populations in southern and eastern Canada.

Establishment of ELISA and serological investigation on Himalayan marmota toxoplasmosis in Qinghai province

Qigang Cai

Qinghai Academy of Animal and Veterinary Science

Purified recombinant protein GST-SAG1 from *Toxoplasma gondii* was used to establish the ELISA diagnostic method of *Toxoplasma* antibodies. Sixty-eight serum samples collected from Himalayan marmota in Qinghai Province were used to detect antibodies against *Toxoplasma* by ELISA. The result showed that 22.06% (15/68) sera samples were positive for antibody against *Toxoplasma gondii*. These results suggest that *Toxoplasma gondii* has infected Himalayan marmotas in Qinghai province.

Posters

Epizootiology of avian cholera

Michael D. Samuel¹ and Thierry M. Work²

¹US Geological Survey, National Wildlife Health Center, 6006 Schroeder Rd., Madison, WI 53711.;

²US Geological Survey, National Wildlife Health Center, Honolulu Field Station, PO Box 50167, Honolulu, HI 96850

Avian cholera is an infectious disease caused by *Pasteurella multocida*, an encapsulated Gram-negative bacterium. The bacterium has a worldwide distribution and produces septicemic and respiratory disease in a wide variety of domestic and wild birds. Pathogenicity of individual strains is highly variable and susceptibility to these bacterial strains varies considerably among avian species. Epizootics of avian cholera typically occur in wetlands with abundant waterfowl populations or in breeding colonies with high densities of birds. Mortality commonly involves multiple species of birds that are susceptible to infection and capable of transmitting the bacterium to other hosts, and natural infection has occurred in over 180 species. Disease transmission among wild birds is believed to occur from bird-to-bird contact and by ingestion of bacteria or aerosol transmission within a contaminated environment. Discharge of pasteurellae from dead or diseased birds is considered an important source of wetland contamination and transmission to susceptible birds. Although, wetlands do not appear to be a long-term disease reservoir, some gregarious species of waterfowl (such as snow geese) are known carriers of pathogenic *P. multocida*.

Cloning and phylogenetic analysis of the NS1-5 genes of giant panda rotavirus isolate strain CH-1 in China

Qi-gui Yan, Yan Lei, Ying-Chun Feng, Kai-yu Wang and Wan-Zhu Guo

College of Veterinary Medicine, Sichuan Agricultural University, Ya'an, Sichuan 625014, China

Rotavirus (RV), a member of the genus Rotavirus of the family Reoviridae, is an important causative agent of diarrhoea diseases of human and animals worldwide. The Asian Rotavirus Surveillance Network reported that 45% of diarrhoea admissions in Asian were positive for rotavirus in nine countries and regions of Asia (2008). However, limited knowledge about animal diarrhoea diseases caused by rotavirus has been published and valuation of genetic relations between human and animal rotavirus isolates is limited. To better understand the rotavirus CH-1 strain isolated from diarrheic faeces of giant panda in 2008, we cloned the NSP1-5 complete coding sequence of the Giant panda rotavirus (GPRV), and sequenced NSP1-5 genes (GenBank accession number: NSP1, GU205762; NSP2, GU188281; NSP3, GU329525; NSP4, GU188282; NSP5, GU329526.). Based on these information and data from GenBank of other genus of RV NSP1-5 genes, phylogenetic analysis was realized. The phylogenetic tree revealed that GPRV NSP1-5 genes were close to that of bovine rotavirus. This research may provide useful information and help us understand GPRV.

Hemolytic phospholipase Rv0183 of *Mycobacterium tuberculosis* induces inflammatory response and apoptosis in alveolar macrophage RAW264.7 cells

Guangxian Xu¹⁻³, Guangcun Deng^{1,2}, Hao Jia¹, Yong Li^{1,2}, Xiaoming Liu^{1,2} and Yujiong Wang^{1,2}

¹Key Laboratory of Ministry of Education for Conservation and Utilization of Special Biological Resources in the Western, Ningxia University, Yinchuan, Ningxia 750021, China; ²College of Life Science, Ningxia University, Yinchuan, Ningxia 750021, China; ³Department of Laboratory Medicine, Ningxia Medical University, Yinchuan, Ningxia, 750004, China.

Mycobacterium tuberculosis are typical intracellular bacteria. The phospholipid metabolic pathway is vital to a number of metabolic pathways in *M. tuberculosis*, and the hemolytic phospholipase Lip (Rv0183) gene is an important component of phospholipid metabolism. To understand the biological function of the Lip (Rv0183) gene in cases of infection by *M. tuberculosis*, we used quantitative RT-PCR and flow cytometric analysis to evaluate the expression of inflammation-related cell factors and cell apoptosis in mouse alveolar macrophage RAW264.7 cells that express Lip (Rv0183). Our results demonstrated that ectopic expression of Lip (Rv0183) significantly increased the expression of IL-6, NF- κ B, TLR-2 and TLR-6 in the RAW264.7 cells. Additionally, the expression of Lip (Rv0183) induced RAW264.7 cell apoptosis. These findings suggested that Lip (Rv0183) was capable of inducing inflammatory responses and cell apoptosis in the host cells, which implies it may play an important role in the pathogenesis of *M. tuberculosis* infection.

