An Introduction to One Health

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Lecture - 04

1. Integrated Human and Animal Disease Surveillance Systems

2. Recent Success of One Health in Control of Emerging Infectious Diseases and the Application of One Health in the Control of Endemic Zoonosis in Resources-Poor Communities

Today the title of my talk is one health. And I would be walking you through the various events, like the zoonotic spill over's from animals to humans which have happened in the past describing a few events in greater details which have happened in India. And also, I would then take you through the modalities of surveillance that we need to set up now to improve our pandemic preparedness.

And how we need to work holistically with various stakeholders and partners to achieve the goal of comprehensive surveillance in a one health approach.

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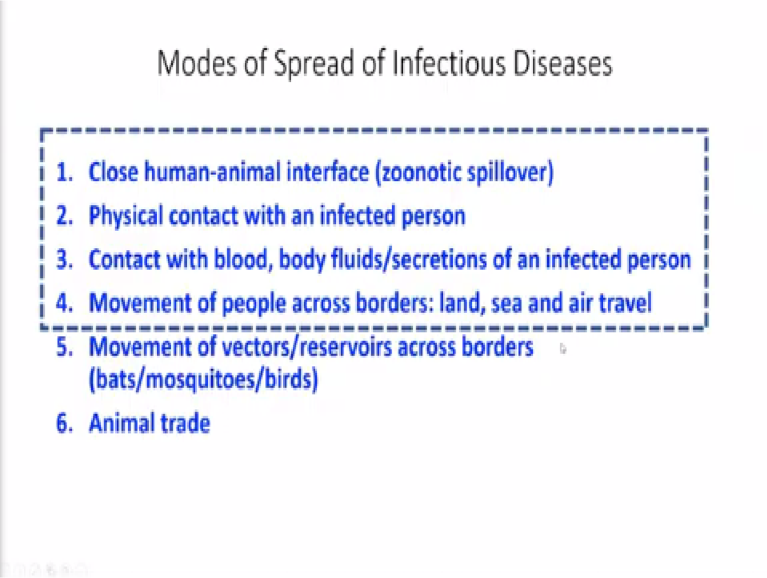

Modes of Spread of Infectious Diseases

1. Close human-animal interface (zoonotic spillover)
2. Physical contact with an infected person
3. Contact with blood, body fluids/secretions of an infected person
4. Movement of people across borders: land, sea and air travel
5. Movement of vectors/reservoirs across borders (bats/mosquitoes/birds)
6. Animal trade

So, there are various known modes of spread of infectious diseases. The most common mode of spread of new infectious diseases that we are now seeing, since the last I would say two decades is the close human to animal interface which is also known as zoonotic spill over. And there have been several diseases, either new or re-emerged diseases which have spread through this route.

Then the other most common mode of spread is physical contact with an infected person, contact with blood, body fluids or secretions of an infected person. Then in the recent past, due to increased air, sea and land travel, there has been lot of spread of infectious diseases due to movement of people across the borders. There are several diseases which have spread rampantly by vectors or reservoirs, like bats, mosquitoes, even wild birds or migratory birds. Then there are instances, when where diseases have spread through animal trade as well.

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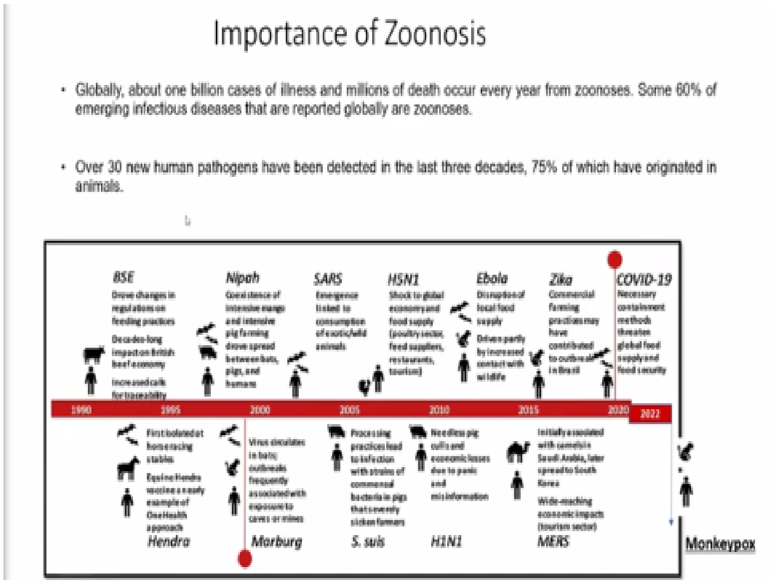

Importance of Zoonosis

- Globally, about one billion cases of illness and millions of death occur every year from zoonoses. Some 60% of emerging infectious diseases that are reported globally are zoonoses.
- Over 30 new human pathogens have been detected in the last three decades, 75% of which have originated in animals.

So, if we look at the what have been the zoonotic diseases in the recent past when globally about 1 million cases of illnesses and millions of deaths occur every year from zoonotic infections. And 60% of these are emerging infectious diseases that are reported globally as zoonosis. And there are over 30 new human pathogens, which have been detected in the last three decades.

Perhaps due to the various modalities that I elucidated in the last slide, 75% of which have originated in animals, which is a huge cause of concern for all of us. Now this is a running line which shows, that since the last three decades how different infections have spread from animals to humans. Starting from bovine spongy form, Encephalitis, Hendra, Nipah, Marburg, SARS as S. suis.

Then avian influenza outbreaks, human influenza outbreaks, Ebola, MERS, Corona virus, then Zika and of course, Covid-19 which has wrecked the entire world. And very recently, in 2022 we saw a global spread of monkey pox disease.

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Now, when we talk of a one health approach. Why do we talk of one health? The reason is that, you are seeing that we have several zoonotic infections which have rampantly spread from animals to humans through various modes. Be it travel, be it vectors, be it close contact with animals and several other modes. So, unless we follow a one health approach, that is we are cognizant of health in animals, in humans, in environment, in vectors.

Unless all that is achieved, we cannot ensure safety to mankind. So, for that it is very important to follow a very comprehensive one health approach. Be it in terms of detection, treatment, disease prevention and various other aspects.

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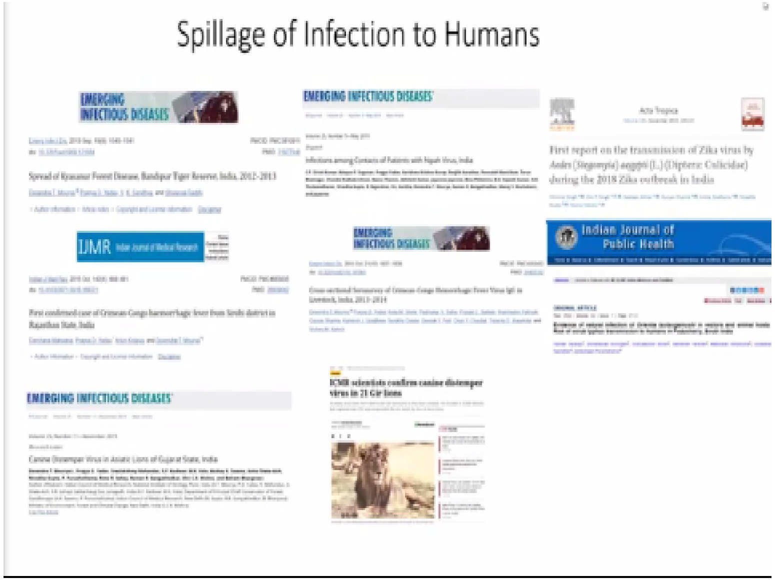

Spillage of Infection to Humans

EMERGING INFECTIOUS DISEASES

Spread of Kyasanur Forest Disease, Bandipur Tiger Reserve, India, 2012–2013

IJMR Indian Journal of Medical Research

First confirmed case of Crimean-Congo haemorrhagic fever from Sirohi district in Rajasthan State, India

EMERGING INFECTIOUS DISEASES

Canine Distemper Virus in Asiatic Lions of Gujarat State, India

EMERGING INFECTIOUS DISEASES

Infections among Contacts of Patients with Nipah Virus, India

EMERGING INFECTIOUS DISEASES

Cross-sectional Serosurvey of Crimean-Congo Hemorrhagic Fever Virus IgG in Livestock, India, 2013–2014

ICMR scientists confirm canine distemper virus in 21 Gir lions

Acta Tropica

First report on the transmission of Zika virus by Aedes (Stegomyia) aegypti (L.) (Diptera: Culicidae) during the 2018 Zika outbreak in India

Indian Journal of Public Health

So, this is a slide, which depicts that how there has been spillage of infections in the recent past, from animals to humans. This is one slide with which depicts that there was spread of Kyasanur forest disease, which is a disease which is found in humans, and or were spread from Kyasanur forest in Karnataka from monkeys, infected monkeys to humans. Now this disease was also found in tigers, in Bandipore tiger reserve in India.

And the source of infection could not be known. But this is not a population which inherently gets KFD either it was reverse synopsis from humans to animals, or contact with some infected monkeys, but the cause could not be deciphered. Then there was first case of Crimean Congo haemorrhagic fever, in a district in Rajasthan, Sirohi district in Rajasthan, which had actually never seen cases of Crimean Congo haemorrhagic fever.

And we all know, that there are a lot of cattle species, which are asymptomatically infected with Crimean Congo haemorrhagic fever. And the ticks that reside on these cattle, can bite humans and spread infection to them. So, again, this could have been the possible route of transmission. Then, we saw an outbreak of canine distemper virus in Asiatic lions of Gujarat. Wherein, the canine distemper virus was responsible for death of several Asiatic lions.

And this aetiology was confused as measles. And later on, ICMR national institute of virology came out that this is canine distemper virus. Again, the source most commonly dogs are infected with this canine distemper virus. Maybe the lions would have got infected by eating some dogs or close contact, so that again remained a question mark. Then of course, most of us know about the recent Nipah virus outbreaks which were seen in Kerala.

And the first outbreak, major outbreak was in 2018, then 2019, and even in 2021, we saw cases of Nipah virus disease. Again, we have been, again Zika virus infection, which is also a zoonotic infection was seen in mosquitoes which were transmitting zika virus from one individual to the other. So, this is also a zoonotic disease which spread very quickly 2014 onwards.

And scrub typhus, which was known as a very covert disease. Nobody used to even check for it, has now spread its tentacles to most parts of the country. And it reflects as very serious disease, in terms of acute encephalitis syndrome and acute respiratory distress syndrome. So, these are diseases, which never caught the attention of people. But now, with them spreading across various domains they have become so important to look at in a routine diagnostic testing.

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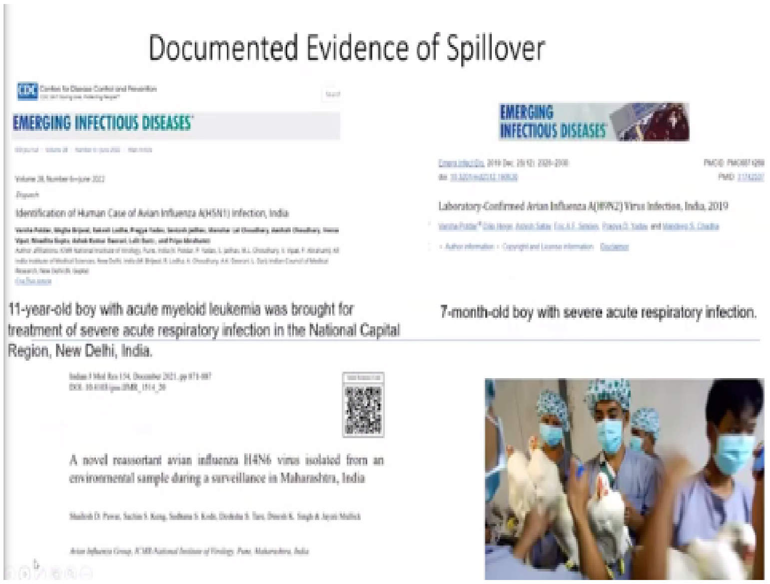

Documented Evidence of Spillover

EMERGING INFECTIOUS DISEASES

Identification of Human Case of Avian Influenza A(H5N1) Infection, India

11-year-old boy with acute myeloid leukemia was brought for treatment of severe acute respiratory infection in the National Capital Region, New Delhi, India.

