

One Health approaches to Zoonotic diseases: *HPAI, MERS and AMR*



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Chair, CODEX TFAMR

One health=One medicine

- Healthy animal
- Safe and healthy food
- Happy people

Standards-setting organizations



Codex = Joint FAO/WHO Codex Alimentarius Commission

OIE = World Organization for Animal Health

IPPC = International Plant Protection Convention (FAO)

OIE approach to 'One Health'

“Protecting animals, preserving our future”

Zoonotic potential of animal pathogens*

- 60% of human pathogens are zoonotic
- 75% of emerging diseases are zoonotic
- 80% of agents having a potential bioterrorist use are zoonotic pathogens
- **Nearly all new human diseases originate from animal reservoirs**

OIE(WAHO) global programs

- **HP Avian Influenza**/FMD
- Rabies
- **Zoonoses**: Brucellosis/TB....
- Food safety/food-borne diseases
- **AMR**
- Wildlife diseases
- New emerging diseases: climate changes

Avian Influenza

Technical Expertise

The **OIE in cooperation FAO and WHO**, provides policy advice, strategy design and technical assistance for the control and eradication of avian influenza.

Prevention & Control: OIE Terrestrial Animal Health Code

BIOSECURITY:

Biosecurity procedures in poultry production (Chapter 6.4)

SURVEILLANCE:

Guidelines for Surveillance for Avian Influenza (Article 10.4.27)

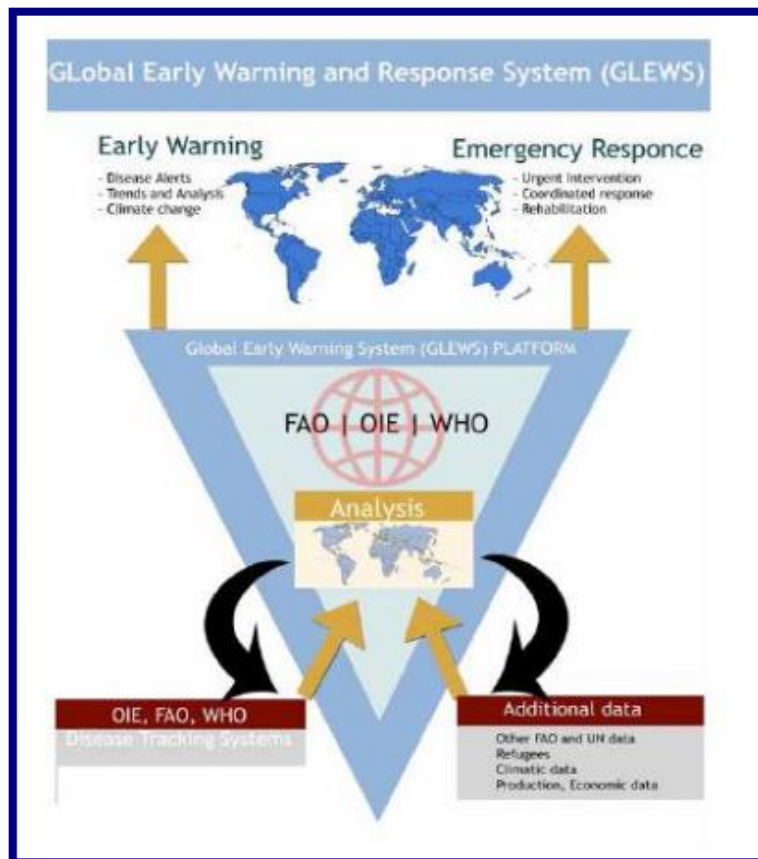
RAPID CONFIRMATION OF SUSPECTS:

Avian Influenza: Manual of Diagnostic Tests and Vaccines for Terrestrial Animals (Chapter 2.3.4)

Avian Influenza

- a global strategy

GLEWS: Global Early Warning System for Major Animal Diseases (including zoonoses)



Formal FAO/OIE/WHO Initiative – integrates the work of their different technical areas

Animal and public health early warning system for emerging infectious diseases

Share disease information and epidemiological analyses to initiate appropriate action

OFFLU:
joint OIE/FAO Network of Expertise for Animal Influenza



Established in 2011 to bring together leading animal influenza experts to protect the health of animals and humans from influenza viruses.

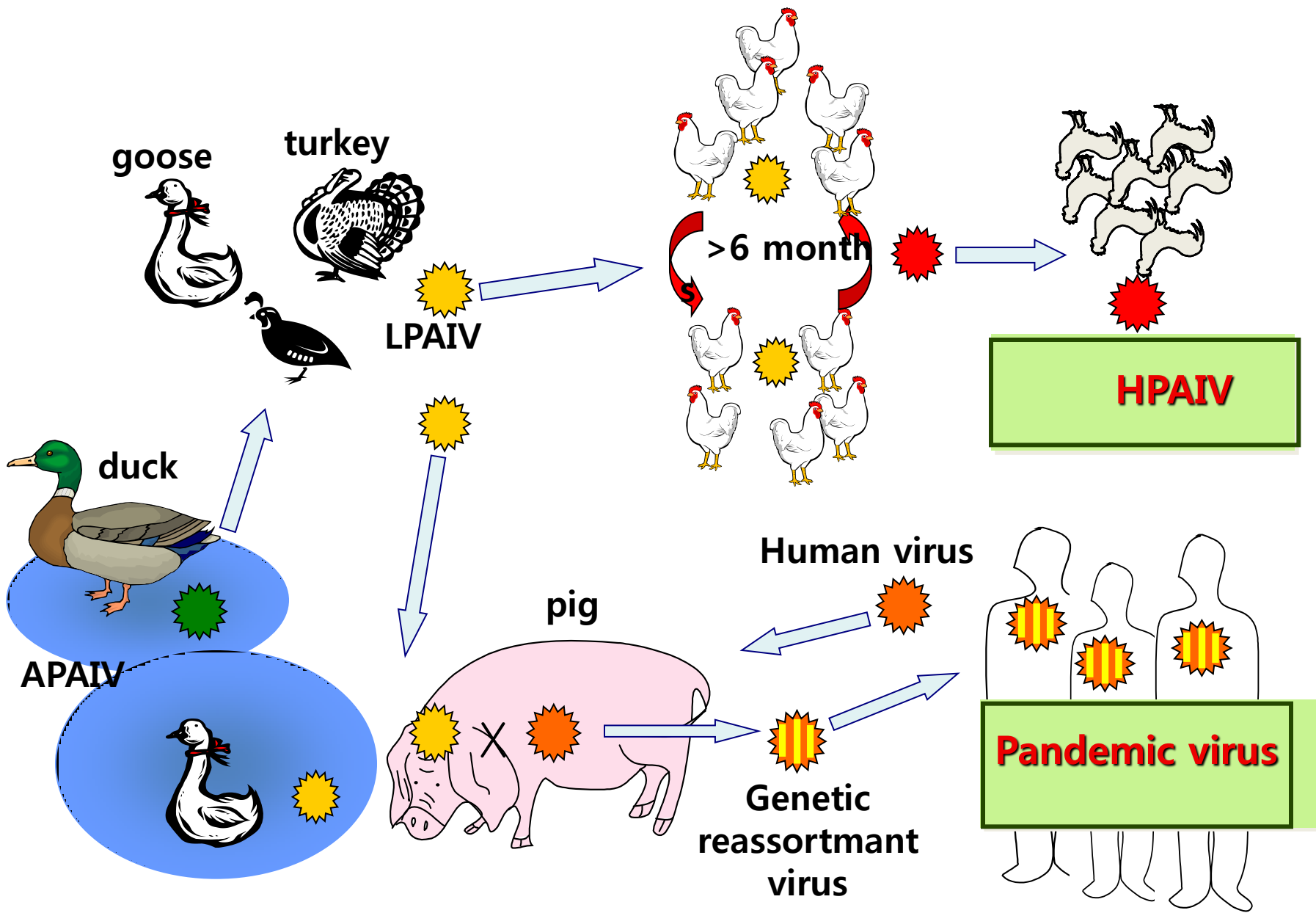


Highly Pathogenic Avian Influenza









HPAI virus and human pandemic virus strain

H5 HPAI Epidemics in Korea

03/04 H5N1

• 19 farms

06/07 H5N1

• 2 wild birds
• 7 farms

2008 H5N1

• 33 farms

10/11 H5N1

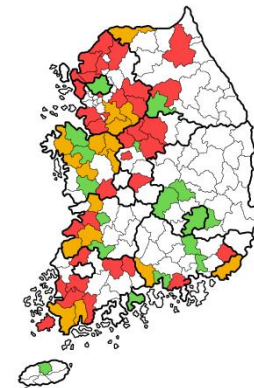
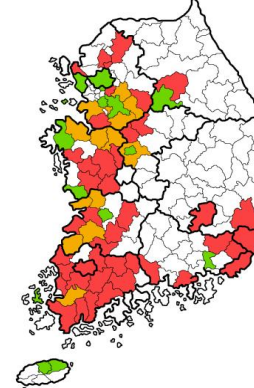
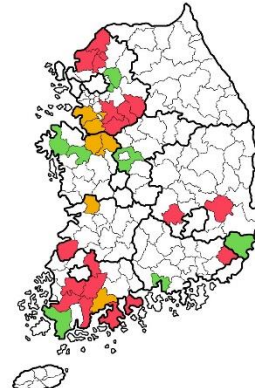
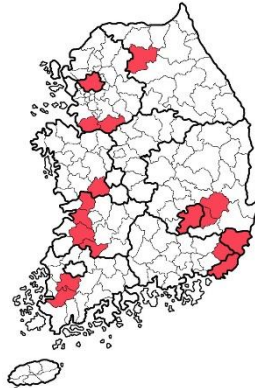
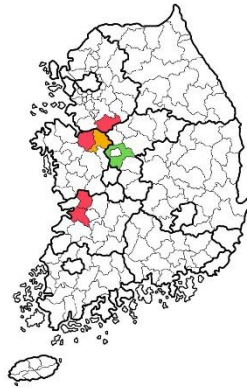
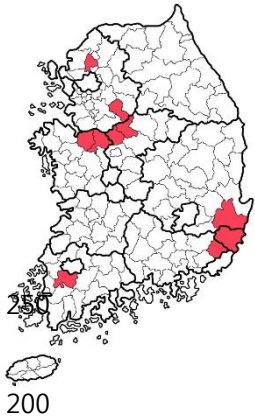
• 20 wild birds
• 53 farms