Construction of the recombinant adenoviral vector co-expressing hemagglutinin and the matrix 2 genes of human H5N1 influenza virus

Yi Hu, Hongguang Sun, Jing Li, Yongqiang Li, Guohui Chuang and Qingyu Zhu

State Key Laboratory of Pathogens and Biosecurity, Beijing 100071, China

We constructed an adenoviral vector co-expressing hemagglutinin and matrix 2 genes of human H5N1 influenza virus by utilizing an internal ribosome entry site (IRES). We obtained the HA and matrix 2 (M2) genes of human H5N1 influenza virus (strain A/Beijing/01/03) by RT-PCR and subcloned them into a pIRES vector. After changing the restriction enzyme sites by PCR amplification, the HA-IRES-M2 fragment was cloned into the shuttle plasmid pAdTrack-CMV, then the linearized shuttle plasmid was cotransformed into BJ5183 bacteria with backbone vector AdEasy-1. The recombinant plasmid was packaged in 293A cells. The recombinant adenovirus was confirmed with PCR and the expression of the HA and M2 genes in the transfected 293A cell were assessed by western blotting. The recombinant plasmid was confirmed by sequencing and restriction endonucleases digestion. GFP expression was observed on the second day and CPE was detected on the tenth day after packaging in 293A cells. The HA and M2 genes were successfully integrated in the genome of the recombinant adenovirus and the expression of HA and M2 could be detected simultaneously. Construction of the recombinant adenoviral vector co-expressing hemagglutinin and matrix 2 genes was successfully obtained, thus providing a basis for the study on new generation AIV vaccine based on recombinant adenovirus.

Pathogenicity of A/Chicken/Hebei/4/2008(H9N2) virus in BALB/c mice

Guangcun Deng^{1,2}, Jianmin Bi³, Fuli Kong³, Xuezhu Li³, Miaojie Zhang³ and Jian Qiao^{3*}

¹Key Laboratory of Ministry of Education for Conservation and Utilization of Special Biological Resources in the Western, Ningxia University, Yinchuan, China; ²College of Life Science, Ningxia University, Yinchuan, China; ³Department of Pathophysiology, College of Veterinary Medicine, China Agricultural University, Beijing, China

We evaluated the pathogenicity of the currently circulating H9N2 virus for mammals using a recently isolated H9N2 avian virus from Northern China in a mouse model without prior adaptation. The results showed that H9N2 virus caused lethal infection in mice without prior adaptation with 100% morbidity and 60% mortality when 6–8 week old BALB/c mice were inoculated intranasally with 100 µl of 10-fold dilutions of Chicken/HB/4/08 H9N2 infectious allantoic fluid. The infected mice presented severe signs of respiratory disease and the majority of mice died 4–6 days post-infection. The fifty percent of mouse lethal dose (MLD₅₀) was 10^{-1.25}/0.1ml and fifty percent of mouse infectious dose (MID₅₀) 10^{-6.75}/0.1ml for the H9N2 virus. Histopathologic changes in infected mice were characterized by diffuse pneumonia with severe alveolar damage, and edema around the small blood vessels. Infected mice were also highly edematous with profuse areas of hemorrhage and significant destruction of bronchial epithelium and increased numbers of neutrophils, fibrin, and suppurative exudates infiltrating the bronchioles. In addition, minor brain hemorrhages were also observed. The virus can replicate in the lung, heart, liver, spleen and kidney but does not spread to the brain and has the highest titers in lung. Our data demonstrated that the currently circulating H9N2 virus found in poultry in Northern China presents enhanced pathogenicity for mammals.

Cloning and analysis of the *Mycoplasma ovipneumonia* Y98 Hsp70 (DnaK) gene

Li Min^{1,2}, Ma Chunji^{1,2}, Zhao Dong^{1,2}, Wang Yujiong^{1,2}, Wang Hongyan², Jin li²,
Chen Xiaohu² and Zhang Xuqiang²

¹Key Laboratory of Ministry of Education for Conservation and Utilization of Special Biological Resources in the Western, Ningxia University, Yinchuan, China; ²College of Life Science, Ningxia University, Yinchuan, China.

Mycoplasma ovipneumonia (MO) can infect and harm bighorn goat and sheep, and lambs and goats aged 1–3 months. It is also the main causative agent of contagious ovine pleuropneumonia. The genome sequences of MO is currently unknown, so there is little research on the molecular level, or research into the antigens involved and genetically engineer a vaccine for MO. In our research, we compared the Hsp70 gene and protein sequence of 14 species of mycoplasma, and we found the conservative sequences and designed degenerate primers. Then, MO Hsp70 gene (Accession No. 1335975) was acquired by homologous cloning combined with chromosome walking. Our results from bioinformatics analysis of MO Hsp70 indicated that the ORF of Hsp70 was 1815 bp in length and encoded 604 amino acids. The GC content was 34.16% and MO Hsp70 gene was highly conserved within Mhp and shared 86% nucleotide and 94% amino acid sequence identities with the Hsp70 genes of all strains deposited in GenBank. The isoelectric point was 5.08, and the C terminal fragment had many α -helical structure, which showed a strong hydrophilicity located on the surface and may be one of the epitopes in MO. These results lay a foundation for further study into the molecular biology of MO, along with possibilities of genetically engineering a vaccine.

Novel hantavirus detected in Yunnan red-backed vole (*Eothenomys miletus*)

Yun-zhi Zhang^{1,2}, Hai-lin Zhang² and Zheng-li Shi¹

¹State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; ²Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China.

