



Centro de Documentación / Documentation Center

Objetivos/ Objectives

Identificar y atender las necesidades de información, adquisición, organización, almacenamiento, generación, uso y difusión de la información en salud pública veterinaria y proveer recursos bibliográficos técnicos-científicos al equipo de profesionales de la unidad y a los usuarios externos.

Identify and take care of the needs of information, acquisition, organization, storage, generation, use and diffusion of the information in veterinary public health and provide technical scientific bibliographical resources to the professional staff of the unit and to the users external.

Temas de interés general / Subjects of general interest

PREVENTING THE NEXT PANDEMIC

An international network for monitoring the flow of viruses from animals to humans might help scientists head off global epidemics **By Nathan Wolfe**

http://www.gvfi.org/docs/SCIENTIFIC_AMERICAN_april2009.pdf

Informaciones disponibles en formato electrónico / Information available in electronic format

Fiebre aftosa / Foot and Mouth Disease



Detection of foot-and-mouth disease virus infected cattle using infrared thermography

Rainwater-Lovett K, Pacheco JM, Packer C, Rodriguez LL
Vet J. 2009 Jun; 180 (3): 317-24

In this study, infrared thermography (IRT) was assessed as a means of detecting foot-and-mouth disease virus (FMDV)-infected cattle before and after the development of clinical signs. Preliminary IRT imaging demonstrated that foot temperatures increased in FMDV-infected animals. The maximum foot temperatures of healthy (n=53), directly inoculated (DI) (n=12), contact (CT) (n=6), and vaccine trial (VT) (n=21) cattle were measured over the course of FMD infection. A cut-off value was established at 34.4 degrees C (sensitivity=61.1%, specificity=87.7%) with the aim of detecting FMDV-infected animals both before and after clinical signs were observed. Seven of 12 (58%) DI and 3/6 (50%) CT animals showed maximum foot temperatures exceeding the 34.4 degrees C cut-off before the development of foot vesicles. In contrast, only 5/21 (24%) VT animals displayed pre-clinical foot temperatures above

this cut-off possibly indicating partial vaccine protection of this group. These results show IRT as a promising screening technology to quickly identify potentially infected animals for confirmatory diagnostic testing during FMD outbreaks. Further evaluation of this technology is needed to determine the value of IRT in detecting animals with mild clinical signs or sub-clinical infections.

Text in English



Identification of cellular genes affecting the infectivity of foot-and-mouth disease virus

Piccone ME, Feng Y, Chang AC, Mosseri R, Lu Q, Kutish GF, Lu Z, Burrage TG, Gooch C, Rock DL, Cohen SN

J Virol. 2009 Jul; 83 (13): 6681-8

Foot-and-mouth disease virus (FMDV) produces one of the most infectious of all livestock diseases, causing extensive economic loss in areas of breakout. Like other viral pathogens, FMDV recruits proteins encoded by host cell genes to accomplish the entry, replication, and release of infectious viral particles. To identify such host-encoded proteins, we employed an antisense RNA strategy and a lentivirus-based library containing approximately 40,000 human expressed sequence tags (ESTs) to randomly inactivate chromosomal genes in a bovine kidney cell line (LF-BK) that is highly susceptible to FMDV infection and then isolated clones that survived multiple rounds of exposure to the virus. Here, we report the identification of ESTs whose expression in antisense orientation limited host cell killing by FMDV and restricted viral propagation. The role of one such EST, that of ectonucleoside triphosphate diphosphohydrolase 6 (NTPDase6; also known as CD39L2), a membrane-associated ectonucleoside triphosphate diphosphohydrolase that previously was not suspected of involvement in the propagation of viral pathogens and which we now show is required for normal synthesis of FMDV RNA and proteins, is described in this report.