14-16 H5N8

• 58 wild birds
• 393 farms

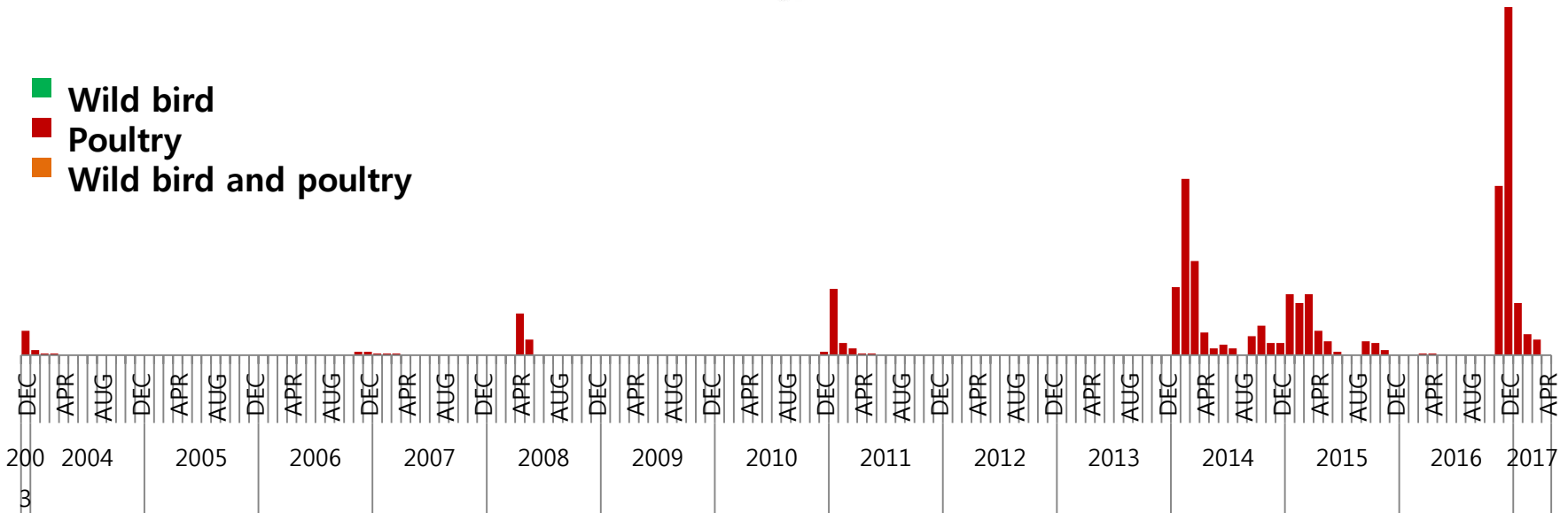
16/17
H5N6/H5N8

• 65 wild birds
• 383 farms

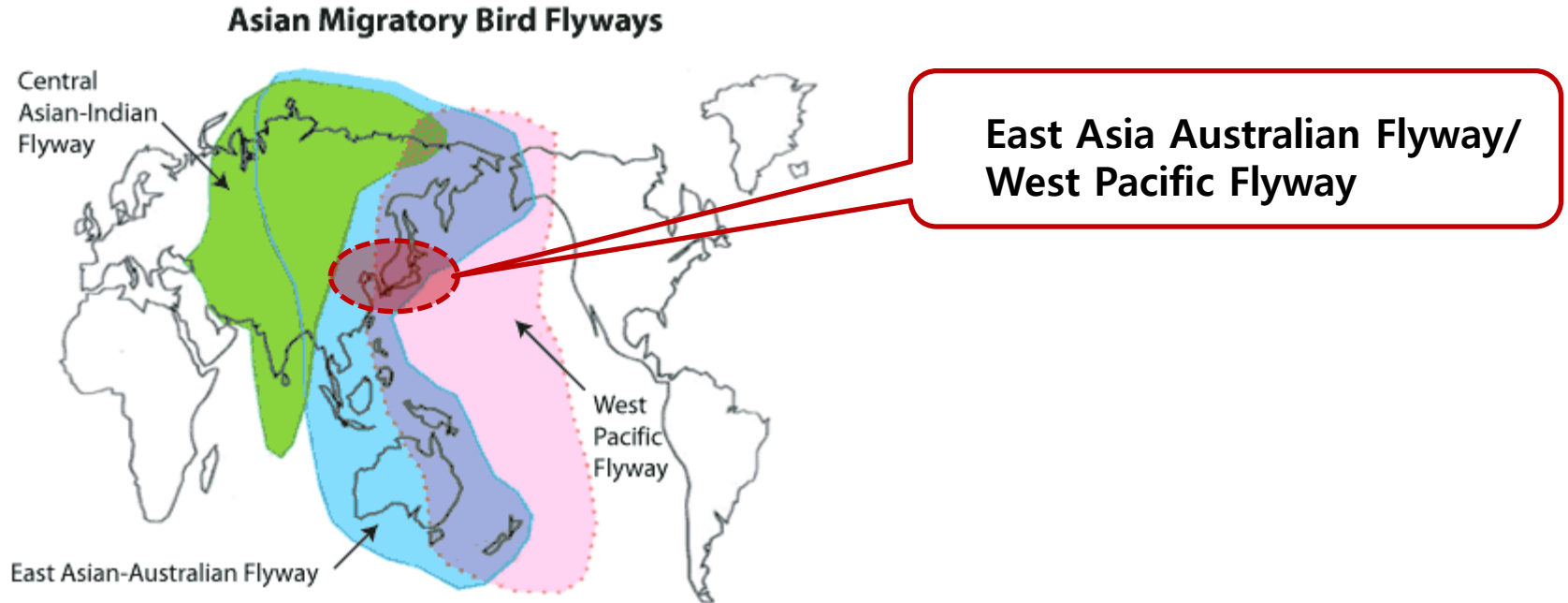
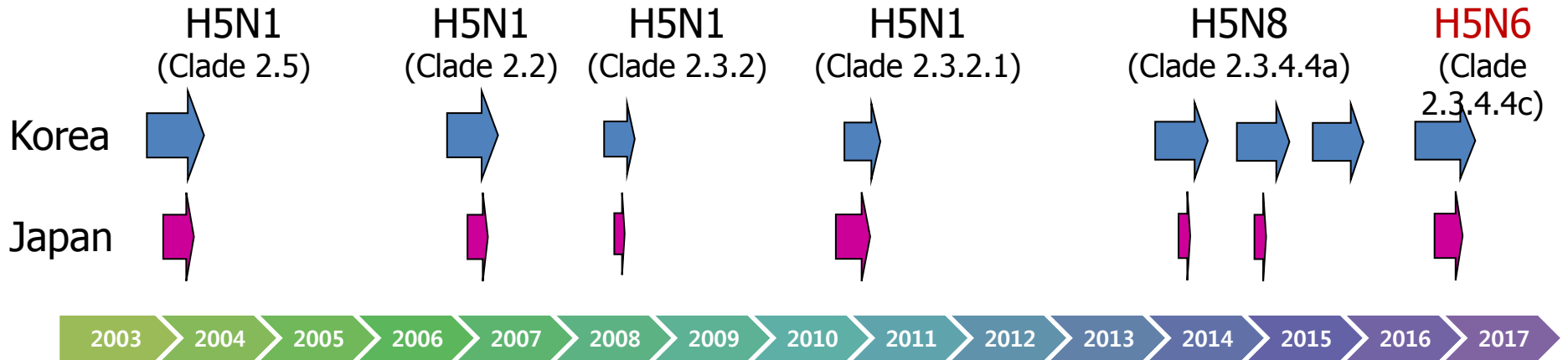


150
100
50
0

■ Wild bird
■ Poultry
■ Wild bird and poultry

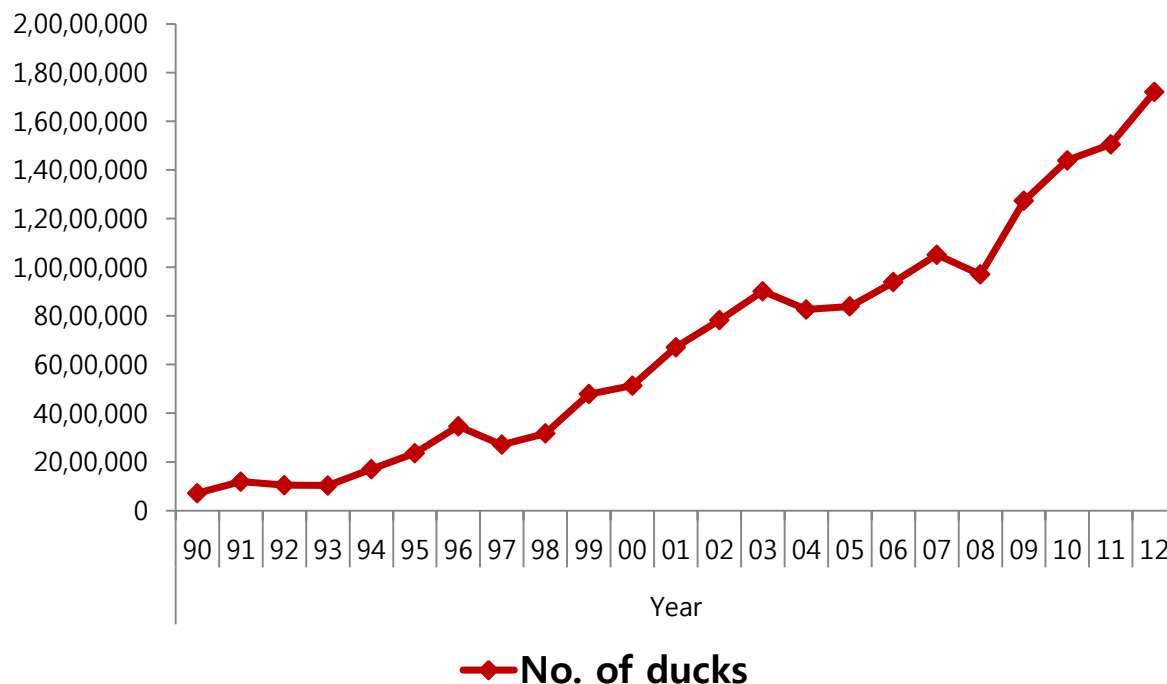


Common Source of H5 HPAI Viruses of Korea and Japan

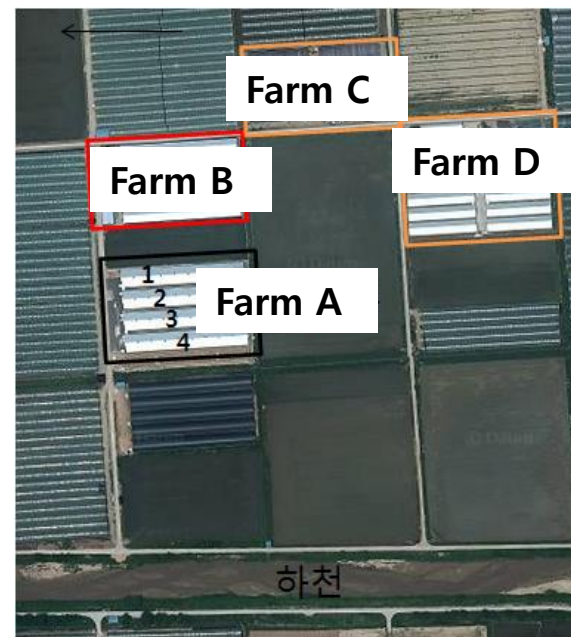


Domestic Duck Industry in Korea

- **Duck industry have been sharply increased**
- **Biosecurity level is low**
- Farms closely located with each other in the plain region
- High risk of transmission of virus: **from wild birds to farm** & farm to farm



Data: Korea Duck Association, 2014

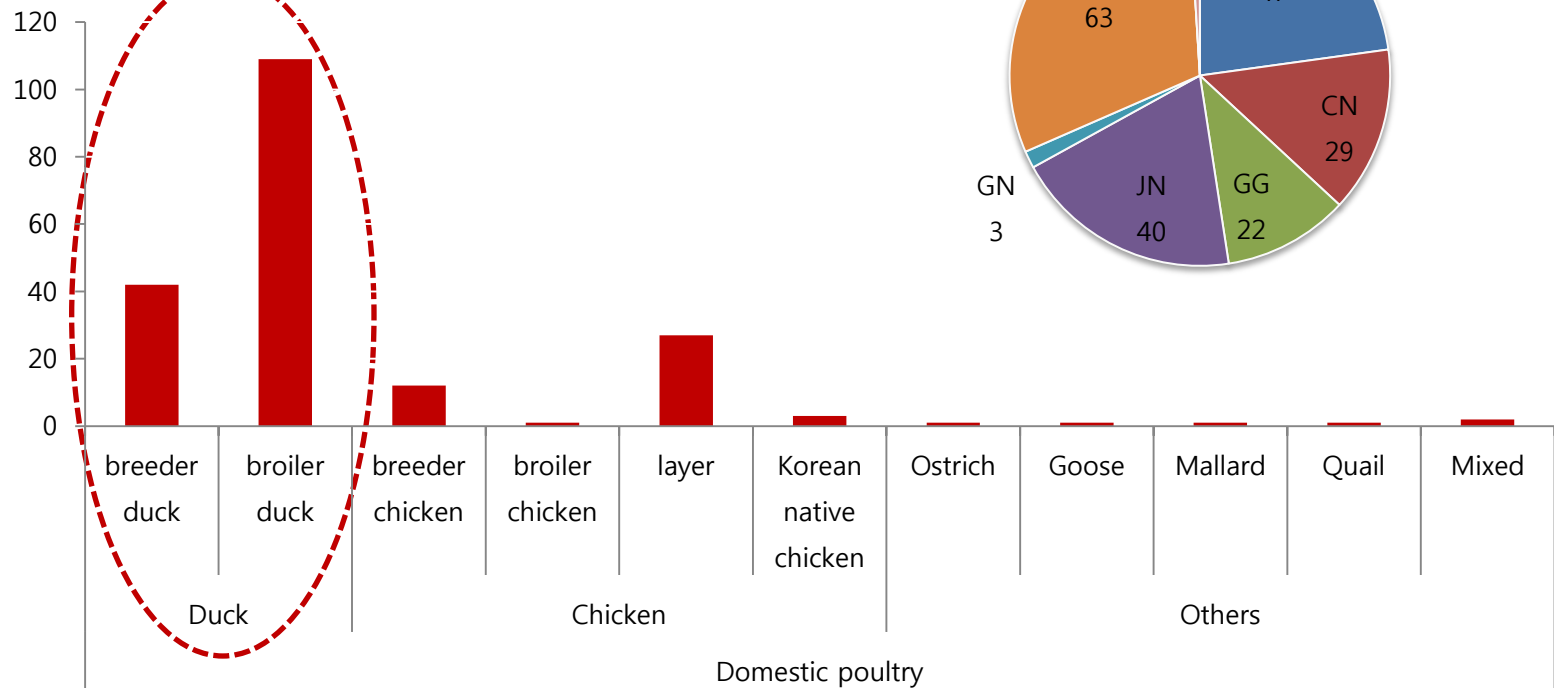


Data: Epidemiological Division of QIA, 2014

Affected species in poultry

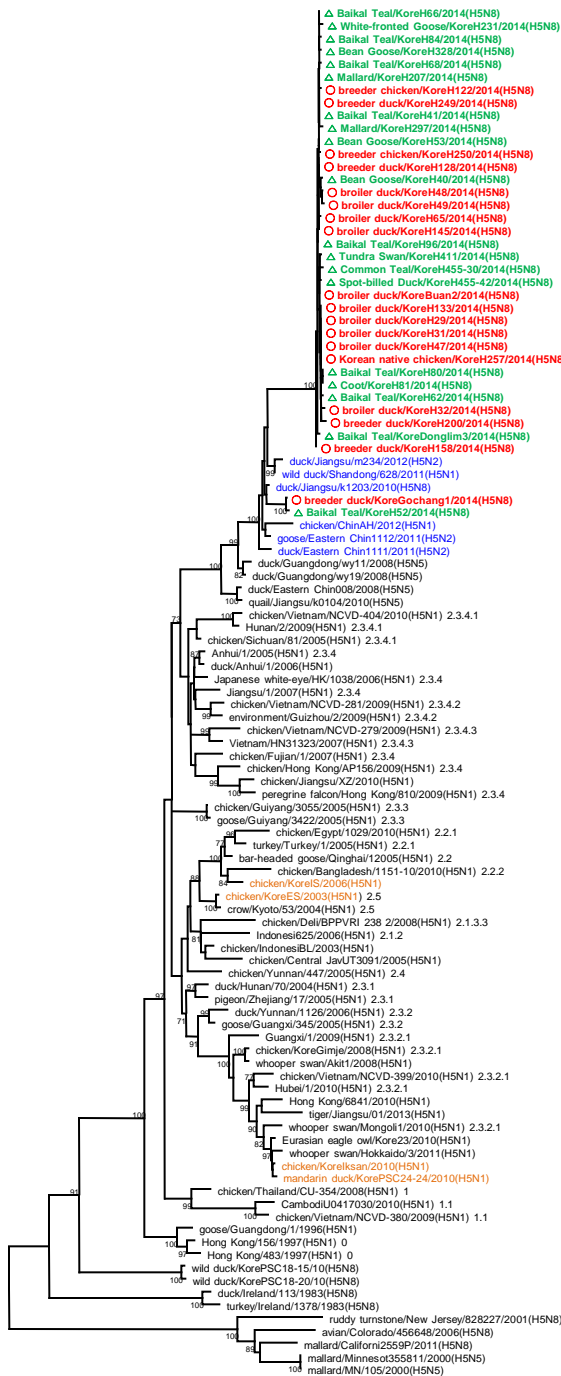
- H5N8 viruses from poultry (202 cases)