Hantaviruses cause two main human zoonoses: hemorrhagic fever with renal syndrome (HFRS) in Asia and Europe; and hantavirus pulmonary syndrome (HPS) in North and South America. Rodents are natural reservoirs of hantavirus. Long-term surveillance of HFRS is necessary to prevent the disease's transmission from animals to humans. In our study, 330 rodents from 12 species were captured in hantavirus endemic areas of Luxi County, Yunnan Province, China, from autumn 2009 to spring 2010, and were tested for hantavirus infection. Among the samples, 23 of 133 *Eothenomys miletus*, 3 of 96 *Rattus flavipectus* and 2 of 25 *Rattus nitidus* registered positive by immunofluorescence assay (IFA). However, the virus was detected in only 23 *Eothenomys miletus*. The sequences of small fragment (S), encoding the nucleocapsid protein, was obtained from virus-infected animal tissue. The sequence comparison of S fragment with other hantavirus indicated that the hantaviruses from *Eothenomys miletus* are closely related to the Tula virus (88% in amino acid sequence). Moreover, the hantavirus sequences detected from positive samples displayed genetic diversity. To our knowledge, this is the first discovery of Tula virus in *Eothenomys miletus*.

Identification of *Plesiomonas shigelloidcs* and *Aermonas schuberti* from doctor fish (*Garra rufa*) and antibiotic sensitivity

Hua Yu^{1,2}, Zhi He², Yu-bao Yan¹, Guang-you Yang², Juan Hu¹ and Minjiang Zhou¹

¹Sichuan Entry-Exit Inspection and Quarantine Bureau of P.R. China, Chengdu, China; ²Veterinary Colledge of SiChuan Agricultural University, Yaan, China

Two bacterial strains were isolated from doctor fish samples (*Garra rufa*). Based on morphological, physiological and biochemical characteristics, the causative bacteria were confirmed as *Plesiomonas shigelloidcs* and *Aermonas schubertii*. Antibiotic sensitivity showed that *P. shigelloidcs* was sensitive to 18 agents, and not sensitive to 2 agents (sulfafurazole and ampicillin). *A. schubertii* was also sensitive to 18 agents, and had no sensitivity to ampicillin and trimethoprim.

Genome properties and phylogenetic analysis of H6N2 and H11N9 avian influenza virus strains from wild birds

Lan-lan Zhang¹, Jian-qi Wang¹, Jin Zhang¹, Hong-liang Chai¹, Yan-bing Li² and Yu-ping Hua¹

¹Northeast Forestry University, Harbin, Heilongjiang 150040, China; ²Animal Influenza Laboratory of the Ministry Agriculture and State Key Laboratory of Veterinary Biotechnology; Harbin Veterinary Research Institute of Chinese Academy of Agricultural Sciences, Harbin, Heilongjiang 150001, China

Wild waterfowls are natural reservoirs of avian influenza virus. We sequenced the genome and evaluated the genetic characteristics and phylogenetic relationships for two H6N2 AIVs [A/mallard/HeiLongjiang/131/2006 (H6N2), A/Mallard/SanJiang/113/2006 (H6N2)] isolated from Sanjiang natural Reserve and a H11N9 AIV [A/OrientalWhite Stork/ZhaLong/183/2006(H11N9)] isolate from Zhalong natural. Sequences were compared with the corresponding sequences published in GenBank. The panorama phylogenetic trees of H6 and H11 genes of AIV and the phylogenetic trees of the other genes were drawn. Results show that eight cDNA fragments contain the entire open reading frame of the corresponding gene. There are seven potential glycosylation sites in the HA gene. The amino acid sequence of the cleavage site has the typical characteristics of the low pathogenic avian influenza virus (LPAIV). The results of comparative sequence analysis indicate that the gene of the isolate viruses are recombinant. Particularly, the PA gene of A/Mallard/SanJiang/113/2006(H6N2) was closely related to A/environment/Qinghai/1/2008(H5N1), with as high as 99.9% homology. In this study, the phenomenon of gene recombination was found in all three of the AIV isolates, especially isolate A/Mallard/SanJiang/113/2006(H6N2) which has the characteristics with recombinant gene fragments of both Eurasian and American lineages of AIV. Our findings indicate the natural geographical distribution of AIVs is more complicated than with the previously used distribution division of Eurasian and American lineages, though the reassortment between these two AIV lineages is generally limited due to geographical constraints. LPAIVs circulating in wild birds have been experiencing genetic reassortment among different subtypes of AIVs, which is inconsistent with the view that wild bird AIVs have reached their maximum adaptability to the host in a "static evolution".

An NDV strain isolation, identification and its complete genome sequence analysis, and the molecular epidemiology of wild bird NDVs isolated in partial regions in Heilongjiang province

Dong-wei Li¹, Huai-ran Liu² and Yu-ping Hua¹

¹Northeast Forestry University, Harbin, Heilongjiang 150040, China; ²Harbin Veterinary Research Institute of Chinese Academy of Agricultural Sciences, Harbin, Heilongjiang 150001, China

Newcastle disease (ND) is regarded worldwide as one of the most devastating diseases of poultry. Wild birds are believed to be the natural hosts of NDV, and NDV can cycle in wild bird population continually. Therefore, monitoring the molecular epidemiology of wild bird originated isolates would illustrate the tendency and variation of NDV. We isolated one strain of Newcastle disease virus (named Mallard/China/HLJ363/06) from a wild duck that did not display typical ND symptoms at Heilongjiang province for our study. We found that the isolate was able to agglutinate chicken red blood cells, which could be inhibited and neutralized by avian Newcastle disease virus (NDV) standard antiserum, but could not be inhibited by avian influenza virus (AIV) standard antiserum (H5 and H9 subtype) and EDS-76 standard antiserum. The results disclosed that the isolate is virulent strain of Newcastle disease virus. Specific primers were designed to amplify the gene fragment by RT-PCR to obtain the complete genome sequence of NDV strain Mallard/China/HLJ363/06. The genomic sequence consists of 15192 nt, which is 6 nt longer than the published full length genome of the NDV strains LaSota. The full length of F genes was amplified, sequenced and analyzed. The results showed that 14 F genes contained an open reading frame (ORF) in length of 1662nt, coding 533 amino acids, and no insertions or deletions were found. A phylogenetic tree was constructed using F gene nucleotide sequences of these 14 isolates and 23 reference strains from GenBank. The 14 isolates were classified into genotype VIIId (13/14) and III (1/14).