Text in English



A web-based system for near real-time surveillance and space-time cluster analysis of foot-and-mouth disease and other animal diseases

Perez AM, Zeng D, Tseng CJ, Chen H, Whedbee Z, Paton D, Thurmond MC

Prev Vet Med. 2009 Jun

Considerable attention has been given lately to the need for global systems for animal disease surveillance that support real-time assessment of changing temporal-spatial risks. Until recently, however, prospects for development of such systems have been limited by the lack of informatics tools and an overarching collaboration framework to enable real-time data capturing, sharing, analysis, and related decision-making. In this paper, we present some of the tools of the FMD BioPortal System (www.fmd.ucdavis.edu/bioportal), which is a web-based system that facilitates near real-time information sharing, visualization, and advanced space-time cluster analysis for foot-and-mouth disease (FMD). Using this system, FMD information that is collected and maintained at various data acquisition and management sites around the world can be submitted to a data repository using various mutually agreed upon Extensible Markup Language (XML) formats, including Health Level Seven (HL7). FMD BioPortal makes available a set of advanced space-time cluster analysis techniques, including scan statistic-based methods and machine learning-based clustering methods. These techniques are aimed at identifying local clusters of disease cases in relation to the background risk. Data and analysis results can be displayed using a novel visualization environment, which supports multiple views including GIS, timeline, and periodical patterns. All FMD BioPortal functionalities are accessible through the Web and data confidentiality can be secured through user access control and computer network security techniques such as Secure Sockets Layer (SSL). FMD BioPortal is currently operational with limited data routinely collected by the Office International des Epizooties, the GenBank, the FMD World Reference Laboratory in Pirbright, and by the FMD Laboratory at the University of California in Davis. Here we describe technical attributes and capabilities of FMD BioPortal and illustrate its functionality by analyzing and displaying information from a simulated FMD epidemic in California.

Text in English (article in press)

Influenza Aviar / Avian Influenza



Avian influenza virus in mammals

Reperante LA, Rimmelzwaan GF, Kuiken T

Rev sci tech Off int Epiz. 2009; 28 (1): 137-159

Highly pathogenic avian influenza viruses of subtype H5N1 are remarkable because of their expanding non-avian host range and wide tissue tropism. They have caused severe or fatal respiratory and extra-respiratory disease in seven naturally infected species of carnivore. However, they are not unique in their ability to cross the species barrier, to cause clinical disease and mortality, or to replicate in extra-respiratory organs. Low pathogenic avian influenza viruses have crossed from birds to swine, horses, harbour seals, whales and mink; have resulted in severe respiratory disease and mortality; and may have spread beyond the respiratory tract in some of these species. They are also transmitted from mammal to mammal in most species, and have become endemic in swine and horse populations, demonstrating their ability to adapt to and become sustained in mammals. Until now, highly pathogenic avian influenza viruses H5N1 have not acquired this ability, but there are concerns that they may adapt to mammalian species and, thus, could spark an influenza pandemic in humans.

Text in English



The Highly Pathogenic Avian Influenza H5N1 - Initial Molecular Signals for the Next Influenza Pandemic

Suzuki Y

Chang Gung Med J. 2009 May-June; 32 (3): 258-263

A new pandemic influenza in the human world may originate from avian reservoirs. Influenza is one of the most widely spread zoonotic infectious diseases. All avian influenza viruses are type A, and they have often caused pandemics throughout human history. The highly pathogenic H5N1 influenza A viruses have now been spreading to many countries in Asia, Europe and Africa. They have infected an increasing number of humans in at least 15 countries in the world. This paper describes recent advances in the mechanism of transmission of highly pathogenic avian influenza to humans and measures for control of a new pandemic.