- Duck (153): 76%**
- Chicken (43): 21%
- Others (6): 3%



2014.5.31

H5 Gene



A

2.3.4.6

B

2.4.4.4

2.3.4.1

2.3.4.2

2.3.4.3

2.3.4.5

2.3.3

2.2

2.5

2.1

2.3.1

2.3.2

2.3.2.1

1.1

H5 Gs/Gd lineage

Korea LPAI H5N8
Ireland HPAI H5N8
American LPAI H5N8

H5N2



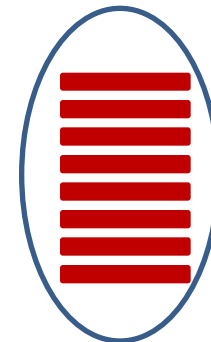
A/duck/Estern China/1111/2011

H5N8



A/duck/Jiangsu/k1203/2010

H11N9



A/environment/Jiangxi/28/2009

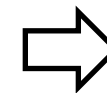
Avian Influenza Viruses in Eastern China during 2009-2011



Layer Chicken farm,
Kumamoto prefecture in Japan(2014.4.13)



Group A
Wild birds: 27 cases
Poultry: 18 cases



Group B
Wild birds: 1 case
Poultry: 1 case

Duck in LBM,
Zhejiang of China
2013
EID online(5.6)

HPAI H5N8 virus of Korea, 2014

❖ Total 47 viruses were analyzed in all 8 segments

Active Surveillance

Duck

- Breeder duck
- Broiler duck

Chicken

- Broiler breeder, Broiler
- Layer, Korean native chicken

Wild bird

- Feces
- Captured birds

LBM

- Live birds market

Minor Poultry

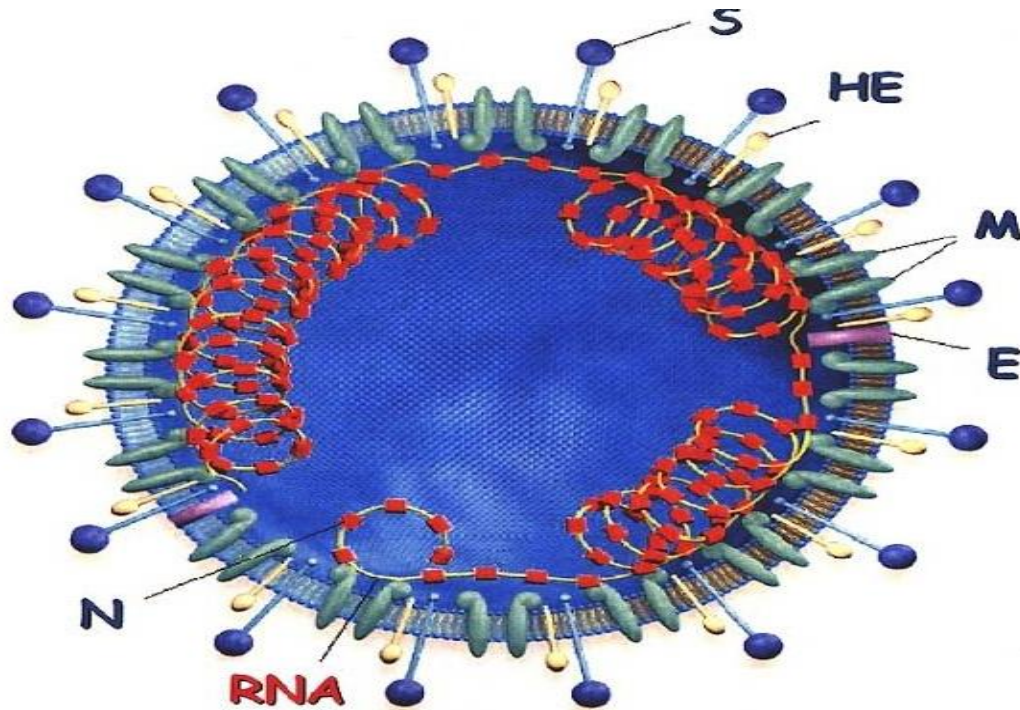
- Pheasant
- Quail

Others

- Raw material for feed
- Pet bird

MERS CoV

Betacoronavirus



Structure of the Coronavirus Virion:

- S = spike glycoprotein (the viral fusion protein),*
- HE = hemagglutinin-acetylase glycoprotein,*
- M = membrane glycoprotein,*
- E = small envelope glycoprotein,*
- N = nucleocapsid phosphoprotein*

Middle East respiratory syndrome coronavirus (MERS-CoV)

- Is thought to have an **origin in animals**
 - Not all community acquired cases of MERS-CoV had reported prior animal contact
 - Evidence suggests that virus has adapted to **camels**
- Is identified in camels in countries in the Middle East and North Africa
- Similar strains of virus were found in humans and camels in the **same locality**



- Clinical symptom is associated **mild respiratory sign in camels**, but morbidity or mortality of aetiology should be investigated
- Immunity to infection is poorly understood, we may not know possibility of reinfection



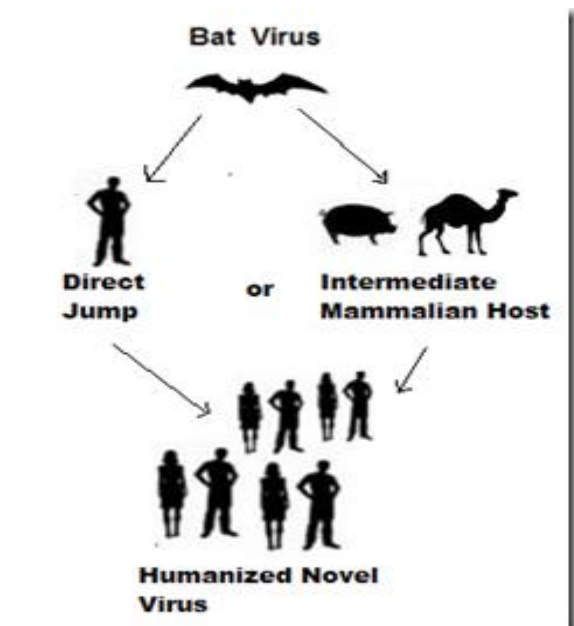
- Several types of investigation are needed
 - **Epidemiological** studies of MERS-CoV infections in camels
 - Pathological effects and **immune response to MERS-CoV**
 - **Relationship** between camel and human cases of virus
 - Effectiveness of **intervention measures** aimed at reducing public health risk
 - Monitor **evolution of the virus**

How dangerous it is

- There are **no vaccines or treatments** available so far.
- MERS-CoV is considered as a serious public health threat to humans by the WHO
 - Infection can cause severe disease in humans
 - Infection appears to be widespread in ***dromedary camels***
 - Coronaviruses may **adapt to new hosts**, and become more easily transmittable between humans

MERS-CoV in other animal species

- Fragment of viral genetic material matching the virus was found on **bat** from Saudi Arabia
- But, current evidence does not indicate a direct link between bats and virus in humans
- Based on receptor studies **other animal species** have been identified as **potential hosts**
- Where MERS-CoV is present, assess the presence of virus in wild and other domestic species



Precaution for at-risk groups

- People working closely with camels may be at higher risk of MERS-CoV infection
 - Farm workers
 - Slaughterhouse workers
 - **Veterinarians**
- Camels infected with MERS-CoV may not show any signs but it can shed virus through **nasal, eye discharge, faeces, milk and urine**
- **Practice good hygiene and avoid direct contact with all of these**

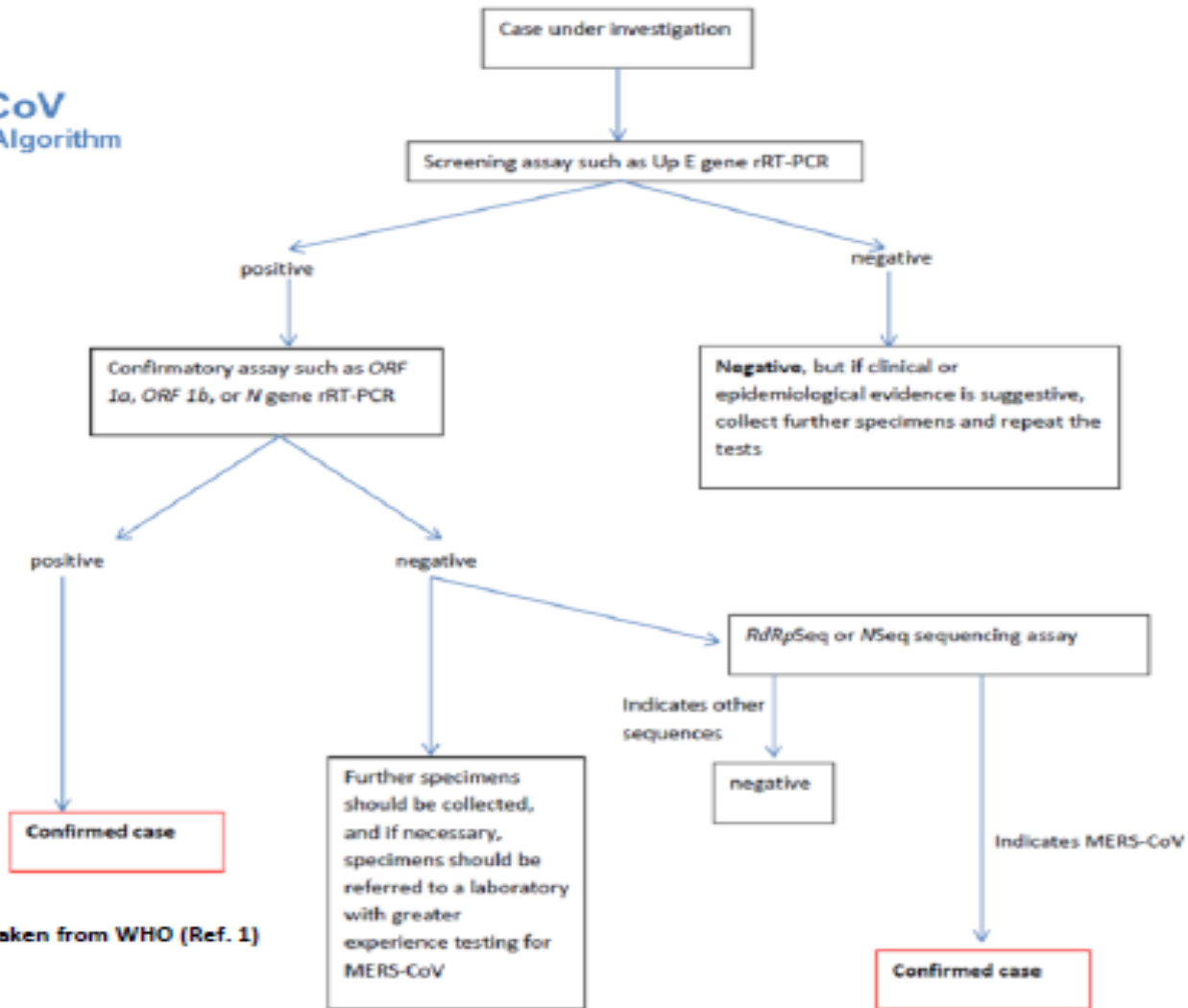


Diagnosis

- **Serological tests** detect antibodies but do not detect the virus itself
- **RT-PCR** tests can detect genetic material of the virus
- Genome sequencing is the best way to confirm
- Positive results from screening tests should be confirmed using a confirmatory test

Algorithm for the molecular detection of MERS CoV

MERS-CoV Detection Algorithm



Algorithm taken from WHO (Ref. 1)

Detection of MERS CoV

✓ The standard method for MERS CoV detection is to detect virus directly

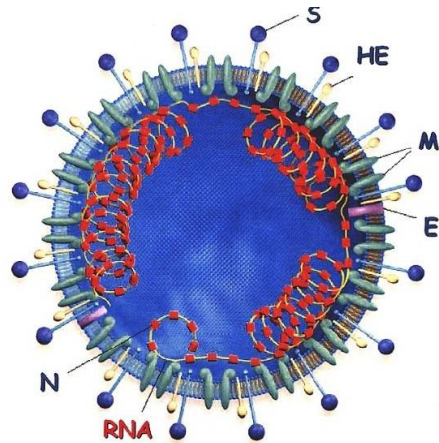
through virus isolation, or PCR

✓ However, these methods require professional skills, lab. equipments, high cost and time-consuming

--- not easy to perform, even worse not match to field situation



BioNote MERS CoV Ag Rapid



Structure of the Coronavirus Virion

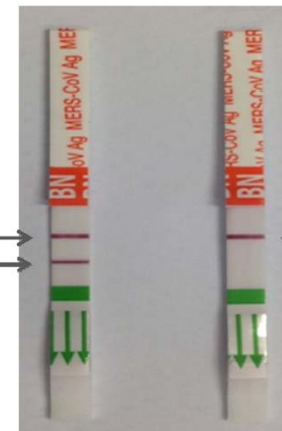
S = spike glycoprotein (the viral fusion protein),
HE = hemagglutinin-acetyltransferase glycoprotein,
M = membrane glycoprotein,
E = small envelope glycoprotein,
N = nucleocapsid phosphoprotein



Peptide for NP



Immunization & mAb development



C
T

C

(A) Positive

(B) Negative

MERS CoV Ag Rapid

without antigen Rapid test ?



MERS in doubt..

Worrying in trouble



Sample transport



Lab. Testing (PCR)



Result Report



Disinfection Isolation

Long time, huge damage

Short time, low damage

Time

With Antigen Rapid Test ?

Immediate field testing by rapid kit



Result within 15 min.



Immediate Disease Control



Prevention & Recommended action



Sick with CHIKUNGUNYA, DENGUE, or ZIKA?

Protect yourself and others from mosquito bites during the first week of illness.