Analysis on gene phylogenesis and amino acid composition of PB1-F2 of AIVs isolated from wild birds

Jin Zhang¹, Yan-bing Li², Hong-liang Chai¹, Lan-lan Zhang¹ and Yu-ping Hua¹

¹Northeast Forestry University, Harbin, Heilongjiang 150040, China; ²Animal Influenza Laboratory of the Ministry Agriculture and State Key Laboratory of Veterinary Biotechnology, Harbin Veterinary Research Institute of Chinese Academy of Agricultural Sciences, Harbin, Heilongjiang 150001, China

We cloned and sequenced PB1-F2 genes of Avian influenza viruses (AIV) isolated from 14 wild birds, and performed analysis on the homology, phylogenetic relationships of the genes and the composition of the corresponding coded amino acids. We found the amino acids 37, 48, 50 of PB1-F2 were arginine, proline, glycine respectively in a H5N1 high pathogenic avian influenza virus (HPAIV) strain, A/lesser_kestrel/Harbin/194/2007(H5N1), which was different from that of other 13 low pathogenic avian influenza virus (LPAIV) strains (glutamine, glutamine and aspartate respectively). To further explore this phenomenon, 1061 AIV strains PB1-F2 genetic sequences downloaded from the NCBI Influenza Virus Resource were compared, and the results showed that the 97 Hong Kong H5N1 subtype, the other H5N1 subtype and the other subtypes of AIV were obviously different in their amino acid composition at these sites. This distinction also presented certain rules and characteristics. We found that the H9N2 subtype AIVs displayed obvious characteristics in temporal and spatial distributions of amino acid composition in these three sites. PB1-F2 genetic phylogenetic analysis showed that the H5N1 and Hong Kong strains had a large genetic distance with other AIVs. Although this difference could not be well explained by genetic stochastic mutation and recombination, its biological significance remains to be further explored.

Survey of infectious status of wild freshwater fish with Metacercaria (*Clonorchis sinensis*) in the western region of Liaoning Province

Xiaogang Liu

Liaoning Medical University

Six species of wild freshwater fish totally 1131 specimens were taken from different rivers in the western region of Liaoning Province, including the never, Gou and Liao rivers. Direct compression was used to check the infection rate of metacercaria of *Clonorchis sinensis*, and the pepsin-HCl artificial digestion method was used to check the average degree. Metacercaria of *Clonorchis sinensis* (MC) were discovered in all six species of freshwater fish. Our results showed there were important differences in the positive rate of MC across the different species of fish ($\chi^2=348.74$, $P<0.0001$). The highest positive rate of 82.76% was for *Pseudorasbora parva* and the lowest rate of 1.46% was for *Phoxinus lagowskii Dybowski*. The largest number of average degree infection was *Perccottus glehnidybowski* (2390 metacercarias per fish), and the lowest was for *Phoxinus lagowskii Dybowski* (32 per fish). The infectious status of metacercaria of *Clonorchis sinensis* in Western Liaoning's wild freshwater fish district is serious, and it is suggested that the relevant departments should take positive and effective preventative measures, and strengthen advocacy in order to protect this ecological environment and human health.

Cloning and molecular characteristic analysis of *prfA* Gene of *Listeria monocytogenes* TA Strain

Qing-ling Meng^{1,2}, Jun Qiao¹, Cai Xue-peng², Xue-nong Luo² and Chuang-fu Chen²

¹Department of Animal Sciences and Technology, Shihezi University, Shihezi, 832003 China;

²State Key Lab of Veterinary Etiological Biology, Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Lanzhou, 730046 China

Listeria monocytogenes (LM) is an important zoonotic pathogen which can cause many diseases in human and animals. LM is one of the four major food-borne bacteria and can contaminate meat, dairy and other animal foods, causing food poisoning. Pathogenicity island 1 in the genome of LM (LIPI-1) encoding *prfA*, *plcA*, *LLO*, *mlp*, *actA*, *plcB* virulence factors plays an important role in LM infection, proliferation and pathogenesis, and is subject to *prfA* regulation. *prfA* gene mutation is implicated in LM virulence. The LM *prfA* gene of TA strains isolated in Xinjiang were PCR amplified and sequenced, and the molecular characteristics analyzed to understand whether genetic variation of *prfA* is related to virulence of the different geographical strains. The complete length of the *PrfA* gene was 714 bp, encoding 237 amino acids. There was one β -roll domain (18-97 ÅÅ), a C domain with α -helix region (110-136 ÅÅ), a D domain with α -helix region (136-155 ÅÅ), a HTH domain with helix-turn-helix (170-196 ÅÅ), a G domain with a leucine zipper domain (211-237ÅÅ) from N_h2-terminal to COOH-terminal in deduced amino acid sequence of *PrfA*. There were some site mutations in the nucleotide sequence of *PrfA* gene for 35 different strain isolated from all over the world. Whether the mutation sites of the *prfA* in HTH domain would affect the conformation stability and *prfA*-DNA binding ability need to be further studied.