EMERGING INFECTIOUS DISEASES

Laboratory-Confirmed Avian Influenza A(H9N2) Virus Infection, India, 2019

7-month-old boy with severe acute respiratory infection.

A novel reassortant avian influenza H4N6 virus isolated from an environmental sample during a surveillance in Maharashtra, India

Then there have been instances, when though avian influenzas fell over to humans in India, has been a rare instance. But still we could find a case of human, a child who was infected with H5N1. He was an immunocompromised child, but he was infected with the virus and had a documented history of contact with poultry. Then we also and this child was of acute myeloid leukaemia.

We also could find a novel reassortant avian influenza H4N6 virus from environmental samples in Maharashtra, which again was a cause of concern. And similarly, we could again find H9N2 infected child in a sample from Delhi. So, there have been reported instances, where avian influenza spill over to humans has also been documented, which again remains a cause of concern because avian influenza is a highly pathogenic virus.

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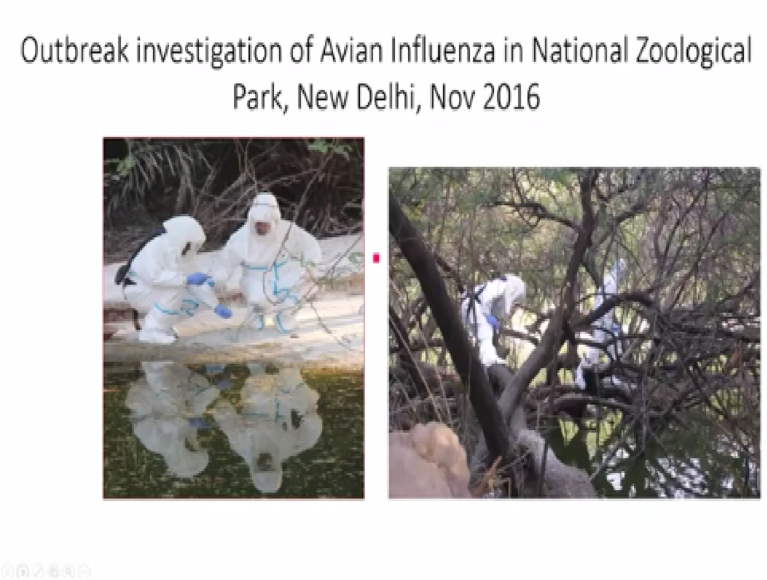

Outbreak investigation of Avian Influenza in National Zoological Park, New Delhi, Nov 2016

This is just to give you a glimpse of avian influenza outbreak that was investigated by the National Institute of Virology of Indian Council of medical research in 2016. And this is the zoo or the national zoological park investigations at Delhi. And you can see how the people are trying to collect samples of dead birds and even their droppings, which were later on examined for the presence of the virus.

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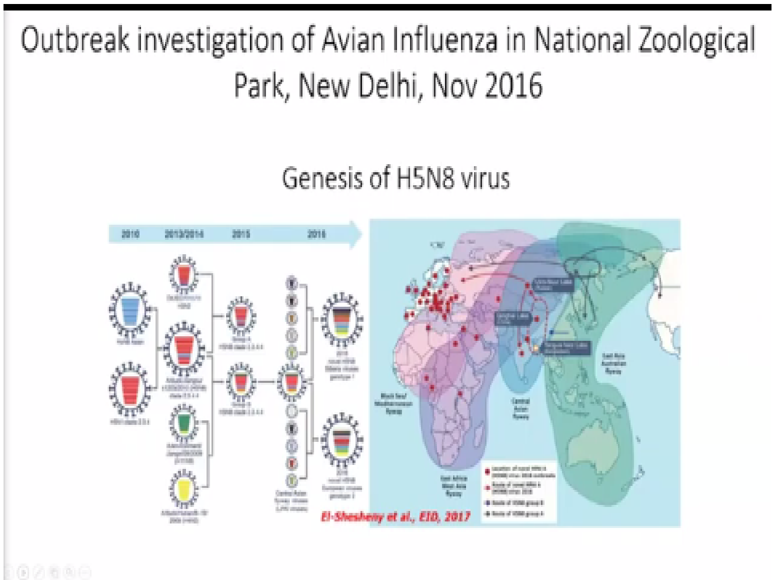

Outbreak investigation of Avian Influenza in National Zoological Park, New Delhi, Nov 2016

Genesis of H5N8 virus

El-Sheshény et al., EID, 2017

And this is how the virus evolved in and this was the Genesis of H5N8 outbreak in Delhi Zoo.

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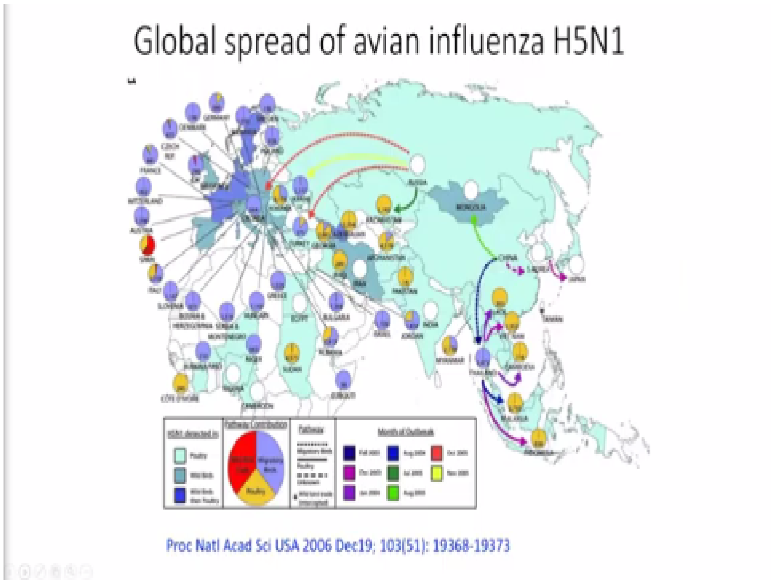

Global spread of avian influenza H5N1

Proc Natl Acad Sci USA 2006 Dec19; 103(51): 19368-19373

Now, this is to give you a glimpse of how quickly viruses can evolve and they can spread globally. So, this is a published paper of 2006 and in 2005, we had a major concern of avian influenza spreading to all corners of the world. And again, its origin was basically from China. And this figure shows you that, how quickly within a year's time the virus spread to many parts of the world. And mainly through migratory birds, wild bird trade, as well as poultry farming.

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HPAI outbreak investigations at the human-animal interface

Central Team Investigations:

- Kerala: Jan 2021: H5N8
- Gujarat: Feb 2021: H5N1
- Maharashtra: Feb 2021: H5N8

And in India, where in very recent times we have detected avian influenza outbreaks, at the animal human interface in states like Kerala, Gujarat and Maharashtra. And at two instances in 2021, it was H5N8 outbreak, and in Gujarat we also found an H5N1 outbreak. So, the point that I am trying to make is that, it is very important to maintain a watch on these emerging viruses through a very robust surveillance.

So, that we are not caught unaware as we were in covid-19 and we have a very major outbreak because influenza viruses have a potential to mutate very fast and cause massive outbreaks.

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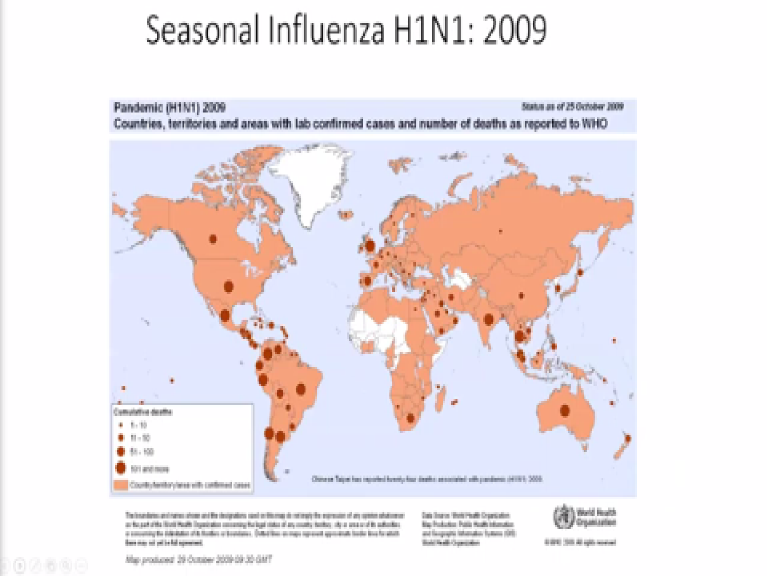

Seasonal Influenza H1N1: 2009

Pandemic (H1N1) 2009

Status as of 25 October 2009

Countries, territories and areas with lab confirmed cases and number of deaths as reported to WHO

Map produced: 29 October 2009 09:30 GMT

And this is to give you a glimpse of how fast the H1N1 or the swine flu of 2009 spread. It quickly emerged the source of infection definitely is not known in this case, where did it emerge. But then it quickly spread to all parts of the world and caused a major pandemic in 2009. And now, this H1N1 2009 strain is a part of our seasonal influenza strains and is routinely detected.

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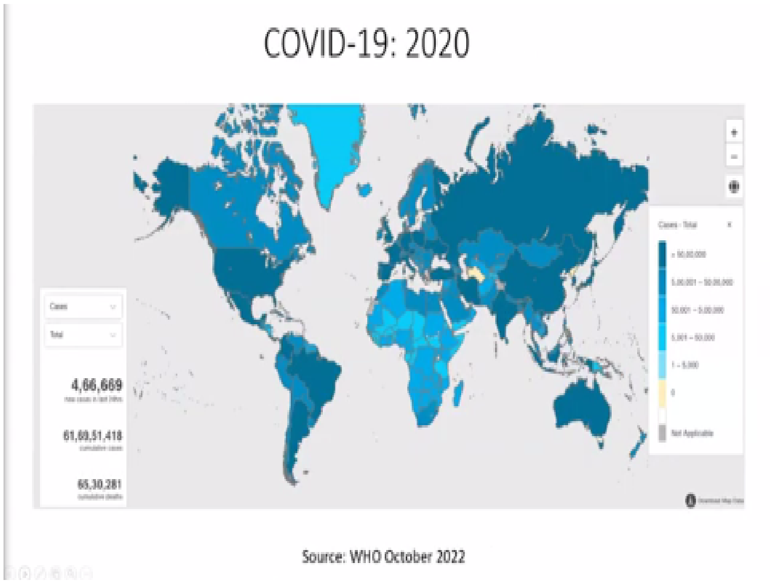

COVID-19: 2020

Source: WHO October 2022

Then of course, covid-19 is a story which is known to everyone how fast the SARS CoV-2 virus emerged and spread to all parts of the world.

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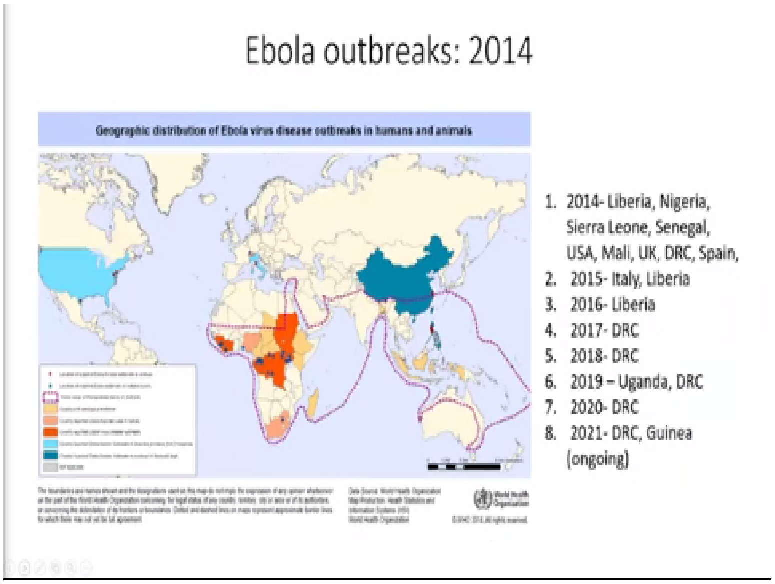

Ebola outbreaks: 2014

1. 2014- Liberia, Nigeria, Sierra Leone, Senegal, USA, Mali, UK, DRC, Spain,
2. 2015- Italy, Liberia
3. 2016- Liberia
4. 2017- DRC
5. 2018- DRC
6. 2019 – Uganda, DRC
7. 2020- DRC
8. 2021- DRC, Guinea (ongoing)

Similarly, the Ebola virus outbreak of 2014 in Africa, was one of the major, most major outbreaks of Ebola that we have seen till now. And the whole world was at vigil. Because this also spreads pretty fast. But the good part about the virus is that it does not have a very high transmission potential. So, so far, the Ebola outbreaks have been restricted to different countries in Africa.