Protect family and friends

- During the first week of illness, chikungunya, dengue, or Zika virus can be found in the blood.
- A mosquito that bites you can become infected.
- An infected mosquito can bite a family member or neighbor and make them sick.



Watch for these symptoms

See your doctor if you develop a fever with any of the following symptoms:

- Muscle or joint pain
- Headache, especially with pain behind the eyes
- Rash
- Conjunctivitis (red eyes)



For more information:

www.cdc.gov/chikungunya
www.cdc.gov/dengue
www.cdc.gov/zika



Protect yourself from mosquito bites

- Wear long-sleeved shirts and long pants.
- Use door and window screens to keep mosquitoes outside.
- Use insect repellent.

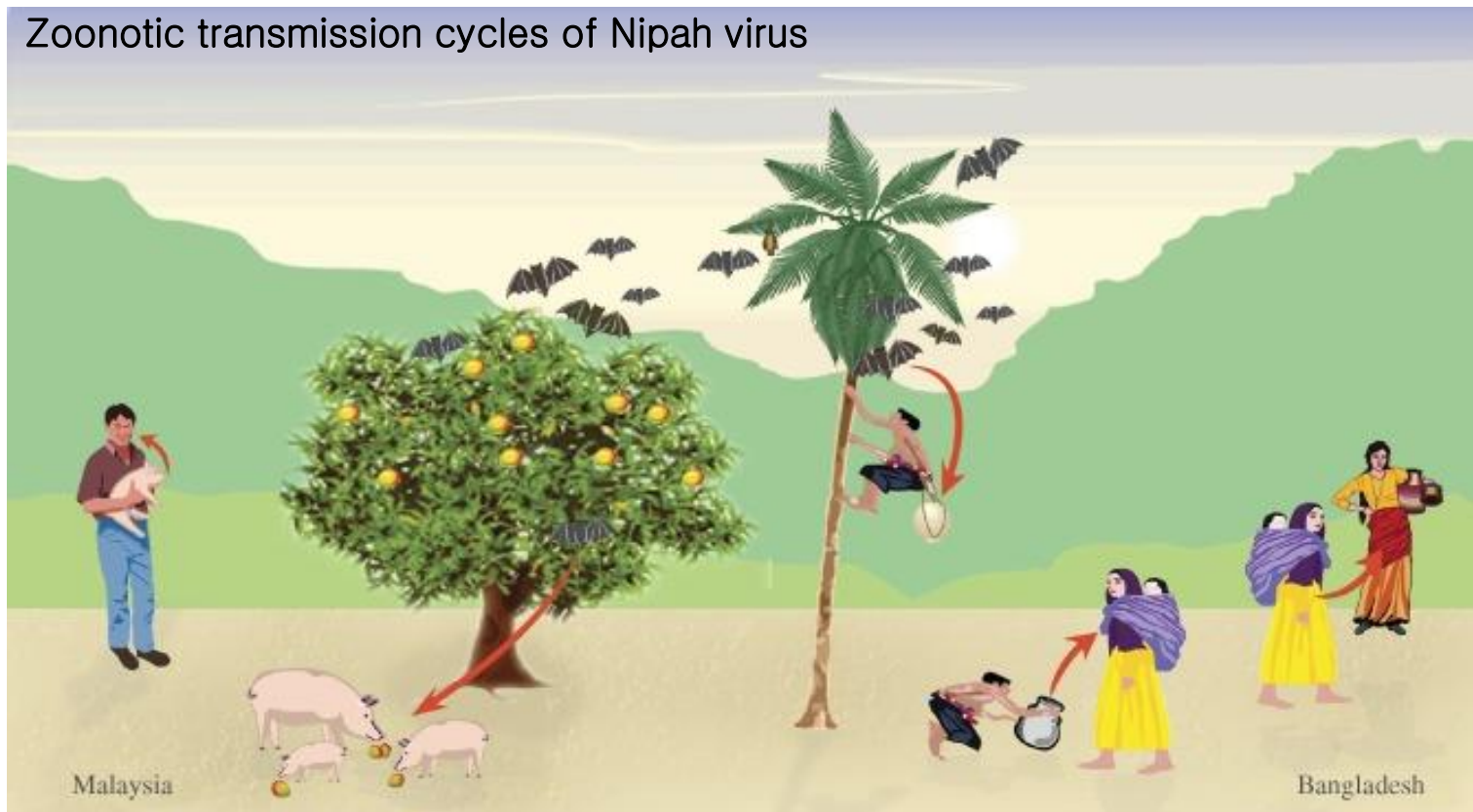


U.S. Department of
Health and Human Services
Centers for Disease
Control and Prevention

Drivers for the emergence of zoonotic diseases

1. Habitat destruction, Human encroachment

- > Drive diverse wildlife species together,
Pushing wildlife and livestock into overlapping environments
- > Facilitate the transfer of novel agents into naive & susceptible species
ex) Outbreak of Nipah virus(Malaysia, 1999)



2. Climate and habitat change

: Significant effect on vector distribution

(Expanding geographical ranges of zoonotic pathogens)

< Climatic factors affecting infection and transmission of vectorborne diseases >

Disease (causative agent)	Vector	Relevant climatic factors	Effects of climatic variability or climate change
Parasitic vectorborne diseases Malaria (<i>Plasmodium vivax</i> , <i>P. falciparum</i>)	Mosquitoes	Temperature, rainfall, humidity, El Niño-related effects, sea surface temperatures	Disease distribution; pathogen development in vector; development, reproduction, activity, distribution, and abundance of vectors; transmission patterns and intensity; outbreak occurrence

Arboviral diseases

Dengue fever (Dengue virus)	Mosquitoes	Temperature, precipitation	Outbreaks, mosquito breeding ,abundance, transmission intensity (extrinsic incubation period)
Yellow fever (Yellow fever virus)	Mosquitoes	Temperature, precipitation	Outbreaks, incidence; distribution, abundance, and breeding of mosquitoes, transmission intensity (extrinsic incubation period)
Chikungunya Fever (Chikungunya virus)	Mosquitoes	Temperature, precipitation	Outbreaks; mosquito breeding and abundance, transmission intensity (extrinsic incubation period)
West Nile virus disease (West Nile virus)	Mosquitoes	Temperature, precipitation	Transmission rates, pathogen development in vector, distribution of disease and vector
Rift Valley Fever (Rift Valley Fever virus)	Mosquitoes	Precipitation, sea surface temperatures	Outbreaks; vector breeding and abundance, transmission intensity (extrinsic incubation period)
Ross River virus disease (Ross River virus)	Mosquitoes	Temperature, precipitation, sea surface temperatures	Outbreaks, vector breeding and abundance, transmission intensity (extrinsic incubation period)
Tickborne encephalitis (Tickborne Encephalitis virus)	Ticks	Temperature, precipitation, humidity	Vector distribution, phenology of host-seeking by vector

Bacterial and rickettsial diseases

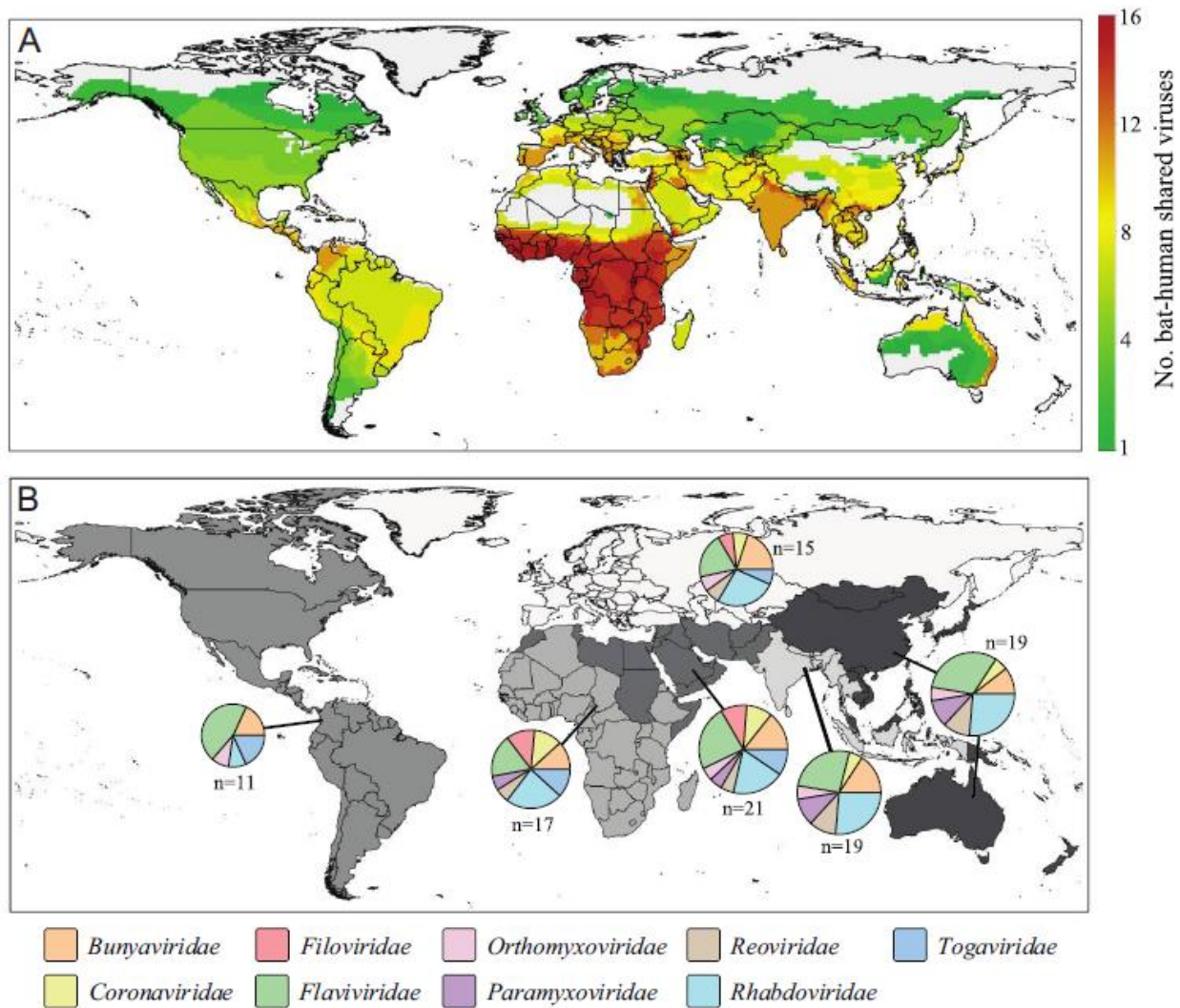
Lyme borreliosis (<i>Borrelia burgdorferi</i> , <i>B.</i> <i>garinii</i> , <i>B. afzelii</i> , or other related <i>Borrelia</i>)	Ticks	Temperature, precipitation, humidity	Frequency of cases, phenology of host-seeking by vector, vector distribution
Tularemia (<i>Francisella tularensis</i>)	Ticks	Temperature, precipitation	Case frequency and onset
Human granulocytic anaplasmosis (<i>Anaplasma phagocytophilum</i>)	Ticks	Temperature, precipitation	Vector distribution, phenology of host-seeking by vector
Human monocytic ehrlichiosis (<i>Ehrlichia chaffeensis</i>)	Ticks	Temperature, precipitation	Phenology of host-seeking by vector
Plague (<i>Yersinia pestis</i>)	Fleas	Temperature, precipitation, humidity, El Niño-related events	Development and maintenance of pathogen in vector; survival and reproduction of vectors and hosts; occurrences of historical pandemics and regional outbreaks, distribution of disease

3. Handling & consumption of bush meat

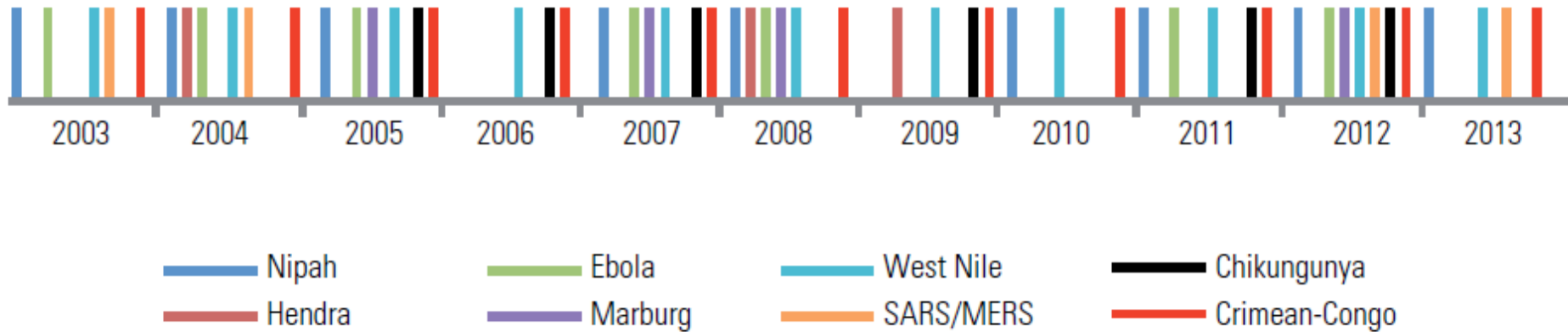
ex) Outbreak of Ebola virus



4. Virus activity expanded



5. Vector activity expanded (bats)



MERS: Middle East respiratory syndrome
SARS: severe acute respiratory syndrome

Schematic summary of zoonotic viral disease outbreaks in the last decade

The color bars above the line indicate the different disease events whereas the small bars below the line define the boundary of each calendar year.

(*Rev. sci. tech. Off. int. Epiz.*, 2014, 33 (2), 569–581)

What kind of animals transmit zoonosis?

Farm Animals

- Cattle
- Swine
- Goats
- Cats & dogs
- Poultry

Wild Animals

- Ticks
- Squirrels
- Raccoons
- Mice/rodents
- Bats
- Others

Bats and emerging zoonotic viruses

: A New Frontier of Emerging Infectious Diseases

“Are Bats Special As Viral Hosts?”