Development of indirect ELISA for detection of antibodies against PPRV Based on recombinant antigen protein

Jun Qiao¹, Qing-ling Meng^{1,2*}, Xue-peng Cai², Chuang-fu Chen¹, and Yan Ren¹

¹. College of Animal Science and Technology, Shihezi University, Shihezi 832003, China; ². State Key Lab of Veterinary Etiological Biology, Lanzhou veterinary research institute, Chinese Academy of Agricultural Science, Lanzhou 730046, China

Peste des petits ruminants (PPR), is an acute high-contact A-type animal infectious disease in goats and sheep caused by peste des petits ruminants virus (PPRV). In recent years, PPR has been epidemic to African, Middle Eastern and South Asian countries, which has posed a tremendous threat to sheep industry of China. Border detection and monitoring of animal serum must be strengthened to protect China from PPR. At present, many detecting techniques such as agarose gel immunodiffusion (AGID), CIE (CIEP), indirect fluorescent antibody test (IFAT), virus micro-neutralization test (VNT), immune capture ELISA (c-ELISA) have been established, but these methods can be time-consuming and complicated with low sensitivity and specificity. There are no commercial test kits for PPR epidemiological investigation and monitoring. It is imperative to develop highly specific, sensitive, and rapid detection methods. In this study, recombinant PPRV H and N proteins expressed in *E. coli* were used as antigens and indirect ELISA was developed for detection of PPRV antibodies. Haemagglutinin (H) protein and nucleoprotein (N) gene of PPRV vaccinal strain were cloned into pET-28a(+) for expression in the transformed *E. coli* BL21(DE3). Recombinant proteins were purified by Ni²⁺ column to prepare coating antigen. An indirect ELISA for detection of antibodies against PPRV was then developed using the purified antigen to coat ELISA plates with the doses of 2.5 µg per wells, and with HRP-SPA as the secondary antibodies. The serum samples of 325 goats, 789 sheep, 132 cattle collected from border areas of Xinjiang were assayed with established indirect ELISA. The detecting results were all negative, which indicated that there were no infections. It is still necessary to inoculate against potential outbreaks from other countries.

Heterogeneity of human H5N1 virus in replication and pathogenicity and its influence on the evolution of the virus in mammals

Yongqiang Li, Jing Li, Yi Hu, Guohui Chang, and Qingyu Zhu

Beijing institute of microbiology and epidemiology, Beijing, 100071

From 1997, H5N1 avian influenza virus began to infect humans directly after crossing the Host Species Barriers. Although it has been suggested transmission occurred in several household clusters and in one case by apparent child-to-mother transmission, human-to-human transmission of H5N1 influenza virus has been limited, due to the host species barriers between birds and humans. But continued incidents of direct transmission of H5N1 viruses from birds to mammalian hosts (humans, felids, and stone martens) may allow the virus to gradually adapt to and spread among mammalian species, including humans. In our research we found it was heterogeneous in plaque forming characteristics for the wild H5N1 avian influenza virus strains isolated from human, besides some smaller ones, many plaques of A/Vietnam/1194/2004 were large in size. Plaque-purified virus of large plaque viruses were less pathogenic in mice and displayed more efficient replication in MDCK cells, compared to plaque-purified virus of smaller plaque viruses. In light of less pathogenicity and more efficient replication, the larger plaque virus had competitive advantage against the smaller plaque virus in mammal cells or animals. The larger plaque virus was more adaptive in mammal cells or animals, and this mammal adapted virus had more chance to escape from the infected mammal host and transmit to other hosts.

The phylogenetic analysis of bat rabies viruses and the evolutionary relationships with their hosts

Lihong Yuan, Dewei Li, and Jinping Chen*

South China Institute of Endangered Animals, Guangzhou, 510260, China; Guangdong Entomological Institute, Guangzhou, 510260, China

Recent studies have suggested that bats are natural reservoirs or hosts for a range of lyssaviruses. We examined the evolutionary relationships between bat lyssaviruses and their hosts by using sequence data of the virus N gene and the bat cytochrome b gene. The resulting information presented in this report provides a comprehensive analysis of these phylogenetic relationships. Phylogenetic analyses revealed multiple incongruent associations between the phylogenies of vespertilionid and pteropodid bats and their lyssaviruses, and some bat lyssaviruses formed several monophyletic clades. Species-specific host restriction was found for bat lyssaviruses in some species sampled from more than one geographic location. Seven RV isolates shared a common ancestor with other clusters, with a nucleotide identity of a high bootstrap value, suggesting that host shifts have occurred in the evolutionary history of these groups. These shifts may be due to either virus biologic traits or host behavioral traits. This finding has implications for the emergence of bat lyssaviruses.

Canine distemper virus raccoon dog isolate animal infection assay

Li Yi, Shen Yang, Jian-ke Wang, Shi-peng Cheng *

Institute of special economic animal and plant science ,CAAS, Jilin 132109,China

Canine distemper is an acute, highly contagious disease found in animals harvested for fur (such as minks, foxes, raccoon dogs) and wild animals (including tigers, pandas). It is caused by canine distemper virus (CDV) which is a member of the genus Morbillivirus of the family Paramyxoviridae. Clinical and morbid anatomical signs of canine distemper have been described in detail, but CDV raccoon dog isolate pathogenesis has not been described clearly. In this study, we successfully replicated the course of canine distemper disease on experimental dogs using raccoon dog tissue virus (strain PS-09). Experimental subjects showed dramatic clinical signs including onset of a cutaneous rash, serous nasal and ocular discharge, conjunctivitis and anorexia after inoculation with the virus. Death usually occurred on after the 28th or 29th day for the first challenge, or 19th day for the second challenge. Pathological changes indicated that there was respiratory, intestinal and nervous system infection. Detecting of virus distribution in vivo by RT-PCR, we found that CDV were distributed in lung, spleen, brain, bile, intestine and its contents. Feces, urine, saliva, blenna narium, and secretion of eyelid were all contained virus. After constructing a phylogenetic tree of raccoon dog CDV H gene and other regions CDV H gene reference strains, we found that strain PS-09 was classified to Asia-1 branch, which is the most predominant strain in China now. Our findings will help better control for and protect against canine distemper.