And of course, cases which have been imported into other countries from Africa, have been documented. But there have not been any massive outbreaks in other parts of the world. But we definitely need to keep a watch on this virus, how it evolves in future, and how much it will spread is something which is not known and needs to be continuously monitored.

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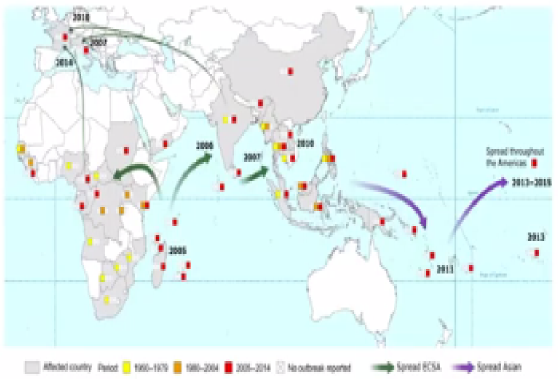
Geographic distribution of Chikungunya: 2006



The Journal of Infectious Diseases, Volume 214, Issue suppl_5, 15 December 2016, Pages S436–S440, https://doi.org/10.1093/infdis/jiw391

Similarly, the chikungunya virus outbreak in 2006, after a quiescence of almost 32 years this virus re-emerged. After significant evolution and it spread to all parts of the world. And India also witnessed a major outbreak of chikungunya virus in 2006. And still, we keep on seeing periodic outbreaks after 3 or 5 months of this virus, it evolves and again causes outbreaks.

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Spread of Zika virus in the world

Front. Microbiol., 23 May 2018

Similarly, the Zika virus which was a relatively very quiescent virus existing in nature in Africa in since 1947. And then first human case isolated in 1954 in Nigeria, it remained a relatively innocuous virus for several decades. But suddenly in 2014, we started seeing outbreaks in the various parts of the world. And then in Brazil in 2015, where it started causing microcephaly in children it became a major cause of concern.

And it was declared as a public health emergency of international concern by WHO in early 2016. And all the countries were advised to quickly set up surveillance, and start monitoring the spread of this virus, and the impacts that it causes, including vector surveillance.

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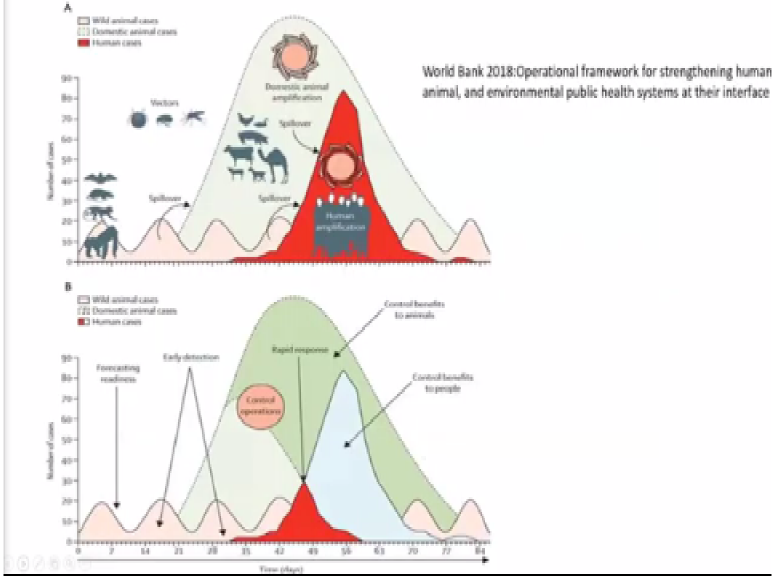

World Bank 2018:Operational framework for strengthening human animal, and environmental public health systems at their interface

So, this is how we have seen it the previous slide just gave you a glimpse of how the infection spread, and how quickly they spread, the zoonotic infections and the population are always got unaware. So, the whole idea now is, this is a slide which has been derived from the World bank document. In the topmost panel, that is figure 8, you can see that first of all there is an amplification of a pathogen in different species, be it non-human primates, or bats, or reservoirs like rats and then monkeys.

So, these are the most common reservoirs for infection and even pigs where infection can spill over from animals to humans. So, first they get infected, the pathogen amplifies in these hosts, non-human hosts for a certain period of time. And then after the pathogen has established itself in these animals, through vectors it spreads over to humans. And this is the point either through domestic animals to humans, or directly to humans if they are in contact with wildlife.

So, this is how the infection spills over. So, now, if you look at the panel B it says that what you should do to prevent the spread of such infections to humans. So, if we have a forecasting readiness, at the first peak that you see where the virus or the pathogen is multiplying in the animals, if we have a way to detect this particular multiplication, and we have a forecasting model, we can prevent it here.

Then, at the time when the pathogen is spilling over through either vectors or by contact with the wildlife of the domestic animals or humans, if we have good detection tools, then we can detect this spill over. And if we have a robust vector surveillance or domestic animal surveillance, we can do a very very quick detection. So, when this detection happens, we are able to prevent the spill over from the vectors or the animals to the humans.

So, these are the tools in which we need to invest now. in terms if we really want to protect ourselves from future pandemics. Pandemics will continue to threaten us, they will continue to come. But we as humans need to improve our readiness, improve our detection tools, so that we are able to identify a threat very early during its emergence. So, that’s the key.

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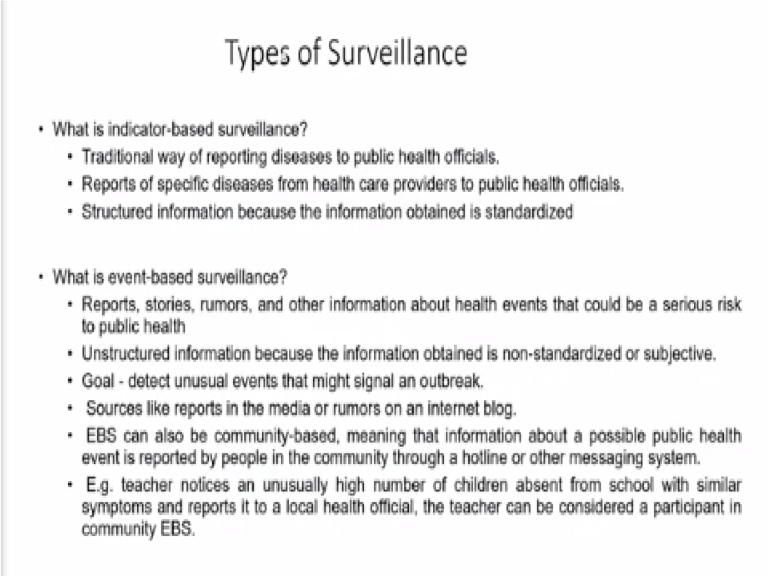

Types of Surveillance

- What is indicator-based surveillance?
  - Traditional way of reporting diseases to public health officials.
  - Reports of specific diseases from health care providers to public health officials.
  - Structured information because the information obtained is standardized
- What is event-based surveillance?
  - Reports, stories, rumors, and other information about health events that could be a serious risk to public health
  - Unstructured information because the information obtained is non-standardized or subjective.
  - Goal - detect unusual events that might signal an outbreak.
  - Sources like reports in the media or rumors on an internet blog.
  - EBS can also be community-based, meaning that information about a possible public health event is reported by people in the community through a hotline or other messaging system.
  - E.g. teacher notices an unusually high number of children absent from school with similar symptoms and reports it to a local health official, the teacher can be considered a participant in community EBS.

Now if we want to achieve all this, then first of all we really need to strengthen our surveillance. Now there are two types of surveillance. One is the indicator-based surveillance, which is a very traditional way of reporting diseases to public health officials and then it reports specific diseases from health care providers to public health officials, because public health officials need to take policy decisions and the cases are seen by the health care providers.

So, there has to be a close link between the two of them. Then structured information is obtained through this surveillance. Because generally our surveillance forms and questionnaires are very standardized. Then we also need, this is indicator-based surveillance exists in our country through the integrated disease surveillance program. What we lack is the, event-based surveillance.

Now event-based surveillance means, that we have a machinery for surveillance which acts on the basis of reports, stories, rumours, media reports, unstructured information, so there are various sources then community reportings, school teacher reportings. So, there has to be a surveillance mechanism, which picks up unstructured information and tries to process it and finds out whether it is useful to examine such events. So, this is one thing on which we need to invest that is on event based surveillance.

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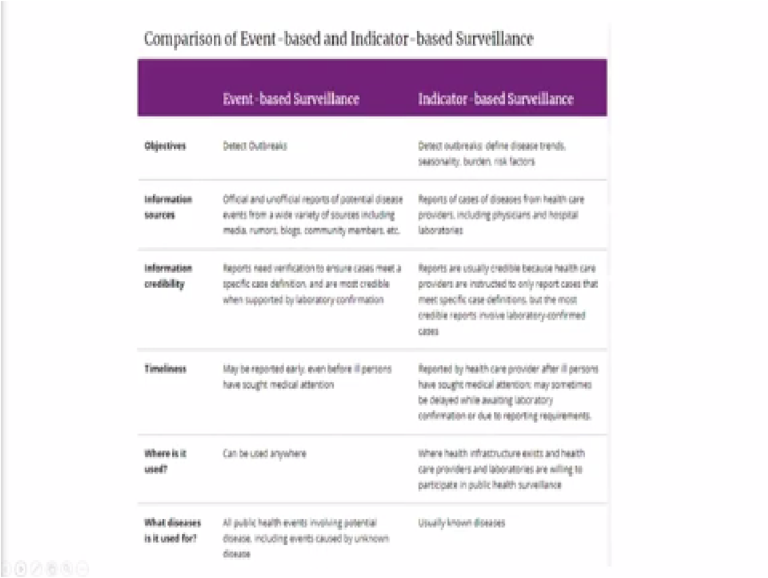

Comparison of Event-based and Indicator-based Surveillance

	Event-based Surveillance	Indicator-based Surveillance
Objectives	Detect Outbreaks	Detect outbreaks; define disease trends, seasonality, burden, risk factors
Information sources	Official and unofficial reports of potential disease events from a wide variety of sources including media, rumors, blogs, community members, etc.	Reports of cases of diseases from health care providers, including physicians and hospital laboratories
Information credibility	Reports need verification to ensure cases meet a specific case definition, and are most credible when supported by laboratory confirmation	Reports are usually credible because health care providers are instructed to only report cases that meet specific case definitions, but the most credible reports involve laboratory-confirmed cases
Timeliness	May be reported early, even before ill persons have sought medical attention	Reported by health care provider after ill persons have sought medical attention; may sometimes be delayed while awaiting laboratory confirmation or due to reporting requirements.
Where is it used?	Can be used anywhere	Where health infrastructure exists and health care providers and laboratories are willing to participate in public health surveillance
What diseases is it used for?	All public health events involving potential disease, including events caused by unknown disease	Usually known diseases

And this is a table, which tells you what is the difference between event-based surveillance and indicator based surveillance. But the point that I want to make here is, that both these surveillances are very important to detect any unknown disease or a novel emerging pathogen.