- High species diversity(925/4,600 mammal(20%)),
- Long life span(~25 years),
- The capacity for long-distance dispersal(travel 200-400mile),
- Dense roosting aggregations(colony size),
- The use of torpor & hibernation
(to conserve energy during cool nights and winter months)



Bats and emerging zoonotic viruses

: A New Frontier of Emerging Infectious Diseases

“Are Bats Special As Viral Hosts?”

Hosting more viruses per species than rodents.

: Bats Carry More Human-Infecting Virus than Rodents

Order	mean no. host/virus	Total viruses		Zoonotic viruses	
		No.	mean/host	No.	mean/host
Bats	4.51	137	2.71	61	1.79
Rodents	2.76	179	2.48	68	1.48

Source : *USDA National Wildlife Research Center - Staff Publications. Paper 1527.*

Bats and emerging zoonotic viruses

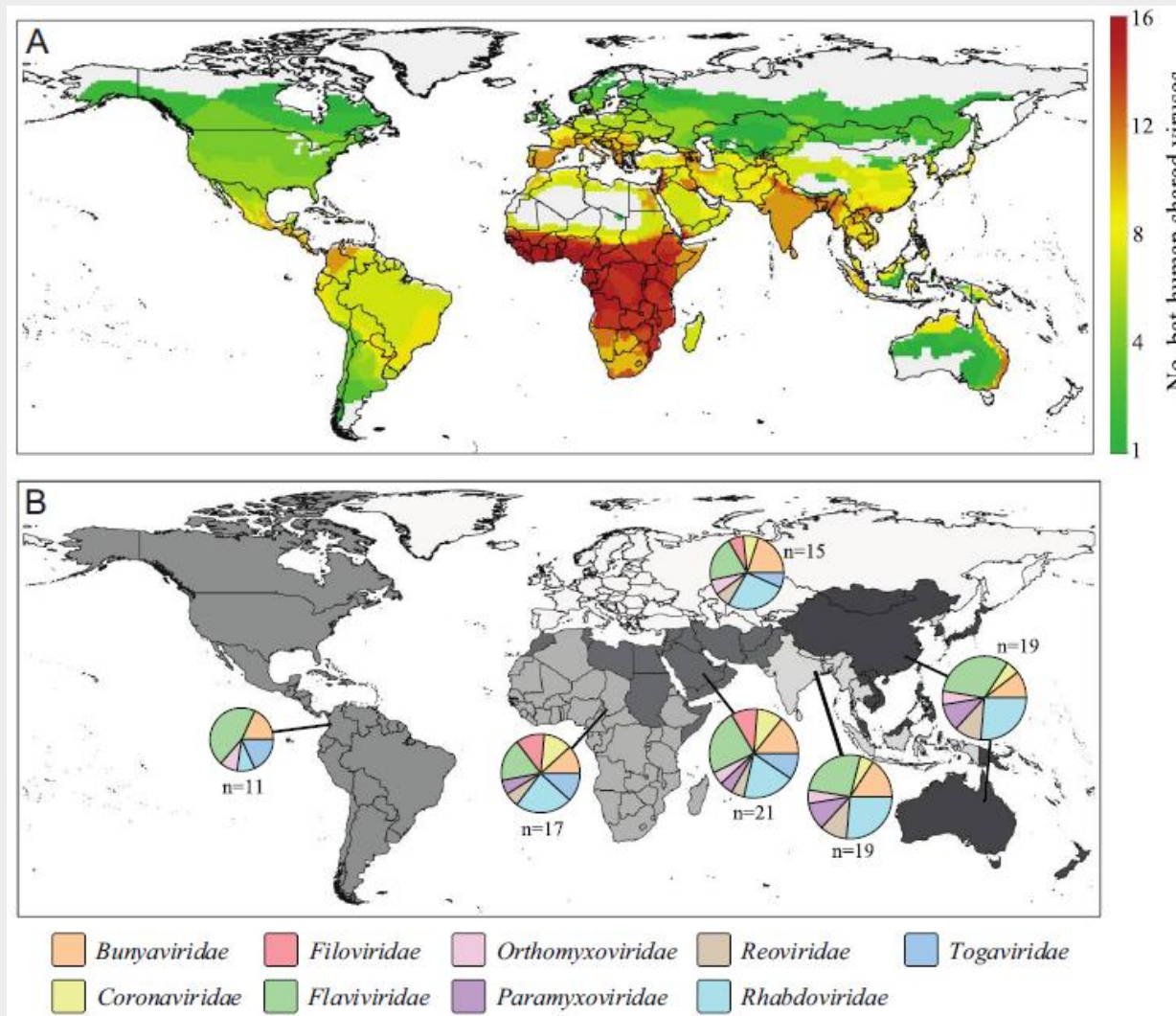


Figure : Distributions of bat-human virus sharing showing numbers of bat-human shared viruses at 17 grid resolution (A)—color represents a linear scale from 1 (green) to 16 (red)—and composition of viruses by family within the six World Health Organization World Regions (B), where the size of the charts is proportional to the number of viruses. Shading denotes region (from lightest to darkest: Europe, South Asia, Africa, Americas, Eastern Mediterranean, Western Pacific), while colors denote viral family (see key).



Rousettus aegyptiacus(Egyptian rousette)



Pteropus alecto(black flying fox)

동물 및 축산물
검역통계

수출입 동축산물 검역현황

- 품목별 수출입현황
- 품목-국가별 수출입현황
- 국가-품명별 수출입현황
- 품목-국가별 불합격수입현황
- 국가-품명별 불합격수입현황
- 품목별 불합격수입현황

2013년 수입축산물 검역현황

2014년 수입축산물 검역현황

열처리 가공육 수입검역현황

수출입 동축산물 검역 현황 조회일자 : 2016-06-10 선택

- 수출입현황은 전체 실적에 대하여 데이터를 제공, 현장검역 데이터 포함한 것입니다.
- 전월 자료는 다음달 10일 이후부터 조회가 가능합니다.
- 당해년도 통계자료는 통계 확정전 잠정치임을 알려드리며 참고용으로만 사용하시기 바랍니다.

품목별 수출입현황

통계분류: 수입동물
 검사기간: 2013년 2월 부터 2016년 1월 까지
 품목/품명: 포유류 / 박쥐 국가: === 전체 ===

조회하기 엑셀

품목	품명	건수	두수(마리/군)
포유류	박쥐	3	316
	품목계 미리	3	316
	품목계 리	0	0
총계 미리		3	316
총계 리		0	0

[초특가] 과일박쥐-한정수량!!입고완료!!!!!!



상품명 : [초특가]과일박쥐-한정수량!!입고완료!!!!!!

판매가격 : 260,000원

적립금액 : 2,500원

남은수량 : 품절

--- 배송방법 선택(필수) ---

- 택배
- 고속버스택배(+10,000원)
- 서울/수도권 퀵배송(배송비후불)

지방

과일박쥐 (수입완료!! 한정분양) 인기상품

판매가격 : 250,000원

배송방법선택 : --옵션 선택--

안전포장선택 : --옵션 선택--

총 상품 금액 0 원



마우스를 올려보세요

Researchers amplify antibiotic of last resort hoping to halt superbugs

By Elizabeth Roberts, CNN

🕒 Updated 1454 GMT (2254 HKT) May 30, 2017



Source: CNN

New "superbug" no antibiotic can combat arrives in U.S. 03:23

News & buzz



Donald Trump likes to 'joke' about a lot of things that aren't...



Hot car deaths reach record numbers in July

Antimicrobial Resistance (AMR)

Why is it of global concern?

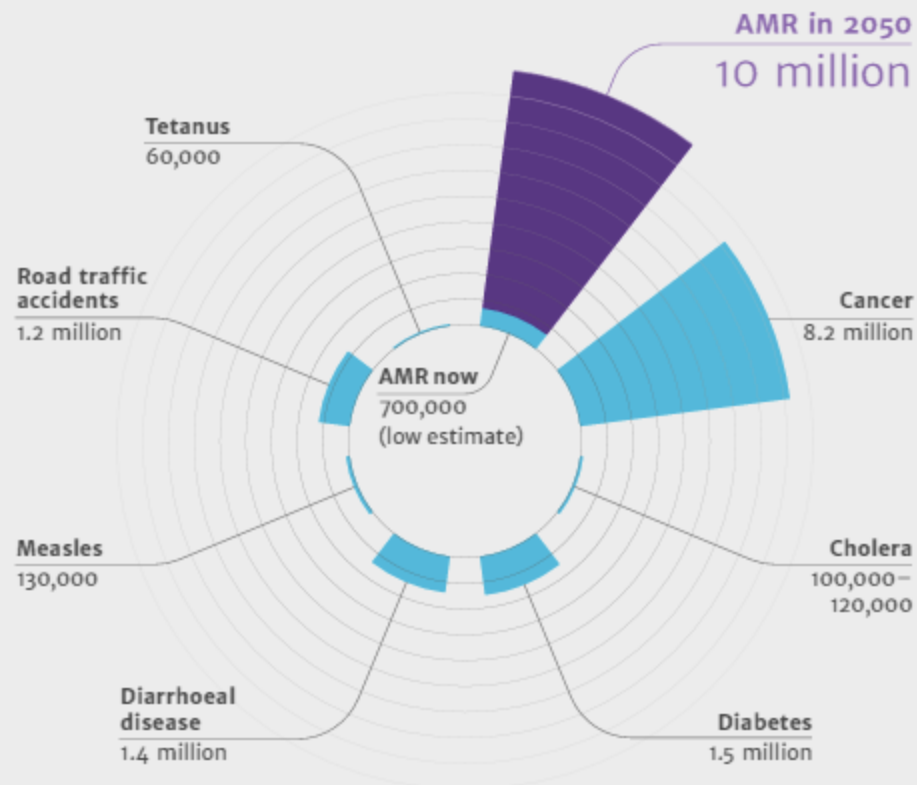
- **There is a lack of coherent global approaches to prevention and containment**

The human, animal and plant sectors have a **shared responsibility** to prevent or minimize the development of antimicrobial resistance by both human and non-human pathogens

- **Harmonization of national antimicrobial resistance surveillance and monitoring programmes, and implementation of international coordination programmes**

- **Implementation of risk assessment**

Deaths attributable to AMR every year compared to other major causes of death



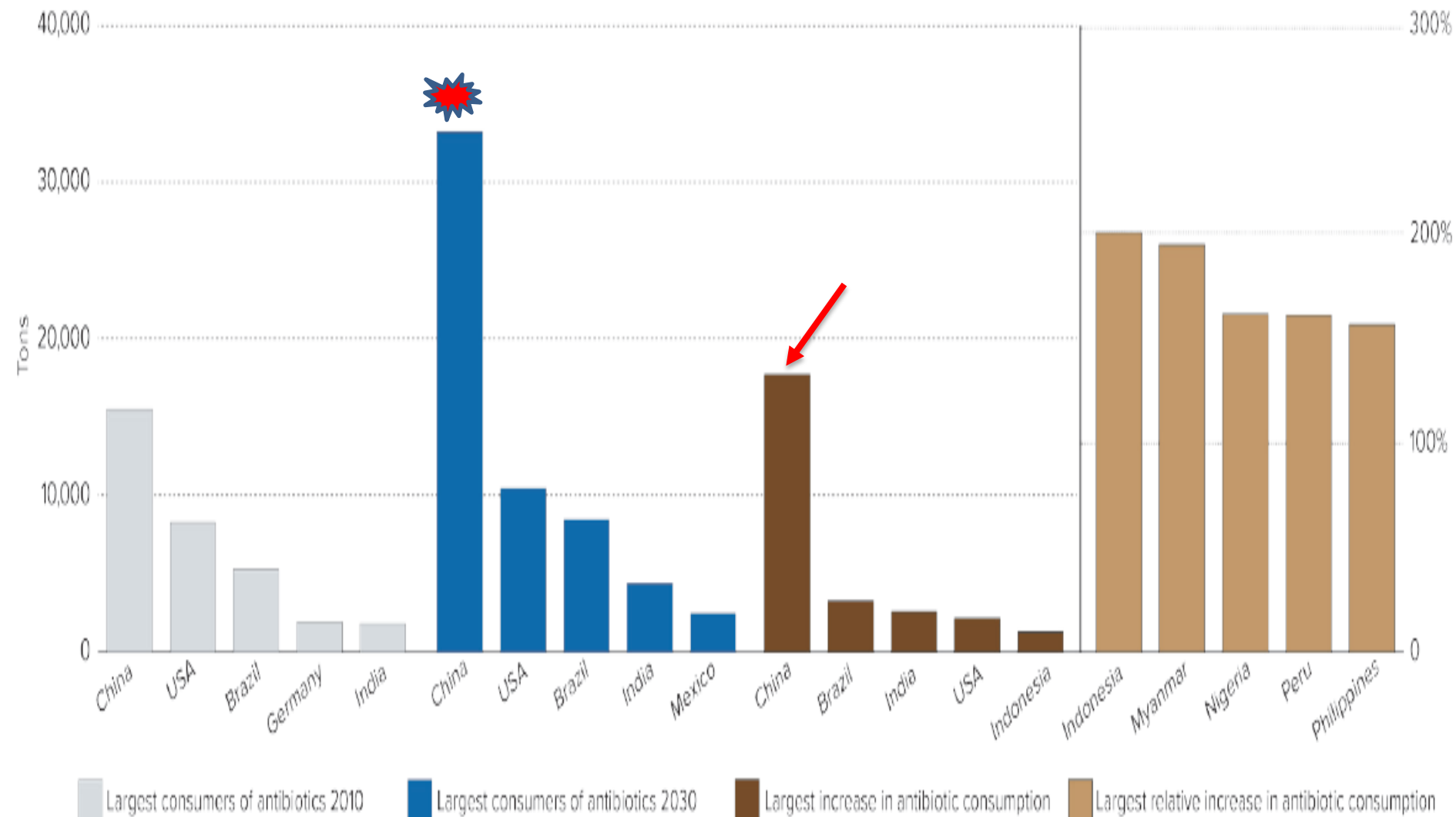


Fig. 1. Antibiotic consumption in livestock in high-consuming countries, 2010–2030 (projected for 2030). Adapted from Van Boeckel et al. 2015