Spatiotemporal relationship of waterbirds migration from Qinghai Lake and HPAI outbreaks in Central Asian-Indian flyway

Dongping Liu^{1,2}, Guogang Zhang^{1,2}, Yunqiu Hou^{1,2}, Hongxing Jiang^{1,2}, Ming Dai^{1,2},
Fawen Qian^{1,2}, Jun Lu^{1,2} and Zi Xing³

¹Key Open Laboratory of Forest Protection of State Forestry Administration Research, Institute of Forest Ecology, Environment and Protection, Chinese Academy of Forestry, Beijing 100091, China; ²National Bird Banding Center, Beijing 100091, China; ³Qinghai Lake National Nature Reserve, Xining 810008, China

Qinghai Lake is the largest inland salt-water lake of China situated northeast Qinghai-Tibet Plateau, a critical important breeding ground and stopover for waterbirds within the Central Asia-Indian flyway. In May 2005, the first major outbreak of HPAI H5N1 virus in wild waterbirds took place in Qinghai Lake, and then followed by other regions in China, the rest of Asia, Europe and Africa, which have raised concerns about the potential role of migratory waterbirds at Qinghai Lake in disseminating the virus. From 2006 to 2007 we marked breeding bar-headed geese (*Anser indicus*), great black-headed gulls (*Larus ichthyactus*) and great cormorants (*Phalacrocorax carbo*) at Qinghai Lake with satellite transmitters to determine their fall migration route and stopovers, and identify any spatiotemporal relationship with HPAI outbreaks. The majority of the marked waterbirds migrated southwestern within the Central Asia-Indian flyway, and only one bar-headed goose migrated in a southeast direction, indicating a connection of East-Asia and Central Asia-Indian flyways, and potential exchange of HPAI virus between them. The migration corridor for marked waterbirds was created based on the Brownian bridge movement model, in which significantly more HPAI outbreaks were found than in a control area outside. The reported outbreaks in migration corridor tended to occur in lower latitude and higher poultry density areas. In addition, probability of HPAI outbreak was not even in the four seasonal stages of marked waterbirds, which is higher in wintering and spring migration season.

Generation of replication-competent recombinant influenza viruses carrying a reporter gene.

Feng Li¹, Liqiang Feng¹, Zhenyuan Dong¹, Xuehua Zheng¹ and Ling Chen^{1,2}

¹Guangzhou Institute of Biomedicine and Health, Chinese Academy of Sciences, Guangzhou 510530, ²Department of Medical Biotechnology, University of Science & Technology of China, Hefei 230026, China

Influenza viruses harboring reporter genes are vital for research but usually require a complementary cell line. Previously there was no way to stably produce large quantity in embryonated eggs. In our study we generated two recombinant A/PR/8/34 (PR8) influenza viruses with neuraminidase (NA) segment carrying enhanced green fluorescent proteins (EGFP). The viral RNA (vRNA) specific packaging signals for NA were largely retained for efficient packaging. An “auto-cleave” 2A peptide was incorporated between NA and EGFP to enable monocistronic expression of two proteins, EGFP and NA proteins, from the same vRNA. Further analysis found that both viruses, with some characteristic differences, could replicate without the need of exogenous NA in cells and were propagated to large quantities while maintaining genome stability after multiple passages in embryonated eggs. These findings will be of great use for basic research, for screening antiviral drugs and to neutralize antibodies.

Japanese encephalitis: wildlife reservoirs

Richard Bowen, Angela Bosco-Lauth and Nicole Nemeth

Colorado State University, Fort Collins, Colorado USA

Japanese encephalitis virus (JEV) is an arthropod-borne virus that circulates throughout Southeast Asia, Japan, and China and is responsible for 30 000–50 000 human cases of encephalitis annually, with as many as 10 000 fatalities. The virus is transmitted primarily by culicine mosquitoes, namely *Culex tritaeniorhynchus*, and the main reservoir hosts are thought to be ardeid birds, such as egrets and herons, and domestic swine. Humans and horses are considered dead-end hosts, but JEV infection in either species can elicit a severe clinical response. The recent expansion of JEV into the Torres Strait of Northern Australia has led to an increased interest in factors that could contribute to disease emergence and establishment in new locations, including the United States. Of particular concern is whether or not there will be any impact by JEV on wildlife, and if so, what role these animals may play in the transmission cycle. In addition to avian wildlife, our investigations into JEV-susceptible mammals revealed that nine-banded armadillos develop viremia in response to JEV infection and, like birds, did not develop clinical disease. Mink were also tested for JEV infection, but failed to develop viremia following inoculation. The results of these investigations suggest that in addition to the known vertebrate reservoir hosts for JEV, there are probably several other species in the wild that could play some role in the sylvatic disease cycle. Continued serological surveillance and experimental infections of various birds and mammals may provide insight into how an emergence of JEV may impact wildlife and also allows for some foresight into methods for early detection of outbreaks.