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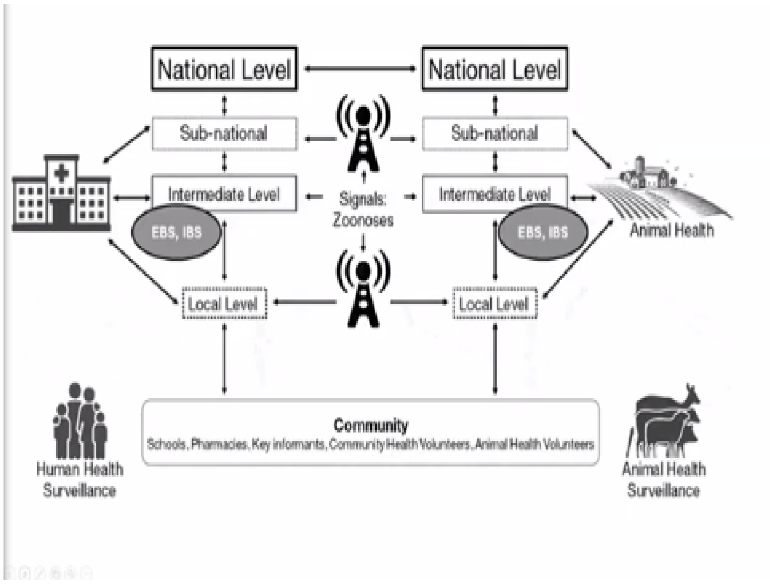

And this is how it operates that both at and especially if we are looking at a one health approach, we really need to have both indicator-based surveillance and event-based surveillance at the level of the human side, as well as the animal side. So, if you look at this figure, it tells you that these surveillance of both event based and indicator based surveillance need to be present as I said on the human and the animal side at national level, at sub-national level, at even intermediate levels and local levels which may be going down to the level of a block or a village.

And when we have these surveillance systems set up, it is also very important to understand that we should be able to process the information that is coming out of these surveillance systems. So, we should be able to pick up signals, we should be able to process the signals, and we should be able to make public health decisions based on the signals that we are picking up.

Any information which is gathered and not reviewed not processed has no meaning. So, we really need to have a very robust system of processing the information as well.

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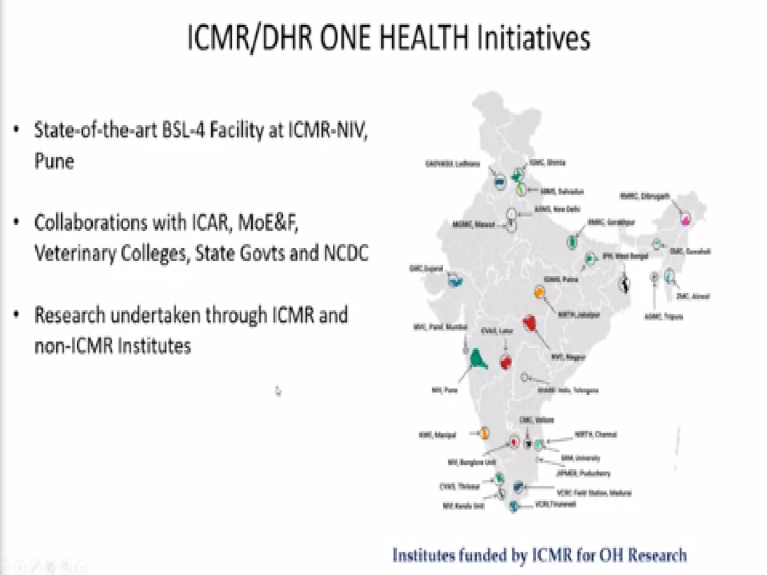

ICMR/DHR ONE HEALTH Initiatives

- State-of-the-art BSL-4 Facility at ICMR-NIV, Pune
- Collaborations with ICAR, MoE&F, Veterinary Colleges, State Govts and NCDC
- Research undertaken through ICMR and non-ICMR Institutes

Institutes funded by ICMR for OH Research

Now, if we look at few initiatives that ICMR has taken, which can be used definitely for a one health based approach that is a state of art biosafety level code facility at ICMR National Institute of Virology, Pune. This is the highest level of laboratory, biosafe laboratory that we have across the world. And this is the only facility available in India, where we can handle any unknown pathogen or high-risk pathogens.

There are existing collaborations with the animal husbandry environment and forest veterinary college state governments, as well as the national centre for disease control. And the figure on the right hand side shows you that, what are the institutes which have been funded by ICMR for undertaking one health research.

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Spread of Monkeypox Disease

Source: CDC

This slide depicts the very recent spread of monkey pox disease across the world.

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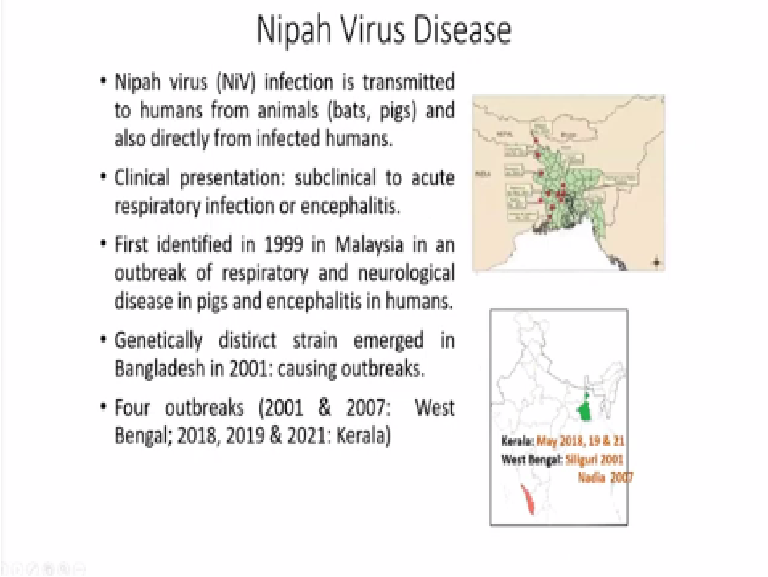

Nipah Virus Disease

- Nipah virus (NiV) infection is transmitted to humans from animals (bats, pigs) and also directly from infected humans.
- Clinical presentation: subclinical to acute respiratory infection or encephalitis.
- First identified in 1999 in Malaysia in an outbreak of respiratory and neurological disease in pigs and encephalitis in humans.
- Genetically distinct strain emerged in Bangladesh in 2001: causing outbreaks.
- Four outbreaks (2001 & 2007: West Bengal; 2018, 2019 & 2021: Kerala)

Now, I want to talk a little about the Nipah virus disease. How it emerged, how it spread in India and how it was tackled. So, when we look at the Nipah virus disease. So, it was first identified in the year 1999 in Malaysia, and as an outbreak of respiratory and neurological disease in pigs and encephalitis in humans. First of all, it was confused as Japanese Encephalitis, but later on it was found that it is a new virus of the measles family.

And it was named as Nipah, on the name of the village in Malaysia where it emerged. And then it started causing distinct outbreaks in Bangladesh in humans and in India four outbreaks have been documented in 2001, 2007 in West Bengal, and thereafter repeated outbreaks in Kerala have been demonstrated.

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Spread of Nipah virus through pigs

- First outbreak of Nipah virus disease was reported in Malaysia in 1998.
- Confused with Japanese encephalitis
- Distinct features, clustering of cases and history of direct contact with pigs.
- In February 1999, the outbreak had spread to Singapore due to importation of live pigs from Malaysia.
- Large numbers of pigs in Malaysia culled and pig importation between Malaysia and Singapore was stopped.
- Consumption of bat bitten fruits by pigs seemed to be the source of infection in pigs.
- This was followed by regular outbreaks in Bangladesh since 2001.

But between this, there was an outbreak in Singapore which was caused by the trade of pigs. Here you can see that the pigs were imported from Malaysia to Singapore and that led to a focal outbreak in the people who were handling the pigs. And then it was identified as the source of infection was the pigs and they were culled.

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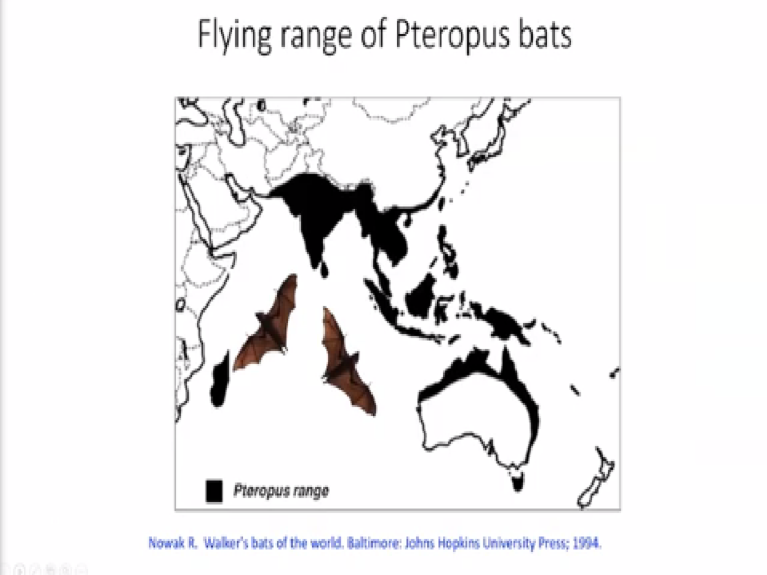

Flying range of Pteropus bats

Nowak R. Walker's bats of the world. Baltimore: Johns Hopkins University Press; 1994.

Now the problem with the Nipa virus disease is that it is spread by Pteropus bats. And if you look at the flight range of Pteropus bats, this is the figure which shows that they actually fly from the tip of Africa to the entire southeast Asia region and even including Australia. So, they fly so their flight range is so big, that they can really spread diseases and Nipah is not the only disease which is spread by bats even diseases like Ebola and several respiratory viruses, novel viruses are spread by and of course rabies is spread by bats.

So, since they have such a big flight range, they really have the potential to cross borders and spread diseases.

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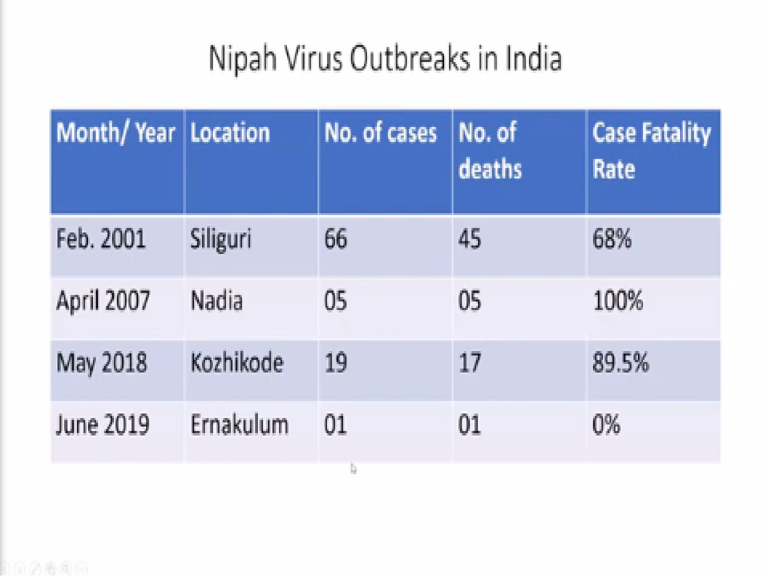

Nipah Virus Outbreaks in India

Month/ Year	Location	No. of cases	No. of deaths	Case Fatality Rate
Feb. 2001	Siliguri	66	45	68%
April 2007	Nadia	05	05	100%
May 2018	Kozhikode	19	17	89.5%
June 2019	Ernakulum	01	01	0%

Now this is a list of the Nipah virus outbreaks in India, after that 2021 outbreak has been added.