CDC 2013 / WHO 2014 19 threats	Animal Link 7 links
URGENT THREATS (3)	
<i>Clostridium difficile</i>	Possible
Carbapenem-resistant Enterobacteriaceae (CRE)	
Drug-resistant <i>Neisseria gonorrhoeae</i>	
SERIOUS THREATS (12)	
Multidrug-resistant <i>Acinetobacter</i>	
<i>Drug-resistant Campylobacter</i>	Possible
Fluconazole-resistant <i>Candida</i> (a fungus)	
<i>Extended spectrum β-lactamase producing Enterobacteriaceae (ESBLs)</i>	Possible
<i>Vancomycin-resistant Enterococcus (VRE)</i>	Possible
Multidrug-resistant <i>Pseudomonas aeruginosa</i>	
<i>Drug-resistant Non-typhoidal Salmonella</i>	Possible
Drug-resistant <i>Salmonella</i> Typhi	
Drug-resistant <i>Shigella</i>	
<i>Methicillin-resistant Staphylococcus aureus (MRSA)</i>	Possible
Drug-resistant <i>Streptococcus pneumoniae</i>	
Drug-resistant tuberculosis	
CONCERNING THREATS (4)	
Vancomycin-resistant <i>Staphylococcus aureus</i> (VRSA)	
Erythromycin-resistant Group A <i>Streptococcus</i>	
Clindamycin-resistant Group B <i>Streptococcus</i>	
<i>Escherichia coli, resistance to FQs</i>	Possible

Swine MRSA & Human infection (HA/CA/LA)

FROM THE FARM AND BACK AGAIN

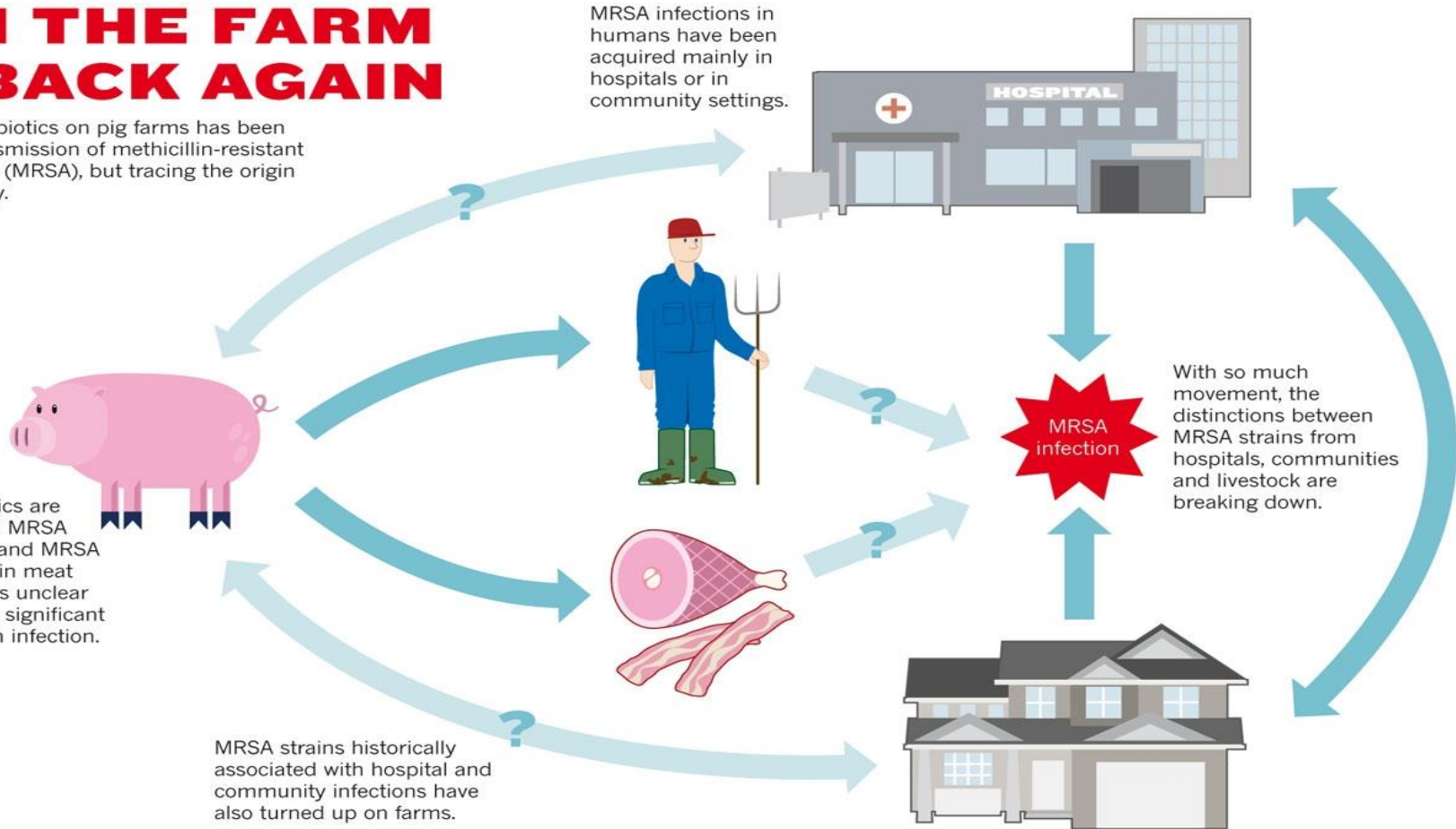
The liberal use of antibiotics on pig farms has been implicated in the transmission of methicillin-resistant *Staphylococcus aureus* (MRSA), but tracing the origin of an infection is tricky.

Pigs fed antibiotics are known to spread MRSA to farmworkers, and MRSA strains show up in meat products, but it is unclear whether this is a significant source of human infection.

MRSA strains historically associated with hospital and community infections have also turned up on farms.

MRSA infections in humans have been acquired mainly in hospitals or in community settings.

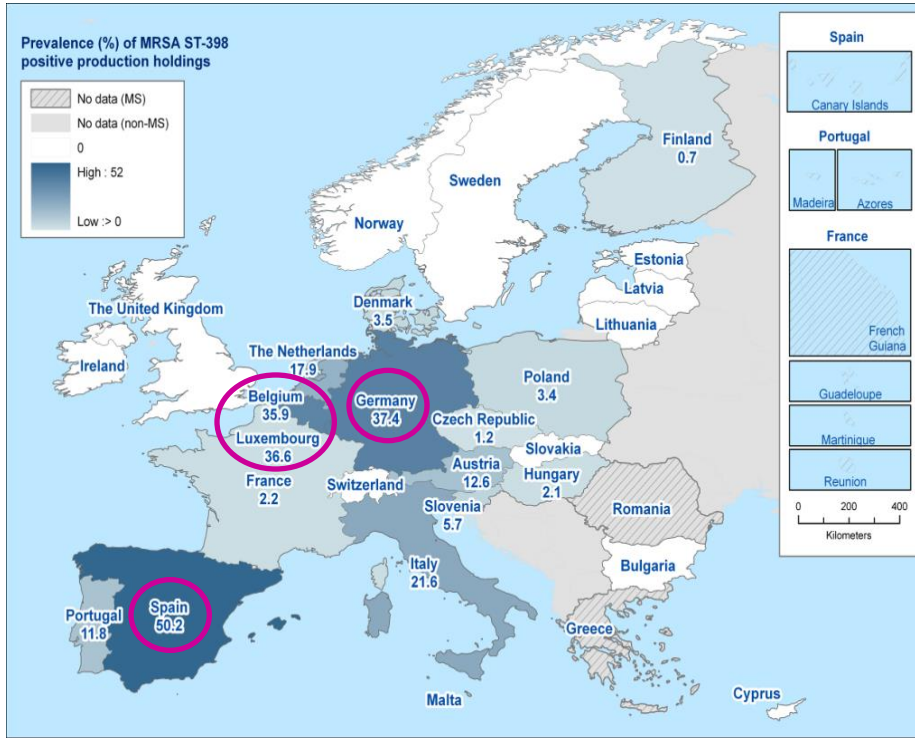
With so much movement, the distinctions between MRSA strains from hospitals, communities and livestock are breaking down.



(Nature, Mole B, 2013)

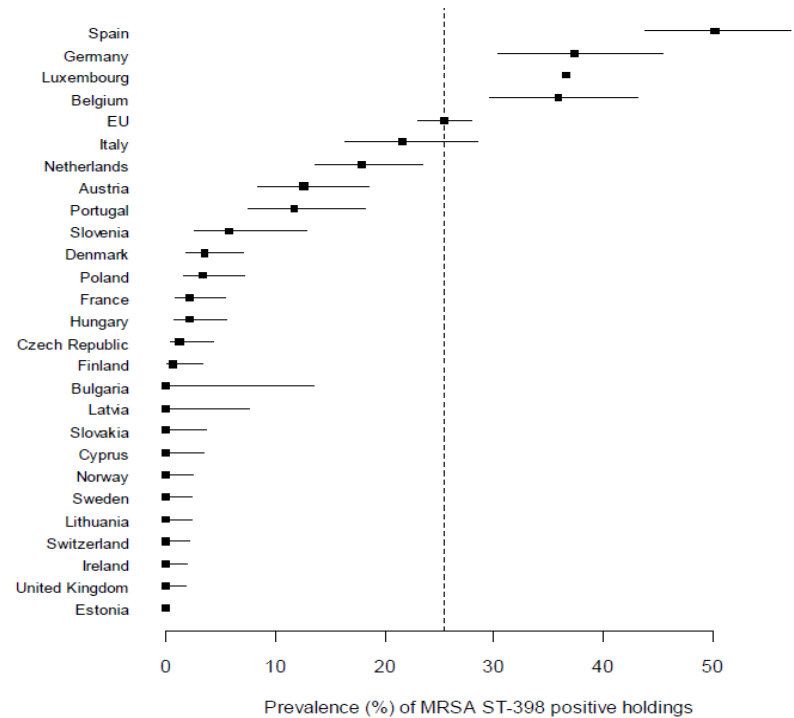
Swine MRSA in EU

EU countries(26)



Prevalence: 26.9%(0-50.2%)

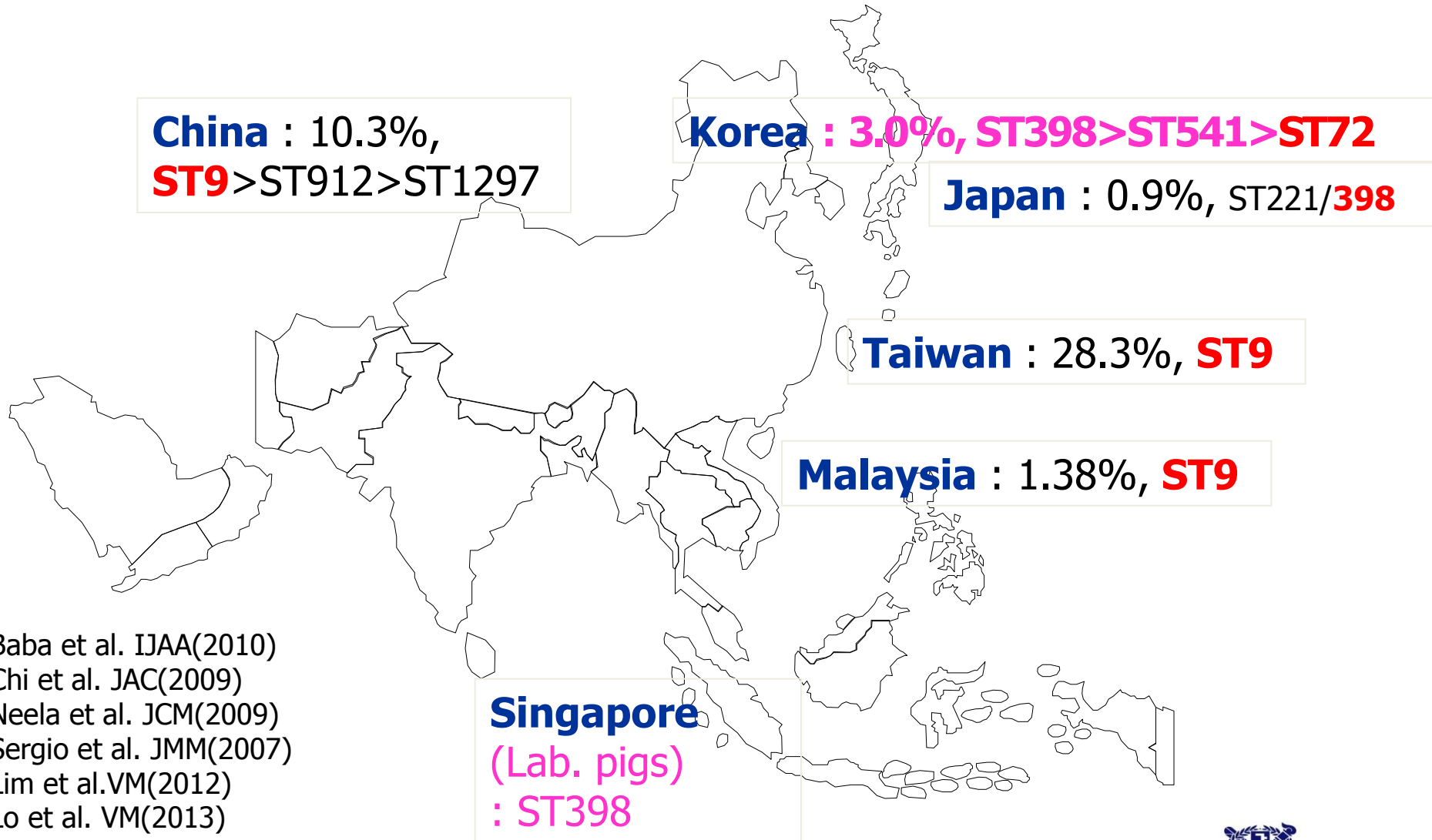
MLST



ST398 : 92.5%

(EFSA Journal 2009)