List of Participants

Alexander Malogolovkin	Malogolovkin@inbox.ru
Alonso Aguirre	aguirre@wildlifetrust.org
Baohua Zhao	zhaobaohua86178@sohu.com
Boripat Siriaronrat	boripat.siriaronrat@fao.org
Catherine Soos	Catherine.Soos@ec.gc.ca
Chengmin Wang	wangcm@ioz.ac.cn
Chenxi Wu	chenxi19860514@126.com
Chheang Dany	wpo@forum.org.kh
Dale Nolte	Dale.L.Nolte@aphis.usda.gov
Dennis Slate	Dennis.Slate@aphis.usda.gov
Erik K. Hofmeister	ehofmeister@usgs.gov
Guangyuan Liu	liuguangyuan2002@sina.com
Guogang Zhang	zm7672@caf.ac.cn
Guohui Chang	changguohui999@yahoo.com.cn
Hanzhong Wang	wanghz@wh.iov.cn
Hong Zhang	hzhang23@yahoo.com, hzhang@zbiomed.com
Hongxuan He	hehx@ioz.ac.cn
Hua Yu	chengduyuhua@163.com
Huan Ji	Jihuan-cynthia@163.com
Ian Barker	ibarker@uoguelph.ca
Jianhua Qin	qjhqqq@sohu.com
Jing Li	lj-pbs@163.com
Jing Luo	luojing@ioz.ac.cn, luojing.lj84@gmail.com
Jinping Chen	Chenjp@gdei.gd.cn
John Baroch	john.a.baroch@aphis.usda.gov
Jonathan M. Sleeman	jsleeman@usgs.gov
Kai Li	jiangqiaokai@163.com

Kai Zhou	zhoukai@ioz.ac.cn
Kamal Gairhe	kamalgairhe@hotmail.com
Karma Rinzin	karinzin@yahoo.com
Ke Wang	15833212097@163.com
Kristy Pabilonia	Kristy.Pabilonia@Colostate.Edu
Li Yi	tcs_yili@126.com, tcscsp@126.com
Liguo Liu	liuliguo91@126.com
Lim Sopheap	Sopheap73@yahoo.com
Lixiang Jiang	jianglixiang2008@sina.com
Loinda Rugay Baldrias	lbaldrias@gmail.com
Maosheng Yang	yms_gy@163.com
Min Li	Limingfm@126.com, lim@nxu.edu.cn
Ming Yang	yangming@synu.edu.cn
Mohammad Mostafa Feeroz	feerozmm@yahoo.com
Nyamba Batbayar	bnyamba@magicnet.mn
Orgil Doolonjin	vetsermongolia@magicnet.mn
Qigang Cai	qgcai@hotmail.com
Qinglong Liang	liangql@ioz.ac.cn
Qiqi Lu	lujq@zzu.edu.cn
Qiumei Shi	shiqiumei@yahoo.com.cn
Qiyong Liu	liuqiyong@icdc.cn
Riana Aryani Arief	rianaarief@yahoo.com
Richard Arnold Bowen	Richard.Bowen@colostate.edu
Shelan Liu	liushelan@yahoo.com.cn
Shipeng Cheng	tcscsp@126.com
Stephanie Shwiff	Stephanie.A.Shwiff@aphis.usda.gov
Sugir TSengee	ssugar352000@yahoo.com
Sunil Chandra Gain	sunil.chandra55@yahoo.com
Tao Zhang	zhangtao@ioz.ac.cn

Thanh Long To	thanhto@fpt.vn
Thierry Work	thierry_work@usgs.gov
Vimol Jirathanawat	vimoljir@dld.go.th
Xiaogang Liu	Lxg7722@163.com
Xuebin Li	Leexuebin@yahoo.com.cn
Yi Hu	huyiamms@163.com
Yi Hu	hy913888@sina.com.cn
Youfang Gu	youfanggu@163.com
Yuehuan Liu	liuyuehuan@sina.com, liuyuehuan@baafs.net.cn
Yu Mu	muyu1985muyu@sina.com
Yukun Li	yukun.li@thermofisher.com
Yung-Fu Chang	yc42@cornell.edu
Yunhai Guo	guoyh@ioz.ac.cn
Yuping Hua	yuping_hua@126.com
Zhengli Shi	zlshi@wh.iov.cn

Attachment: Author Guidelines for Integrative Zoology

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The acceptance criteria for all papers are the quality and originality of the research and its significance to our readership. Except where otherwise stated, manuscripts are double-blind peer reviewed by two anonymous reviewers and the Editor. Manuscripts should be written so that they are intelligible to the professional reader who is not a specialist in the particular field. They should be written in a clear, concise, direct style. If extensive alterations are required, the manuscript will be returned to the author for revision.

Submission of manuscripts

Word document only via email to inz@ioz.ac.cn. All manuscripts should be double-spaced and include line numbers, preferably within the page. All pages should be numbered consecutively in the top right-hand corner, beginning with the title page. The top, bottom and side margins should be at least 30 mm.

Author guidelines

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- A cover letter explaining why you consider the manuscript suitable for publication in Integrative Zoology.
- A title page including all authors and their affiliations and email addresses.
- An abstract of 250 words or less that effectively summarizes your study.
- Check that the manuscript follows the Author Guidelines for Integrative Zoology and that the sections are in the correct order.
- Check you have indicated the ethics approval system.
- Cross-checked all referencing and checked the formatting of these.
- Ensure your manuscript is in DOC (Microsoft Word) format.
- All tables and figures are presented at the end of the text.
- Check that only SI values have been used throughout the manuscript.
- At least one colleague has read through your manuscript.