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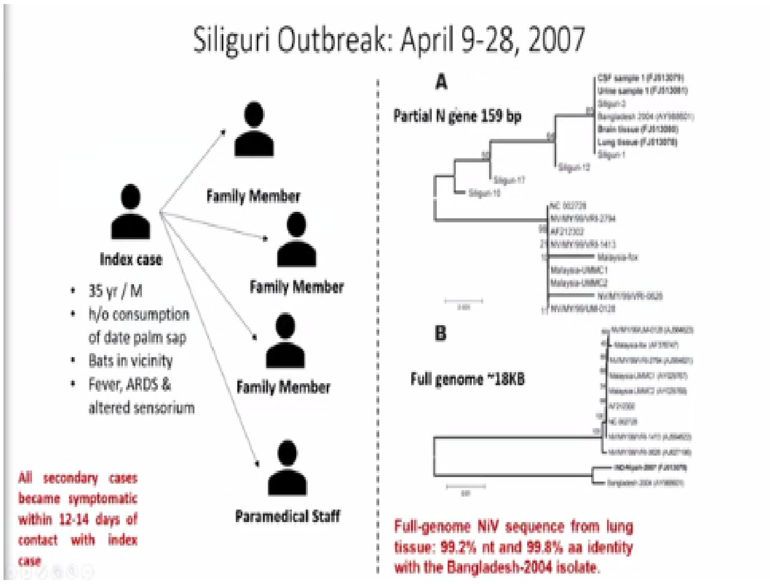

Siliguri Outbreak: April 9-28, 2007

Index case

- 35 yr / M
- h/o consumption of date palm sap
- Bats in vicinity
- Fever, ARDS & altered sensorium

All secondary cases became symptomatic within 12-14 days of contact with index case

Full-genome NiV sequence from lung tissue: 99.2% nt and 99.8% aa identity with the Bangladesh-2004 isolate.

Now I like to speak a little bit about the first identified outbreak in 2001, we really could not identify the Nadia outbreak, what was the cause of the outbreak. But in Siliguri outbreak in 2007, we could distinctly see that the index case was a 35-year-old male, spread the infection to three of the family members and one of the paramedical staff and when we looked at the genome sequences of this particular outbreak.

We could see that we had a very high sequence identity with the Bangladesh isolate; which was more than 99 percent identity. And all the index case, as well as the contacts, all of them died. So, this was almost 100 percent mortality in this outbreak, which was a great cause of concern.

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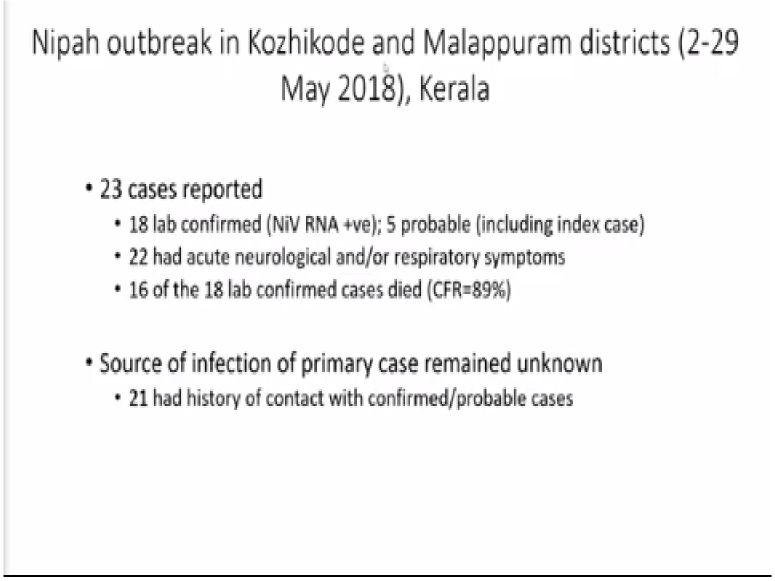

Nipah outbreak in Kozhikode and Malappuram districts (2-29 May 2018), Kerala

- 23 cases reported
  - 18 lab confirmed (NiV RNA +ve); 5 probable (including index case)
  - 22 had acute neurological and/or respiratory symptoms
  - 16 of the 18 lab confirmed cases died (CFR=89%)
- Source of infection of primary case remained unknown
  - 21 had history of contact with confirmed/probable cases

Then subsequently, we had an outbreak of Nipah virus in Kozhikode and Malappuram districts, which was one of the really concerning outbreaks with an 89% mortality, 23 cases were reported in this outbreak, wherein 18 were lab confirmed, 22 had acute neurological sequelae and 16 of the 18 lab confirmed cases died, with the case fatality rate of 89%. Now source of the infection in the primary case remained unknown. So, we never knew where the infection came from.

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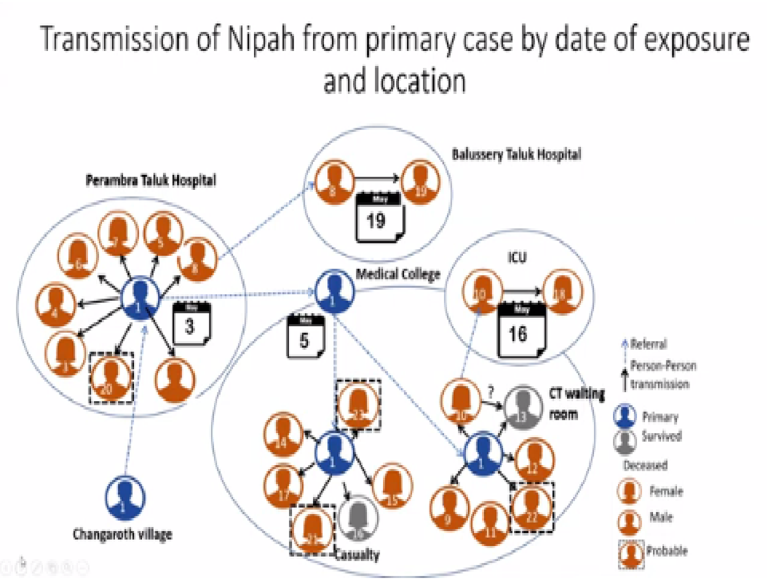
Transmission of Nipah from primary case by date of exposure and location

And this is how like, the first person that is number one who came from a village in Kerala, really infected, he was taken to the hospital. Wherein he infected like all the contacts, which the people who came in contact, they were the family people, as well as the health care professionals they were all infected by this person. Then since he deteriorated, he was taken to a medical college.

And in the medical college, in the casualty, as well as the CT scan waiting room, again this person infected several health care workers, as well as the hospitalized patients. And this infection or trend continued from 3rd of May to 16th of May, wherein this person really infected several people. So, here you can see that, how one infected case really infected many other people.

The reason being, because like nobody in Kerala had detection capacity for Nipah at that point in time. And by the time they really identified it is a confirmed Nipah virus disease, this person had infected many other people and most of them died. So, here I want to highlight, that how important it is to really detect the spread of infection in a very early stage. In terms of having very strong laboratory capacity, to detect what the infection is.

And to take appropriate precautions in terms of isolating the patient, wearing proper PPE while handling the patient, which were not taken during the Nipah virus outbreak in turn, killing so many people, both healthcare workers, family people, family contacts, as well as the hospital people who are hospitalized for other illnesses.

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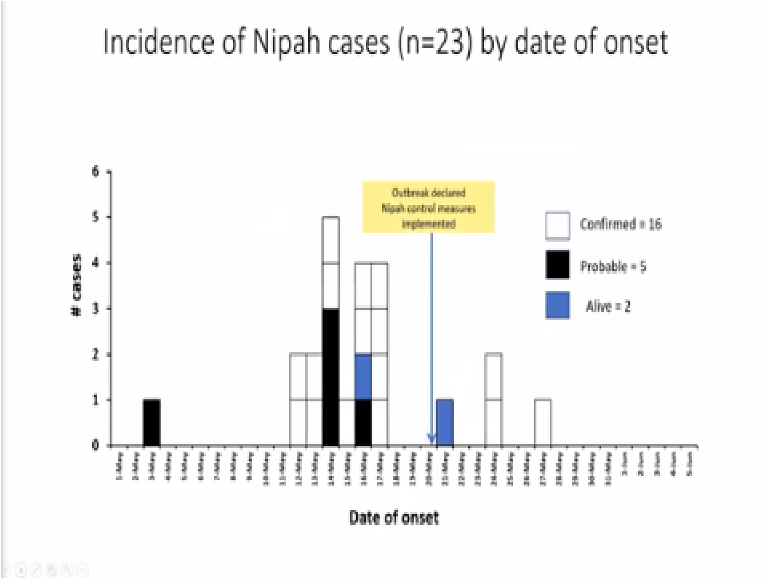

Incidence of Nipah cases (n=23) by date of onset

So, this is how like between 3rd of May and 27th of May, how the infection continued to spread creating probable cases and only two of them survived, rest of them died.

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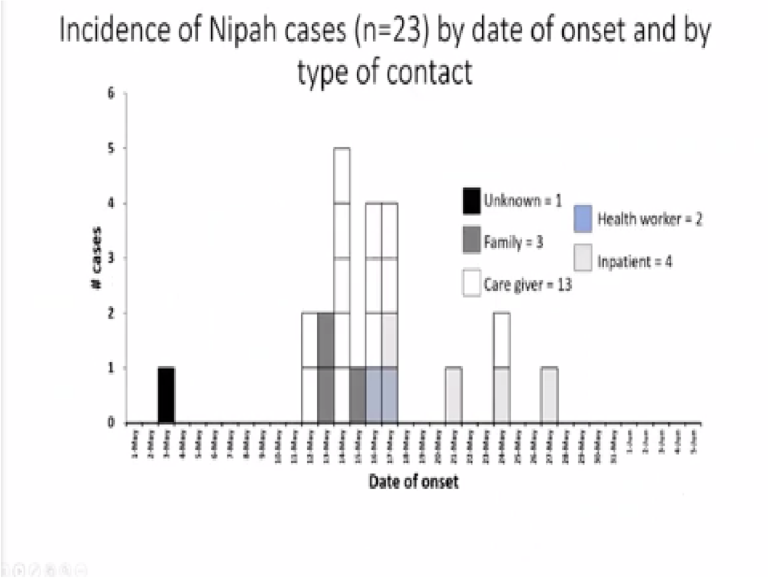

Incidence of Nipah cases (n=23) by date of onset and by type of contact

Again, this is the incidence of cases of Nipah cases by date of onset and type of contact. I would not go into the details here.

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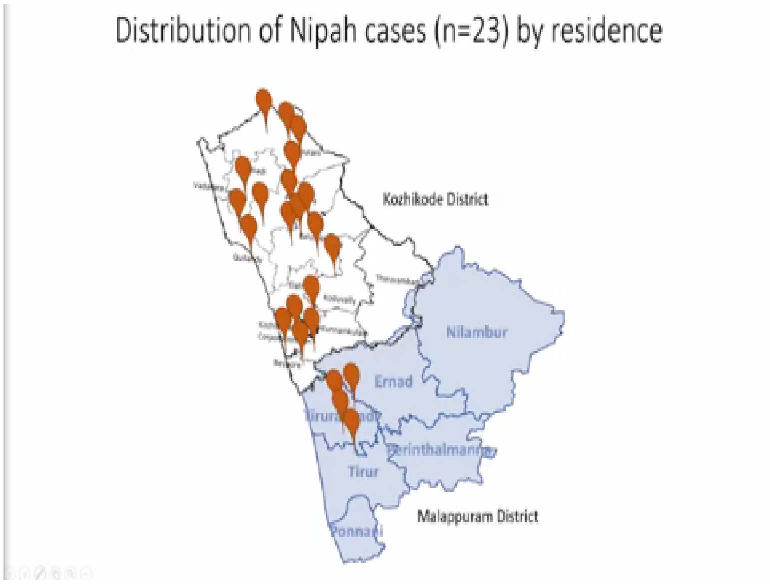

Distribution of Nipah cases (n=23) by residence

And now this is the slide which depicts that how the infection emerged and spread. Like it emerged in Kozhikode, many people got infected and ultimately, they travelled and spread it to Malappuram district as well.