Swine MRSA in Asian Countries



Baba et al. IJAA(2010)
Chi et al. JAC(2009)
Neela et al. JCM(2009)
Sergio et al. JMM(2007)
Lim et al.VM(2012)
Lo et al. VM(2013)

Prevalence of MRSA in Asia

China:

Pig; 6.4-16.7%

Pig farmers; 1.7 -10.7%

w/o contact 1.4% w/ contact 14.3%

Korea:

Breeder & Imported pig ; high MRSA

Japan:

ST221/ST398/6/9

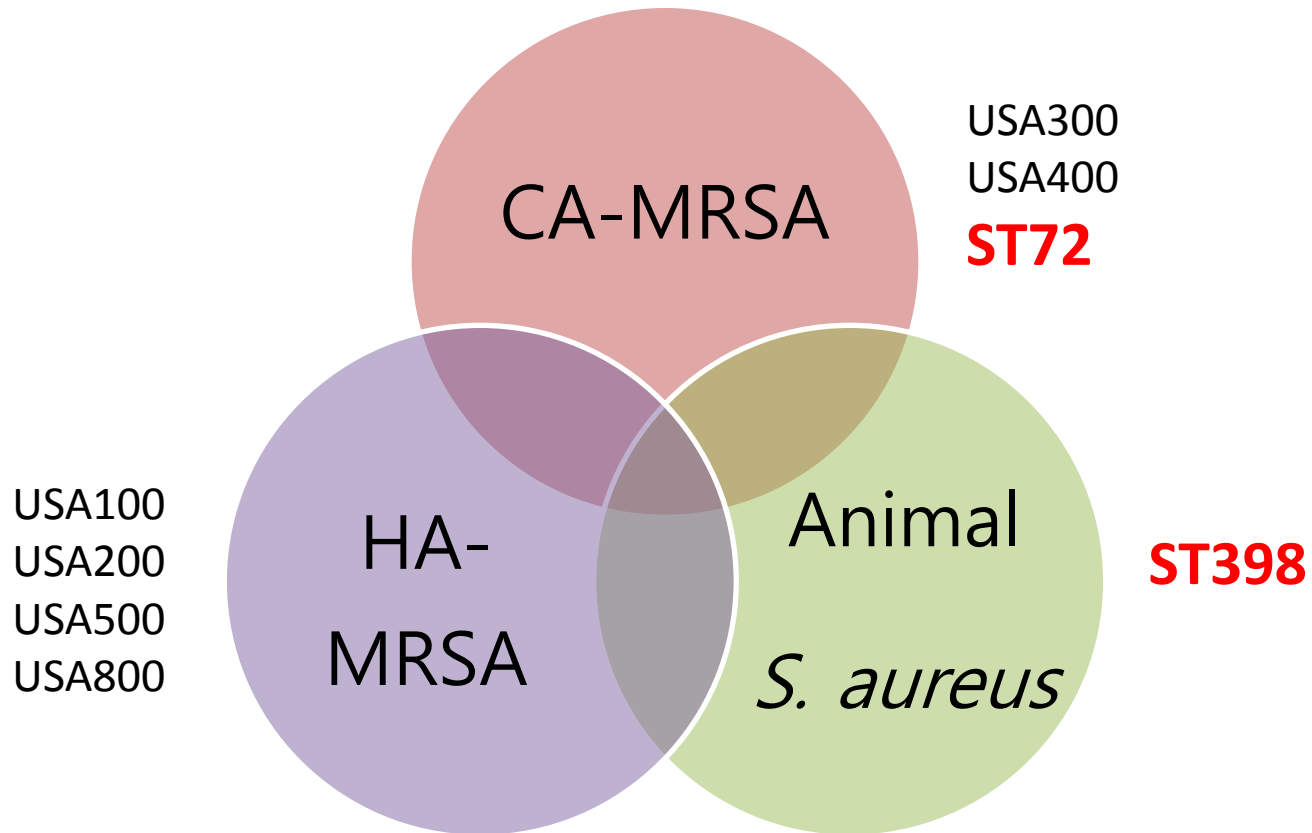
Thailand: ST9

Malaysia: ST9

Nepal: ST9 w/ bovine mastitis

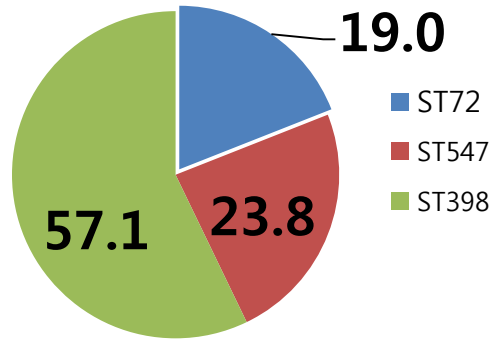
(17th ISSSI 2016, Korea)

Re-emerging MRSA in US



Human & non-human MRSA in Korea

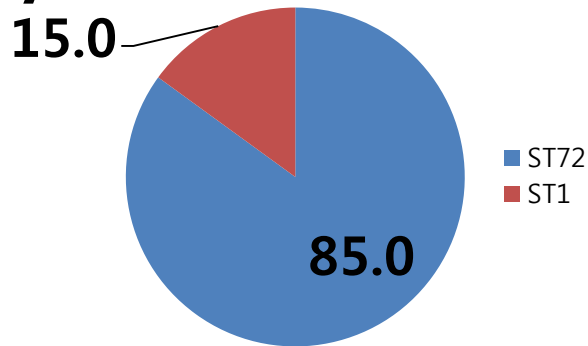
Pigs



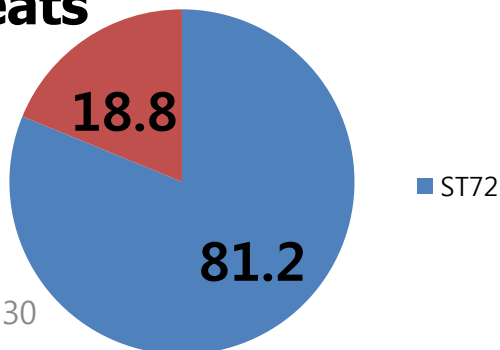
➤ ***ST72 is a predominant type both humans and non-humans***

- Human : 35%
- Non-Human : pigs 19%, **cattle 85%**
meats 81%

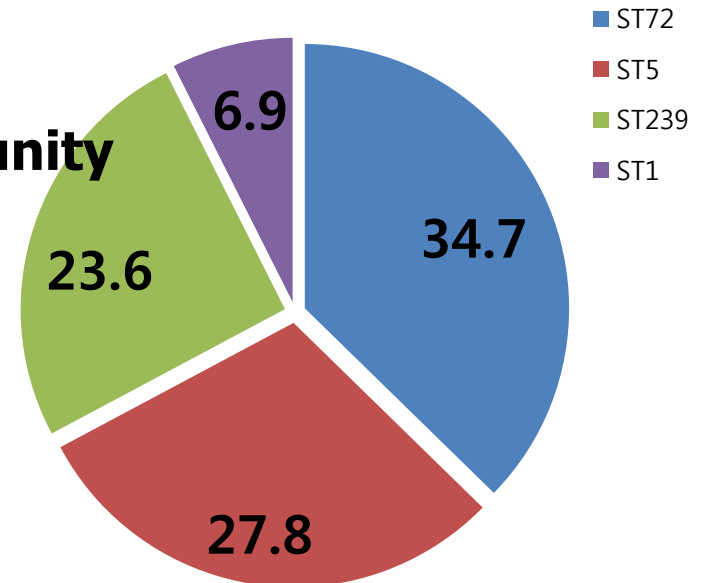
Dairy cattle



Raw meats



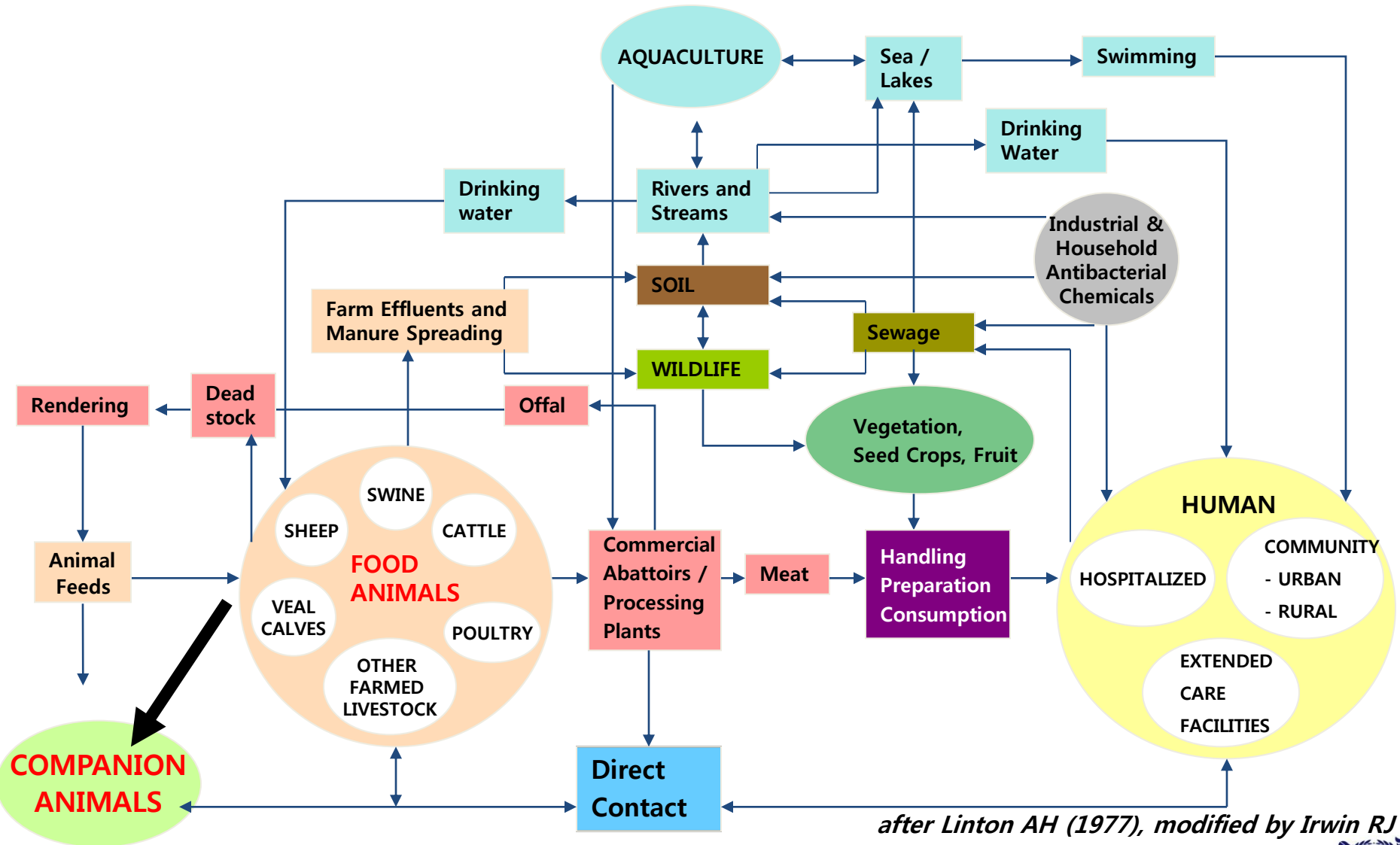
Human Community



Lim et al. VM(2012); Nam et al. FPD(2011)
Lim et al. JMB(2010)); Kim et al.JAC(2007)

- *Although the prevalence of MRSA in food animal products in Korea is still maintained at the low level, **occurrence and increase in multiple resistant LA MRSA lineage and virulent HA MRSA lineage** can be potential threat to public as animal related job workers and consumers are constantly exposed to these MRSA lineages.*

Epidemiology of antimicrobial resistance



after Linton AH (1977), modified by Irwin RJ



Companion animal and AMR





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Diagnostic Microbiology and Infectious Disease

journal homepage: www.elsevier.com/locate/diagmicrobio



Notes

Dissemination of multidrug-resistant *Escherichia coli* in Korean veterinary hospitals[☆]

Jeong Hwa So^a, Juwon Kim^b, Il Kwon Bae^b, Seok Hoon Jeong^{b,*}, So Hyun Kim^c, Suk-kyung Lim^a, Yong Ho Park^d, Kyungwon Lee^b

Zoonoses and Public Health



Journal of Veterinary
24(5) 924–931
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sagepub.com/journals
DOI: 10.1177/104066:
<http://jvdi.sagepub.com>

SHORT COMMUNICATION

Occurrence of antimicrobial resistance and virulence genes, and distribution of enterococcal clonal complex 17 from animals and human beings in Korea

Ka Hee Kwon, Sun Young Hwang, Bo Youn Moon, Young Kyung Park, Sook Shin, Cheol-Yong Hwang, Yong Ho Park¹

Detection of CC17 *Enterococcus faecium* in Dogs and a Comparison with Human Isolates

K. H. Kwon, B. Y. Moon, S. Y. Hwang and Y. H. Park

Department of Microbiology and Brain Korea 21 Program for Veterinary Science, College of Veterinary Medicine, Seoul National University, Seoul, Korea

Impacts

- This is the first report of *Enterococcus faecium* CC17 isolated from dogs with enterococcal infections in Korea.
- This is the first genetic comparison of *E. faecium* isolated from canine and human patients based on results from pulsed field gel electrophoresis (PFGE) and multilocus sequence typing (MLST).
- The results suggest that the CC17 lineage is more able to infect dogs as well as humans than other lineages.