Attachment: About the Wildlife Disease Association

History of the Wildlife Disease Association

In March 1951 a group of 28 US and Canadian scientists interested in wildlife diseases founded the Wildlife Disease Committee. The rest, as they say, is history - eventually becoming what we know as the Wildlife Disease Association (WDA) in 1952. Today, the WDA is an international scientific society of wildlife professionals, veterinarians, epidemiologists, biologists, ecologists, research scientists and other individuals involved with wildlife diseases and related disciplines, promoting research, management, education, communication, consultation and collaboration. The WDA sponsors an annual scientific conference and publishes the Journal of Wildlife Diseases. Read more at www.wildlifedisease.org/index.html

Focus of the WDA

- Endangered Species – WDA members together with international, state, provincial, federal, and private agencies are intimately involved in efforts to preserve and improve the status of endangered species populations. Examples include monitoring the status of the black-footed ferret in Wyoming, USA, trying to control losses of Tasmanian devils associated with Devil facial tumor disease, and investigating factors contributing to the woylie decline in West Australia.
- Game and Furbearing Animals – Extensive research and surveillance provides multiple benefits to wildlife through private and public agencies by enhancing understanding the impact of diseases on wild animal populations.
- Wildlife Conservation – Members, working as and/or with wildlife biologists, investigate the effects of environmental toxins, global warming, habitat alterations, and introduction of exotic species on the health of native wildlife.
- Wildlife Translocation – Many members are engaged in translocation of wildlife between areas. Efforts are made to prevent the introduction of disease and to monitor the health of animals following translocation.
- Wildlife Rehabilitation – Veterinarians, clinically oriented specialists and other professionals affiliated with the WDA are increasingly interested in the rehabilitation of sick and injured wildlife, especially rare, threatened and endangered species.
- Zoological Parks – Zoo veterinarians supervise the care of a large variety of species and provide husbandry and veterinary care for many captive populations of threatened and endangered species from all over the world. In addition, they work with wildlife and other resource managers on the management of free-ranging wildlife population health.
- Public Health – WDA members contribute substantially to knowledge about

arthropod-borne encephalitis, rabies, tularemia, Lyme disease, hantaviruses, plague, environmental toxins, and many other wildlife diseases potentially affecting human health.

- Livestock and Poultry –Wildlife specialists participate in laboratory, clinical and field research to control diseases in wildlife that can be economically devastating to domestic livestock. Among these diseases are malignant catarrhal fever, brucellosis, tuberculosis, viscerotropic velogenic Newcastle disease, and African swine fever.
- Comparative Medicine – Many WDA members with specialty training in the health and biological sciences are involved in basic research using wildlife as models of diseases found in humans or domestic animals.
- Ecosystem Health – Because no species exist independent of its environment, many WDA members are addressing the complex issues of ecosystem health. Topics of special concern include aquatic animal health, as many marine mammals and sea birds serve as biomarkers for the assessment of the health of the marine environment, and the multiple interactions resulting from human and domestic animal encroachment into wild habitats.
- Wildlife Disease Ecology – Understanding the transmission dynamics and impacts of diseases in wildlife populations is crucial to the future conservation management of wildlife. Thus, members conduct research on both endemic and exotic diseases in wildlife populations, to understand the transmission, ecology and impacts of diseases in these populations.

WDA Management Team

Management of the Wildlife Disease Association rests with several groups of people. These groups include:

- Officers: The officers of the Association include President, Vice-President, Secretary, and Treasurer.
- Council: The government and operation of the Association is vested in the Council, made up of the officers, seven Members-at-Large (i.e., six regular members and one student member), Editors, and an elected representative from each Section.
- Editors: The editors for the Association include those for the Journal of Wildlife Diseases, the Supplement to the JWD and the web page.
- Managers: The WDA managers include the Executive Manager and Business Manager.

WDA Recognition and Awards

The WDA gives several awards and provides funding to recognize outstanding work in wildlife health and service to the WDA. These awards include:

- WDA Distinguished Service Award: The DSA is the highest award of the Wildlife Disease Association. The purpose of the DSA is to honor a WDA member of long standing who, by his/her outstanding accomplishments in research, teaching and other activities, including participation in WDA affairs, has made a noteworthy contribution furthering the aims of the Wildlife Disease Association.
- WDA Emeritus Award: The Emeritus Award is an honorary category of membership awarded by the Council to members of the WDA who have retired from their profession and who in the opinion of Council have contributed significantly to the study of wildlife diseases.
- WDA Duck Award: The Duck Award is presented to recipients to acknowledge a particularly embarrassing incident (e.g., foible/mistake) that usually occurs at the annual meeting of the WDA.
- WDA Student Awards: The WDA offers a scholarship and two awards to encourage student participation in the Association and our annual conference, and to recognize outstanding student research.
- Tom Thorne and Beth Williams Memorial Award: The Award is presented in acknowledgement of either an exemplary contribution or achievement combining wildlife disease research with wildlife management policy implementation or elucidating particularly significant problems in wildlife health.
- Carlton M. Herman Founder's Fund: The main scope of activities supported by the fund is the relation of population health and density to changes in habitat. The scope includes all animals, including the human species. Activities may include invited lectures, funding of research, presentation of medals in acknowledgement of contributions, support of publications, or other activities as determined by the trustees of the Fund. [Award Info]
- WDA In Memoriam: This section profiles those WDA members who made significant contributions to the WDA and to wildlife and ecosystem health worldwide.

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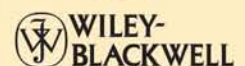
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