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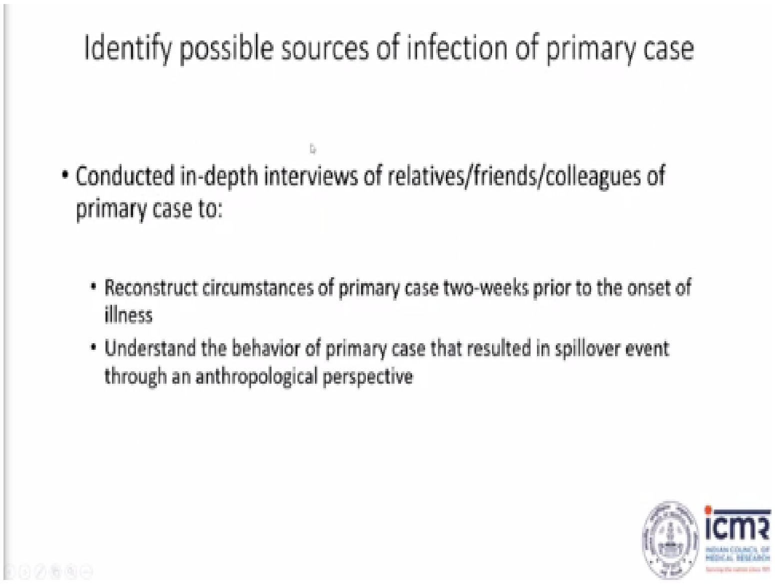

Identify possible sources of infection of primary case

- Conducted in-depth interviews of relatives/friends/colleagues of primary case to:
  - Reconstruct circumstances of primary case two-weeks prior to the onset of illness
  - Understand the behavior of primary case that resulted in spillover event through an anthropological perspective

Now, after the Nipah virus outbreak in Kerala, there was a huge concern, that since this virus was restricted only to Bangladesh and West Bengal which is very close to Bangladesh and they shared the borders, suddenly how this virus came to Kerala. So, there was lot of speculation, is it bioterrorism, is it release of the virus to Kerala and there were no answers. So, it became extremely important to find the source of infection, to understand where it is coming from.

So, there were lot of interviews, there were lot of qualitative interviews, to understand that what do they think, what were their consumption practices, did they come in contact with bats, did they eat any half-eaten fruit, or where the index case acquired the infection from.

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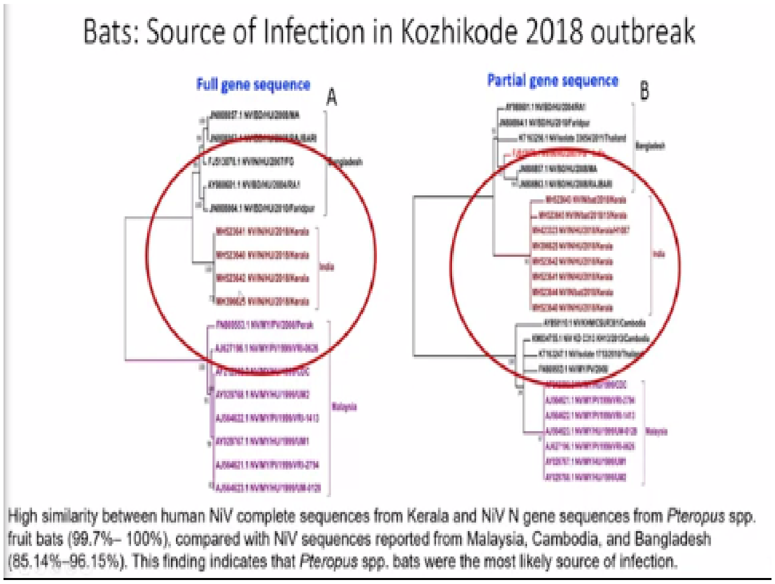
Bats: Source of Infection in Kozhikode 2018 outbreak

High similarity between human NiV complete sequences from Kerala and NiV N gene sequences from *Pteropus* spp. fruit bats (99.7%– 100%), compared with NiV sequences reported from Malaysia, Cambodia, and Bangladesh (85.14%–96.15%). This finding indicates that *Pteropus* spp. bats were the most likely source of infection.

So, fortunately, after a lot of fact finding, again ICMR NiV Pune did bat surveys over there. And they caught trapped bats from the localities from where the index case was found. And to our surprise we saw that, when we compared the full gene sequence of humans which you can see on the left-hand side, and the partial gene sequence from the bats, there was again a very close similarity. More than 99 percent similarity between the two sequences.

And also, a close match with the Bangladesh sequence to the extent ranging from 85 to 96%. But definitely this also indicated that, we were not exactly similar to the Bangladesh stream, as we were in the West Bengal outbreaks. We had a slight divergence from the Bangladesh stream, which indicated that Nipah virus is somewhere multiplying within our limit, within our environment, within the bats that visit India or migrate to India.

So, it becomes imperative to keep on seeing that how we keep on monitoring the situation in bats and keep on doing bat surveys within our country.

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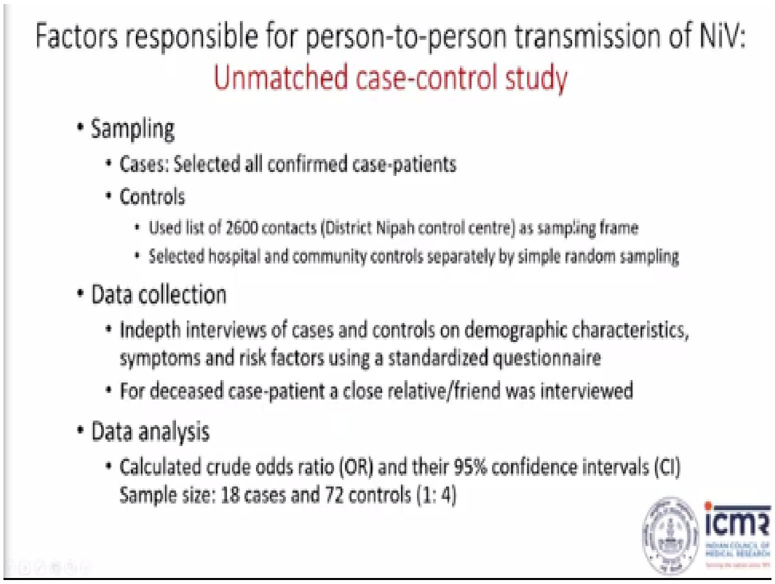

Factors responsible for person-to-person transmission of NiV: Unmatched case-control study

- Sampling
  - Cases: Selected all confirmed case-patients
  - Controls
    - Used list of 2600 contacts (District Nipah control centre) as sampling frame
    - Selected hospital and community controls separately by simple random sampling
- Data collection
  - Indepth interviews of cases and controls on demographic characteristics, symptoms and risk factors using a standardized questionnaire
  - For deceased case-patient a close relative/friend was interviewed
- Data analysis
  - Calculated crude odds ratio (OR) and their 95% confidence intervals (CI) Sample size: 18 cases and 72 controls (1: 4)

We also did again to do more fact finding in terms of identifying the risk factors. We also did an unmatched case control study, whereas cases were we selected all confirmed cases and controls were selected from the list of 2600 primary and secondary contacts, which we had enlisted during the Nipah outbreak. We did in-depth interviews and did data collection, and calculated the odds ratio against confidence intervals of 95 percent. Our sample size was 18 cases and 72 controls in1 is to 4 ratio.

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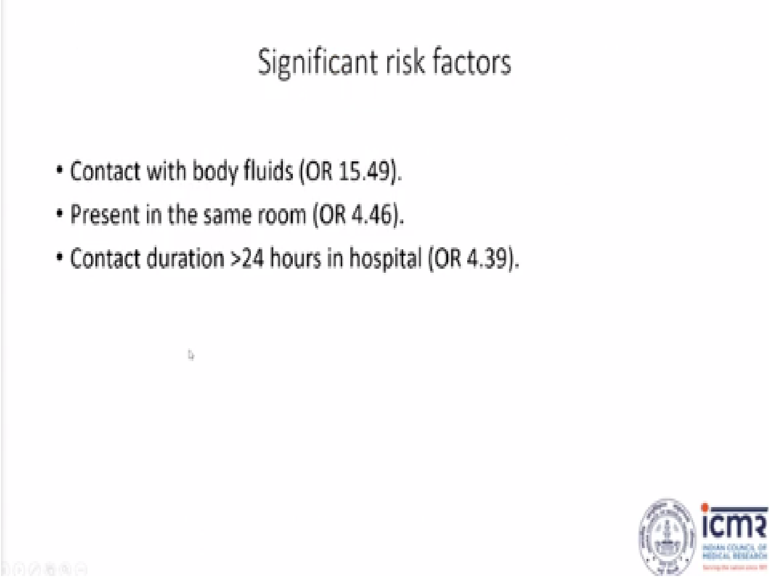

Significant risk factors

- Contact with body fluids (OR 15.49).
- Present in the same room (OR 4.46).
- Contact duration >24 hours in hospital (OR 4.39).

So, the study concluded that the significant risk factors were for acquisition of Nipah infection were contact with body fluids with an odds of 15. Then presence in the same room as the infected patient, with an odds of 4.5. Then the contact duration of more than 24 hours in hospital again with an odds of more than four.

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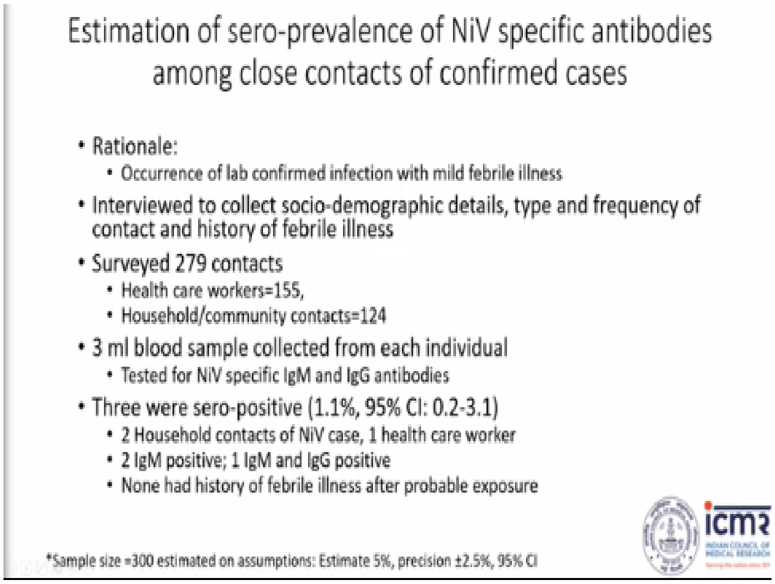

Estimation of sero-prevalence of NiV specific antibodies among close contacts of confirmed cases

- Rationale:
  - Occurrence of lab confirmed infection with mild febrile illness
- Interviewed to collect socio-demographic details, type and frequency of contact and history of febrile illness
- Surveyed 279 contacts
  - Health care workers=155,
  - Household/community contacts=124
- 3 ml blood sample collected from each individual
  - Tested for NiV specific IgM and IgG antibodies
- Three were sero-positive (1.1%, 95% CI: 0.2-3.1)
  - 2 Household contacts of NiV case, 1 health care worker
  - 2 IgM positive; 1 IgM and IgG positive
  - None had history of febrile illness after probable exposure

*Sample size =300 estimated on assumptions: Estimate 5%, precision ±2.5%, 95% CI

Then we also wanted to understand that, what is the prevalence of Nipah antibodies in close contacts of confirmed cases. So, our objective was to understand whether we have any asymptomatic cases of Nipah. Because this was something a research question which was unanswered and nobody knew how many asymptomatic cases, we have for Nipah. So, our study revealed, that really in terms of Nipah virus infection, there were only 3 people who were sero-positive, who had a documented contact from with a Nipah patient.

So, out of the 279 contacts which we checked for antibodies, we could only find 3 people who were sero-positive. So, this gives us an indication that most of the Nipah virus disease is asymptomatic. Most of the Nipah virus disease is symptomatic, we do not have asymptomatic infection to a significant proportion. So, in our study there were only 1.1 percent individuals who did not exhibit symptoms.

But still exhibited antibodies which is a very low proportion as compared to other diseases. If you look at Dengue or even Covid-19 where 60 to 80 percent of the infection is asymptomatic. So, this gives us a clue on how to investigate Nipah virus outbreaks in future. I would like to stay here and I would like to emphasize that, the reason why I took you through the Nipah virus outbreak, and how we investigated it, what kinds of studies we conducted.

This to give you an idea that, whenever we have a new outbreak or an outbreak of a novel pathogen. These are the kind of exercises that we have to do to understand the spectrum of disease, the risk factors proportion of asymptomatic infection, then source of infection, then also augmenting our laboratory capacity for early detection in future. So, these are the steps which are required and we need to gear up in future with these steps to be able to combat epidemics and pandemics.