Journal of Veterinary Diagnostic Investigation
24(3) 489–498
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DOI: 10.1177/1040638712440985
<http://jvdi.sagepub.com>

Genetic and phenotypic characterization of methicillin-resistant staphylococci isolated from veterinary hospitals in South Korea

Bo Youn Moon, Jung-Ho Youn, Sook Shin, Sun Young Hwang,¹ Yong Ho Park¹

Molecular Characterization of Extended-Spectrum- β -Lactamase-Producing and Plasmid-Mediated AmpC β -Lactamase-Producing *Escherichia coli* Isolated from Stray Dogs in South Korea

Migma Dorji Tamang, Hyang-Mi Nam, Geum-Chan Jang, Su-Ran Kim, Myung Hwa Chae, Suk-Chan Jung, Jae-Won Byun, Yong Ho Park, and Suk-Kyung Lim

Bacterial Disease Division, Animal, Plant, and Fisheries Quarantine and Inspection Agency, Anyang, Gyeonggi-do, Republic of Korea

J. Microbiol. Biotechnol. (2014), 24(3), 386–393
<http://dx.doi.org/10.4014/jmb.1310.10088>

jmb

Characterization of Veterinary Hospital-Associated Isolates of *Enterococcus* Species in Korea

Yeon Soo Chung^{1†}, Ka Hee Kwon^{1†}, Sook Shin¹, Jae Hong Kim¹, Yong Ho Park¹, and Jang Won Yoon^{1,2*}

¹Department of Veterinary Microbiology, College of Veterinary Medicine, Seoul National University, Seoul 151-742, Republic of Korea

²College of Veterinary Medicine, Kangwon National University, Chuncheon 200-701, Republic of Korea

blaDHA-1/ CMY-2 β -lactamase-producing E. coli detected in dogs

Similar PFGE pattern of AR Enterococci have been found in companion animal, their owners and vet doctors

Isolation and characterization of antimicrobial-resistant *Escherichia coli* from national horse racetracks and private horse-riding courses in Korea

Yeon Soo Chung¹, Jae Won Song¹, Dae Ho Kim¹, Sook Shin¹, Young Kyung Park¹, Soo Jin Yang², Suk Kyung Lim³, Kun Taek Park^{1,*}, Yong Ho Park^{1,*}

¹Department of Veterinary Microbiology, BK21 PLUS Program for Creative Veterinary Science Research, and Research Institute for Veterinary Science, College of Veterinary Medicine, Seoul National University, Seoul 08826, Korea

²Department of Animal Science and Technology, College of Biotechnology and Natural Resource, Chung-Ang University 2nd Campus, Anseong 17546, Korea

³Animal and Plant Quarantine Agency, Anyang 14086, Korea

Limited information is available regarding horse-associated antimicrobial resistant (AR) *Escherichia (E.) coli*. This study was designed to evaluate the frequency and characterize the pattern of AR *E. coli* from healthy horse-associated samples. A total of 143 *E. coli* (4.6%) were isolated from 3,078 samples collected from three national racetracks and 14 private horse-riding courses in Korea. Thirty of the *E. coli* isolates (21%) showed antimicrobial resistance to at least one antimicrobial agent, and four of the AR *E. coli* (13.3%) were defined as multi-drug resistance. Most of the AR *E. coli* harbored AR genes corresponding to their antimicrobial resistance phenotypes. Four of the AR *E. coli* carried class 1 integrase gene (*intI1*), a gene associated with multi-drug resistance. Pulsed-field gel electrophoretic analysis showed no genetic relatedness among AR *E. coli* isolated from different facilities; however, cross-transmissions between horses or horses and environments were detected in two facilities. Although cross-transmission of AR *E. coli* in horses and their environments was generally low, our study suggests a risk of transmission of AR bacteria between horses and humans. Further studies are needed to evaluate the risk of possible transmission of horse-associated AR bacteria to human communities through horse riders and horse-care workers.

Keywords: *Escherichia coli*, antimicrobial resistance, class 1 integron, cross-transmission, horse

**AR-ESBL-*E.coli*
have been found in
either horses,
environment and
human-in-contact**



Contents lists available at ScienceDirect

Comparative Immunology, Microbiology and Infectious Diseases

journal homepage: www.elsevier.com/locate/cimid



Prevalence and characterization of *Staphylococcus aureus* and *Staphylococcus pseudintermedius* isolated from companion animals and environment in the veterinary teaching hospital in Zambia, Africa

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ABSTRACT

The Republic of Zambia consists of only one veterinary teaching school at the University of Zambia (UNZA) where students and veterinarians are exposed to many bacterial pathogens including *Staphylococcus aureus* (SA) and *Staphylococcus pseudintermedius* (SP). The aim of this study was the characterization and antimicrobial susceptibility profile of eleven SA and 48 SP isolates from the veterinary hospitals' in- and outpatients and the environment. No isolate was resistant to ceftiofime by disk diffusion test and the corresponding resistance gene *mecA* was not found. In contrast, the resistance rates of SA to penicillin (63.6%) and trimethoprim-sulfamethoxazole (36.4%) and SP to penicillin (52.1%) and tetracycline (25.0%) were the highest. A variety of sequence types (STs) without a predominant type including numerous novel types were determined, especially for SP (39.6%). The *spa* typing provided a clonal assignment for all SAs (100%) and 24 SPs (50%) with three and two novel types, respectively. This study has provided an overview of SA and SP in the veterinary teaching hospital at UNZA. However, for a better understanding of these species regarding pathogenesis and transmission, further studies on the prevalence and characterization of SA and SP from veterinary staff, pet owners, and farm animals in Zambia is needed.

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AR *S.aureus* and *S. pseudintermedius* have been detected in companion animal and their owners.

Human-to-Dog Transmission of Methicillin-Resistant *Staphylococcus* *aureus*

Engeline van Duijkeren,^{*}

Maurice J.H.M. Wolfhagen,[†] Adrienne T.A. Box,[‡]
Max E.O.C. Heck,[§] Wim J.B. Wannet,[§]
and Ad C. Fluit[‡]

Methicillin-resistant *Staphylococcus aureus* (MRSA) was cultured from the nose of a healthy dog whose owner was colonized with MRSA while she worked in a Dutch nursing home. Pulsed-field gel electrophoresis and typing of the staphylococcal chromosome cassette *mec* (SCC*mec*) region showed that both MRSA strains were identical.

Emerging Infectious Diseases

Vol. 10, No. 12, December 2004



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BRAZILIAN JOURNAL OF MICROBIOLOGY

<http://www.bjmicrobiol.com.br/>



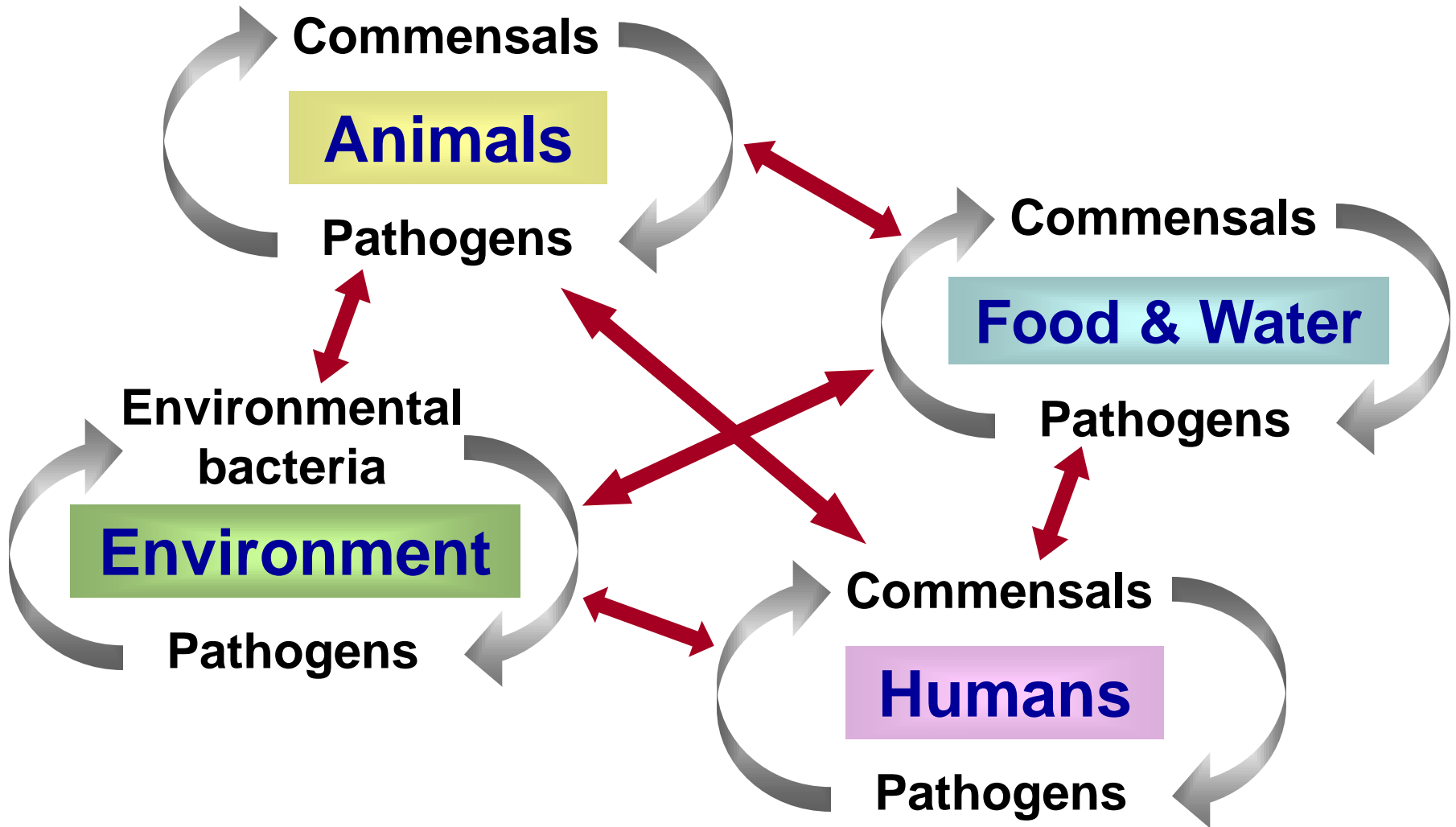
Medical Microbiology

Resistance patterns, ESBL genes, and genetic relatedness of *Escherichia coli* from dogs and owners



A.C. Carvalho^{a,b,*}, A.V. Barbosa^b, L.R. Arais^b, P.F. Ribeiro^b, V.C. Carneiro^b,
A.M.F. Cerqueira^b

Transmission of AMR



S. Korea Elected Chair of CODEX Ad Hoc Task Force

- Korea has been elected to head an ad hoc T/F of CODEX (July 3th, 2016)
- Korea will lead efforts in producing global guidelines regarding *the reduction and prevention of the use of antimicrobial resistant microorganisms in environment, farm and fishery products, and food from 2017-2020 (4yrs)*
- Create global guidelines to monitor the use of **antimicrobial resistant materials** by 2020.

국제식품규격위원회 항생제 내성 특별위원회 (CODEX TFAMR)

CAUSES OF ANTIBIOTIC RESISTANCE



Antibiotic resistance happens when bacteria change and become resistant to the antibiotics used to treat the infections they cause.



Over-prescribing of antibiotics



Patients not finishing their treatment



Over-use of antibiotics in livestock and fish farming



Poor infection control in hospitals and clinics



Lack of hygiene and poor sanitation



Lack of new antibiotics being developed

www.who.int/drugresistance

#AntibioticResistance



Ad hoc Codex Intergovernmental Task Force on Antimicrobial Resistance (TFAMR)

FAO/WHO ID No:	CX-804
Reference:	CX/AMR
Terms of Reference:	<p style="text-align: right;">2017</p> <p>Objectives To develop science-based guidance on the management of foodborne antimicrobial resistance, taking full account of the WHO Global Action Plan on Antimicrobial Resistance, in particular objectives 3 and 4, the work and standards of relevant international organizations, such as FAO, WHO and OIE, and the One-Health approach, to ensure that Members have the necessary guidance to enable coherent management of antimicrobial resistance along the food chain.</p> <p>Terms of reference (i) To review and revise as appropriate the Code of Practice to Minimise and Contain Antimicrobial Resistance (CAC/RCP 61-2005) to address the entire food chain, in line with the mandate of Codex. (ii) To consider the development of Guidance on Integrated Surveillance of Antimicrobial Resistance, taking into account the guidance developed by the WHO Advisory Group on Integrated Surveillance of Antimicrobial Resistance (AGISAR) and relevant OIE documents.</p> <p>NOTE: The Task Force shall complete its work within three (max four sessions), starting in 2017.</p>
Status:	Active
Host:	Republic of Korea

CODEX 항생제 내성 특별위원회 의장 위촉식 및 제1차 전문가 자문회의 개최

- 식품의약품안전처(처장 손문기)는 국제식품규격위원회(CODEX) '항생제 내성 특별위원회' 의장으로 박용호 교수(서울대 수의학과)를 위촉하고, 3월 10일 특별위원회 운영을 위한 제1차 전문가 자문회의를 개최한다고 밝혔다.
- 의장으로 위촉된 박용호 교수는 오는 '18년까지 2년 간 항생제 내성 특별위원회 의장으로서 국제회의를 주재하고 항생제 내성 저감화 등을 위한 논의를 주도하는 역할을 맡게 된다.

박용호 서울대 교수, CODEX 항생제 내성 특별위원장 선임

한국, CODEX 항생제 내성 특별위원회 의장국, 내성 저감 국제논의 이끈다

등록 : 2017.03.10 12:34:53 수정 : 2017.03.10 12:34:53 윤성준 기자 ysj@dailyvet.co.kr



식품의약품안전처가 국제식품규격위원회(CODEX) 항생제 내성 특별위원장으로 서울대학교 수의과대학 박용호 교수를 위촉했다고 10일 밝혔다.

“One Health” approach



Human health communities



Animal health communities



Environmental communities



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Kim KY

QIA

Jung BY

Lim SK

Jung SC



Gunma University Graduate School of Medicine

Yasuyoshi Ike

Dr. Tomita/Dr. Tanimoto

Univ. of Idaho

Bohach G

Seo KS

Lim JY

So JH



Korea FDA/CDC