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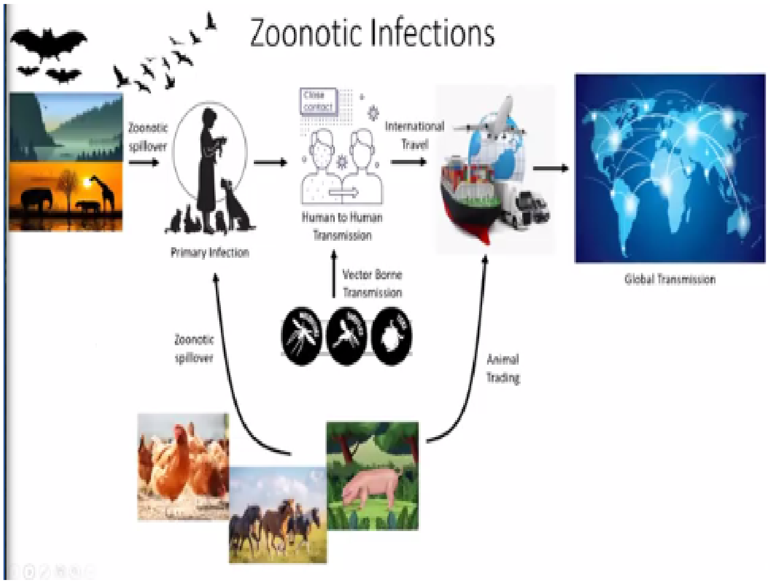

So, again, this is a slide which really depicts that zoonotic infections can really come either from the natural flora and fauna, wild animals, poultry, domestic animals, horses, animal trading. And then first of all, after they establish well in the animal reservoirs, they start spilling over to humans and it takes time to establish; for these pathogens to establish themselves for human-to-human transmission.

So, it does not happen immediately, it happens after a few or a considerable number of cycles of animal replication, then animal to human spillover, and then eventually the pathogen tries to establish itself for human-to-human transmission.

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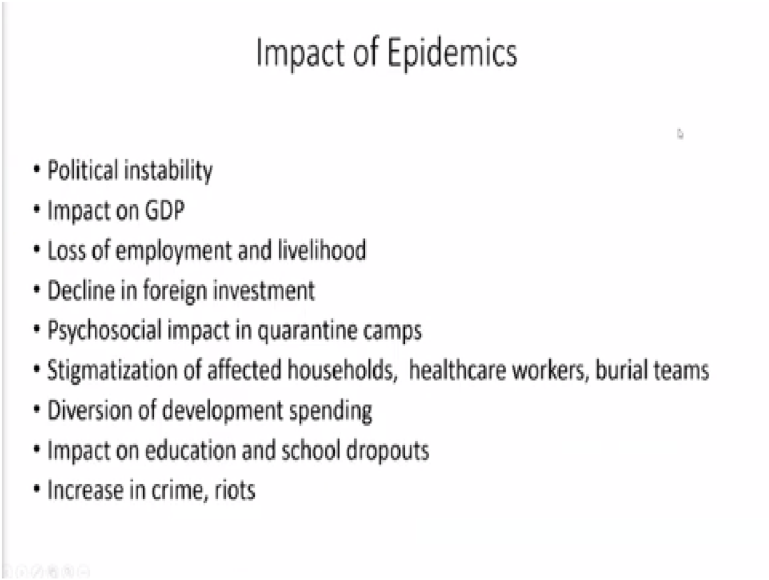

Impact of Epidemics

- Political instability
- Impact on GDP
- Loss of employment and livelihood
- Decline in foreign investment
- Psychosocial impact in quarantine camps
- Stigmatization of affected households, healthcare workers, burial teams
- Diversion of development spending
- Impact on education and school dropouts
- Increase in crime, riots

Now what are the impacts of epidemics? Impacts are huge. They lead to political instability, they impact the GDP of the country, they lead to loss of employment and livelihood. There is a decline in foreign investment and definitely economy of the country is affected. Then the people who are quarantined, or in camps, or isolated, they really undergo a huge psychosocial impact.

There is stigmatization of households, healthcare workers, burial teams which we have repeatedly seen in covid-19 as well as Nipah. Then there is a diversion of development spending; so whatever fund is allocated for development is diverted towards combating the pandemic and it affects the development, overall development of the country. There is an impact on education, there are school dropouts.

And when there is increase in economic crisis, there is definitely poverty which leads to increase in crime and rights. So, the impacts of epidemics are many, and we should make all concerted efforts to really avert any future epidemics or pandemics to a large scale.

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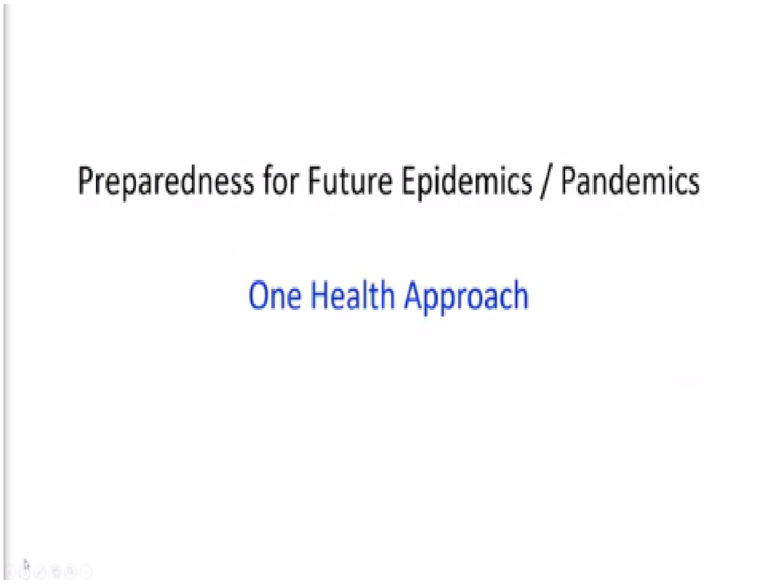

Preparedness for Future Epidemics / Pandemics

One Health Approach

And the answer is, that we really need to prepare ourselves for future epidemics and pandemics through a one health approach.

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Surveillance: One Health Approach

Surveillance

Human

Animal

Vector

Environment

Organized sector

- Zoos
- Sanctuaries
- National parks
- Abattoirs
- Farms

Un-organized sector

- Livestock in human dwellings
- Wet markets

Now when we talk of one health approach, it will involve setting up surveillance very robust sentinel surveillance at the human level, animal level, vector as well as environment. Now there are there is a one health group at the level of the PSA, or the principal scientific advisor to the Prime Minister when in all the sectors are being brought together now. And surveillance is being set up at all levels, both in terms of organized sector as well as unorganized sector.

Like organized sector if I talk of, then ICMR is planning to set up surveillance at zoos, wildlife sanctuaries, national parks, abattoirs and farms, where we have a very well characterized population, human population that is regularly coming into contact with animals. And they definitely are a source where we can detect any zoonotic spillover. So, surveillance is being set up at these sites.

Then definitely, it is also equally important to look at the unorganized sector in terms of livestock in human dwellings and wet markets. And definitely food safety, animal surveillance is equally important.

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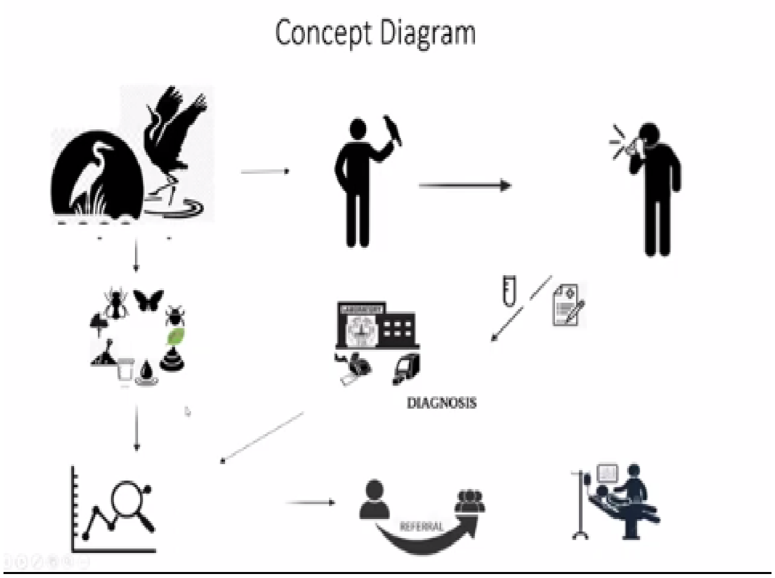
Concept Diagram

Now this is a concept diagram which shows that what ICMR is trying to do in terms of setting up surveillance. So, as I said that, we are trying to set up surveillance both in zoos, wildlife sanctuaries which is depicted here, bird sanctuaries. And also set up environmental surveillance to pick up humans who are showing early signs of any kinds of disease whether it is a respiratory disease, whether it is acute fever, jaundice, conjunctivitis, fever with rash, acute encephalitis.

So, we will pick up these individuals who are exhibiting some kind of syndromic illness and through a comprehensive laboratory approach we are going to test them. And whatever remains undiagnosed, we will sequence them to understand that what is the ultimate pathogen. So, there is an effort to develop a novel pathogen discovery platform, which will enable us to understand what new pathogens are; we are seeing at the animal human interface.

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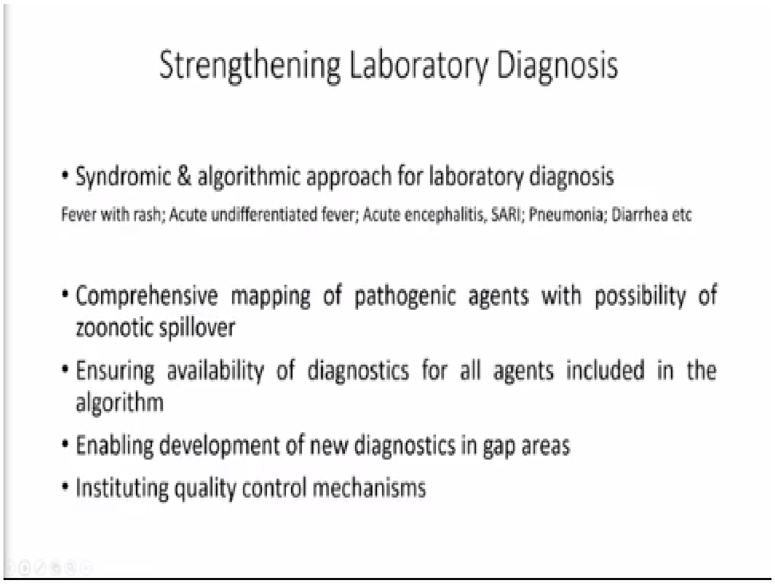

Strengthening Laboratory Diagnosis

- Syndromic & algorithmic approach for laboratory diagnosis

Fever with rash; Acute undifferentiated fever; Acute encephalitis, SARI; Pneumonia; Diarrhea etc

- Comprehensive mapping of pathogenic agents with possibility of zoonotic spillover
- Ensuring availability of diagnostics for all agents included in the algorithm
- Enabling development of new diagnostics in gap areas
- Instituting quality control mechanisms

For all these exercises, like whenever we have a sample with us of an ill patient it is very important to have a very robust laboratory capacity for detecting that sample. What is it? And definitely for this, we have done a comprehensive mapping of pathogenic agents with a possibility of zoonotic spill over. We are strengthening our laboratories to have diagnostic capacities for these pathogens which have a potential of zoonotic spill over.

So, what I am trying to say is that, first a comprehensive list has been developed, what all pathogens can jump from animal to humans, and then we are trying to supplement our labs with diagnostic kits and methods for detecting those spill over pathogens. We are developing new algorithms, and also trying to institute quality control mechanisms at our lab. So, that we do not do any wrong diagnosis.

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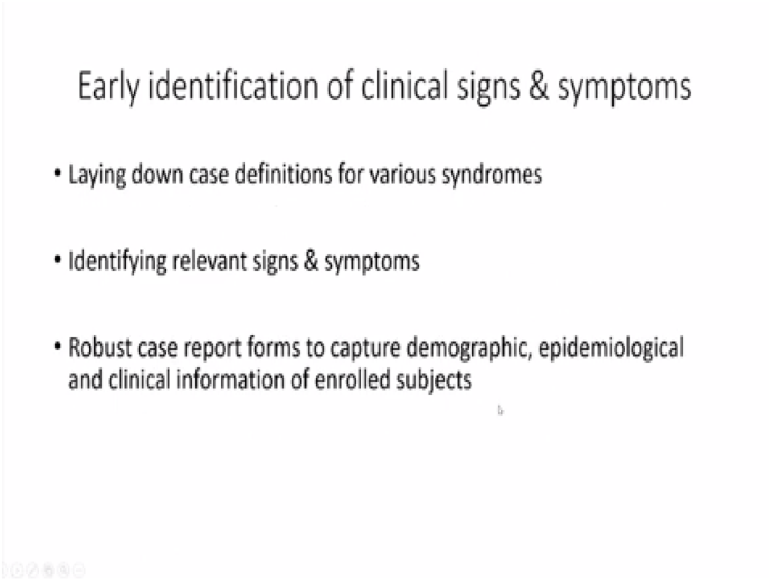

Early identification of clinical signs & symptoms

- Laying down case definitions for various syndromes
- Identifying relevant signs & symptoms
- Robust case report forms to capture demographic, epidemiological and clinical information of enrolled subjects

Then we are also laying down case definitions for various syndromes of zoonotic pathogens. And mapping the relevant signs and symptoms developing robust case report forms to capture demographic, epidemiological and clinical information, which is extremely important. Because, if you detect a novel infection, you really need to go back to the communities, the households and see where the infected patient resides.

And if there is a need to quarantine the area or like make it a containment zone. It is very important to do take all these public health measures to contain the spread of infection, as we all have seen in Covid-19.

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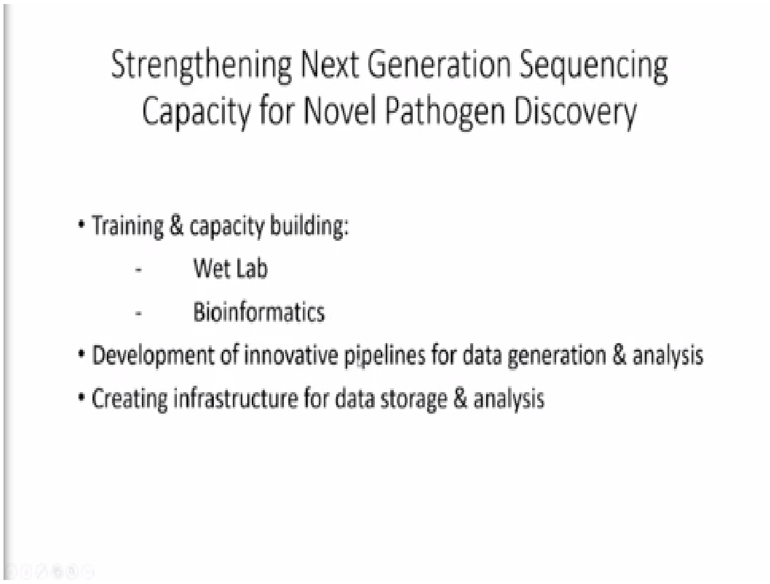

Strengthening Next Generation Sequencing Capacity for Novel Pathogen Discovery

- Training & capacity building:
  - Wet Lab
  - Bioinformatics
- Development of innovative pipelines for data generation & analysis
- Creating infrastructure for data storage & analysis

Then the most important thing to identify novel pathogen is that, whatever diagnostic assets and kits we have, are able to detect pathogens that are known to us. Now something which is unknown we do not have kits for. So, the next generation sequencing and capacity for novel pathogen discovery, at the level of wet lab and having very innovative bioinformatics pipelines for data generation analysis storage is very important to identify any novel threat due to an infectious pathogen that we may see in future.

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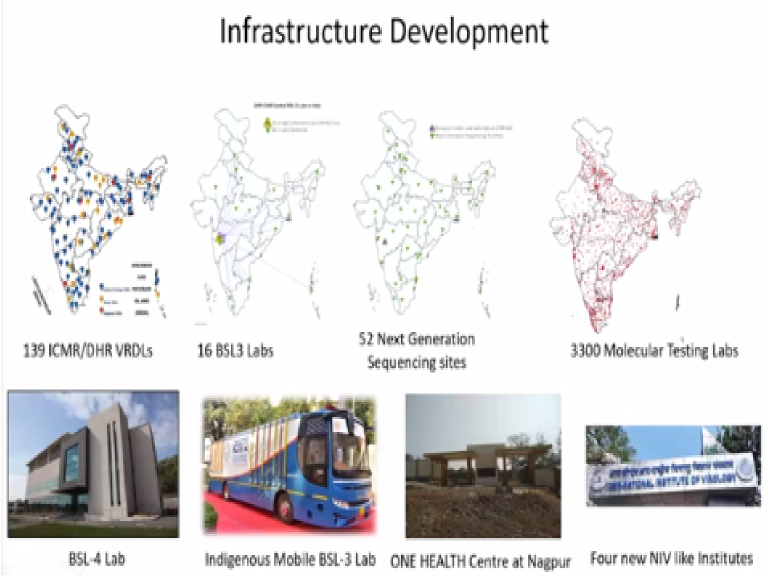

Infrastructure Development

139 ICMR/DHR VRDLs

16 BSL3 Labs

52 Next Generation Sequencing sites

3300 Molecular Testing Labs

BSL-4 Lab

Indigenous Mobile BSL-3 Lab

ONE HEALTH Centre at Nagpur

Four new NIV like Institutes

Again, if we talk of the infrastructure that we have for, like having all these capacities of good labs, of good surveillance of novel pathogen discovery. This is the rich network that we have available at ICMR and in collaboration with various stakeholders and partners, we have virus research and diagnostic laboratories across the country. We have biosafety level 3 labs which are very well aligned with the biosafety level code lab, which is the highest lab as I said.

We also have an indigenous mobile biosafety level 3 lab, which can be taken to places like I, as I showed you the Nipah virus outbreak in Kerala, where there was a delay in diagnosis. So, now we have a mobile lab, which can be taken to any part of the country and diagnosis can be given in a few hours and the outbreak can be contained very quickly. Then we have next generation sequencing facilities at almost 52 sites.

And these are public health laboratories which are working on infectious pathogens. During Covid-19 pandemic, we have scaled our molecular testing capacity to almost 3300 labs. And now we are also coming up with a dedicated one health centre at Nagpur, which was recently inaugurated by the honourable Prime minister. And will specifically focus on one health related surveillance, research, diagnostic capacity and innovative solutions.

And we also to have upcoming four National Institute of Virology, like institutions in different parts of the country, which will again focus on emerging, re-emerging viral infections particularly of one health importance.

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Mobile BSL-3 Features

- Automated negative air pressure system
- Airtight & Access Controlled
- Biological waste decontamination system
- Safety features: Biometrics, CCTV, Fire fighting, Geo tagging & Vehicle performance monitoring
- Self sufficient for standalone operations
- Data recording systems
- Price: 6 crores INR (approx. 1 M US $)

This is to just give you a glimpse of the mobile BSL-3 laboratory that we have. This is a complete solution in terms of a negative air pressure system and a biological waste decontamination system. It has all geo tagging, biometrics, CCTV and all modern, it’s a modern equipped facility.

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Fully Indigenous Mobile BSL-3 Laboratory

ICMR & Klenzaids Partnership

Asia’s first mobile BSL3+ laboratory in a bus

These are the interiors, where you can see that, there are biosafety cabinets, RTPCR machines, ice making machines, centrifuges, autoclaves everything that you need to go and test in times of outbreaks at the sites.

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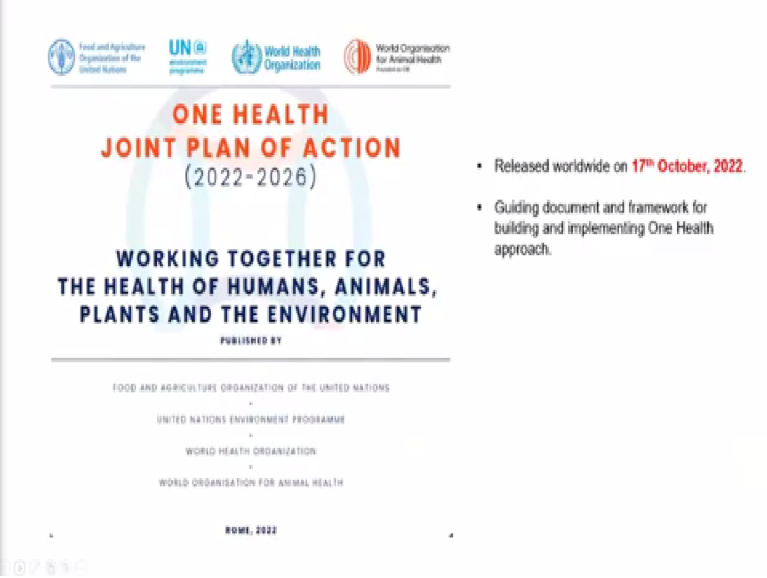

ONE HEALTH
JOINT PLAN OF ACTION
(2022-2026)

WORKING TOGETHER FOR
THE HEALTH OF HUMANS, ANIMALS,
PLANTS AND THE ENVIRONMENT

PUBLISHED BY

FOOD AND AGRICULTURE ORGANIZATION OF THE UNITED NATIONS
•
UNITED NATIONS ENVIRONMENT PROGRAMME
•
WORLD HEALTH ORGANIZATION
•
WORLD ORGANISATION FOR ANIMAL HEALTH

ROME, 2022

- Released worldwide on 17th October, 2022.
- Guiding document and framework for building and implementing One Health approach.

Recently, WHO has also released a one health joint action plan, which I encourage all of you to go and look at.

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Global One Health Joint Action Plan

Published on 17.10.2022

Quadripartite Agreement

- Food and agriculture organization
- United Nations Environment Programme
- World Health Organization
- World organisation for animal health

Action track 1: Enhancing One Health capacities to strengthen health systems

Action track 2: Reducing the risks from emerging and re-emerging zoonotic epidemics and pandemics

Action track 3: Controlling and eliminating zoonotic, neglected tropical and vector-borne diseases

Action track 4: Strengthening the assessment, management and communication of food safety risks

Action track 5: Curbing the silent pandemic of Antimicrobial Resistance (AMR)

Action track 6: Integrating the Environment into One Health

This is a very initial document which lays down certain action tracks, which all countries must follow to have a very comprehensive one health based surveillance. And this talks about strengthening of health care systems, then risk reduction for emerging epidemics and pandemics then also controlling and eliminating zoonotic and vector borne infections. Then strengthening the assessment management and communication of food safety risks.

Then curbing the silent spread of antimicrobial resistance and integrating the environment component also into one health.

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Key Actions

- Surveillance for early detection
- Strengthen laboratory infrastructure
- Trained workforce
- Strengthen healthcare
- Multi-stakeholder engagement
- Strong research infrastructure
- Appropriate governance
- Political support
- International collaboration

So, I would encourage all of you to go and see this. Now ultimately, I would like to enumerate the key actions which are required at our end in collaboration with all relevant stakeholders and partners are setting up surveillance for early detection of diseases of epidemic pandemic potential, as I have shown you in my presentation. Strengthen laboratory infrastructure, to be able to test and detect novel pathogens.

Then it is very important to train our workforce and also sustain the trained workforce, we should not lose them. Then strengthen healthcare infrastructure, in terms of having good isolation facilities, good well-trained staff, in terms of handling patients who are critically ill with a very highly pathogenic infectious disease. It is extremely important to have a multi-stakeholder engagement.

Because when we talk of one health, it cannot be one organization or agency alone, it is many together. Then have a strong research infrastructure, to be able to give innovative solutions to curb the spread of epidemics and pandemics. Appropriate governance is a must. We should have very strong well-defined governance pathways, to avoid any confusion and delays in our execution processes.

Political support is extremely important, without which nothing can be achieved. Then we also need to enter into robust international collaborations, to be able to draw upon the experiences, knowledge of many other countries who may be doing something much better than us.

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One Health involves everyone.

Working together is key to One Health.

So, one health involves everyone. And the key for one health is collaborating, communicating and coordinating, as well as working together. So, that is all from my side and thank you very much.