Text in English



Immunity to avian influenza A viruses

Doherty PC, Brown LE, Kelso A, Thomas PG

Rev sci tech Off int Epiz., 2009; 28 (1): 175-185

While the basic principles of immunity to the influenza A viruses are probably similar for all vertebrates, detailed understanding is based largely on experiments in laboratory mice. Elements of the innate response limit early virus replication, although high pathogenicity strains can trigger effusive cytokine/chemokine production and lethal shock. Virus clearance is normally mediated via CD8+ effector T cells but, in their absence, the class-switched antibody response can ultimately achieve the same goal. Protection against reinfection is optimally provided by antibody (IgG and IgA) specific for the homologous viral haemagglutinin, and priming against the neuraminidase and the low abundance, conserved M2 protein can also have an effect. Influenza virus-specific plasma cells and CD8+ T cells persist in the long term and the recall of the CD8+ T cell response can lead to earlier virus clearance. The characteristics of the aging immune system and possible, novel vaccine strategies are also considered.

Text in English

Influenza A (H1N1)



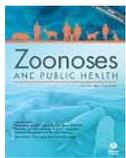
Emergence and pandemic potential of swine-origin H1N1 influenza virus

Neumann G, Noda T, Kawaoka Y

Nature 2009 Jun; 459 (7249): 931-939

Influenza viruses cause annual epidemics and occasional pandemics that have claimed the lives of millions. The emergence of new strains will continue to pose challenges to public health and the scientific communities. A prime example is the recent emergence of swine-origin H1N1 viruses that have transmitted to and spread among humans, resulting in outbreaks internationally. Efforts to control these outbreaks and real-time monitoring of the evolution of this virus should provide us with invaluable information to direct infectious disease control programmes and to improve understanding of the factors that determine viral pathogenicity and/or transmissibility.

Text in English



The Role of Swine in the Generation of Novel Influenza Viruses

Ma W, Lager KM, Vincent AL, Janke BH, Gramer MR, Richt JA

Zoonoses Public Health 2009 May

The ecology of influenza A viruses is very complicated involving multiple host species and viral genes. Avian species have variable susceptibility to influenza A viruses with wild aquatic birds being the reservoir for this group of pathogens. Occasionally, influenza A viruses are transmitted to mammals from avian species, which can lead to the development of human pandemic strains by direct or indirect transmission to man. Because swine are also susceptible to infection with avian and human influenza viruses, genetic reassortment between these viruses and/or swine influenza viruses can occur. The potential to generate novel influenza viruses has resulted in swine being labelled 'mixing vessels'. The mixing vessel theory is one mechanism by which unique viruses can be transmitted from an avian reservoir to man. Although swine can generate novel influenza viruses capable of infecting man, at present, it is difficult to predict which viruses, if any, will cause a human pandemic. Clearly, the ecology of influenza A viruses is dynamic and can impact human health, companion animals, as well as the health of livestock and poultry for production of valuable protein commodities. For these reasons, influenza is, and will continue to be, a serious threat to the wellbeing of mankind.

Text in English



Unraveling the mystery of swine influenza virus

Wang TT, Palese P

Cell 2009 Jun; 137 (6): 983-5

Influenza virus outbreaks occur with regularity, but the severity of outbreaks is not consistent. The recent flu epidemic caused by an H1N1 swine influenza virus presents an opportunity to examine what is known about virulence factors and the spread of infection to better prepare for major influenza outbreaks in the future.

Text in English



Use of revised International Health Regulations during influenza A (H1N1) epidemic, 2009

Katz R

Emerg Infect Dis. 2009 Aug

Strong international health agreements and good planning created a structure and common procedure for nations involved in detection and evaluation of the emergence of influenza A (H1N1). This report describes a timeline of events that led to the determination of the epidemic as a public health emergency of international concern, following the agreed upon procedures of the International Health Regulations. These events illustrate the need for sound international health agreements and should be a call to action for all nations to implement these agreements to the best of their abilities.

Text in English

<http://www.cdc.gov/eid/content/15/8/pdfs/09-0665.pdf>

Inocuidad de los Alimentos / Food Safety



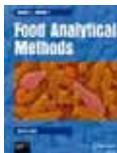
Assessment of personal hygiene and practices of food handlers in municipal public schools of Natal, Brazil

Campos AK, Cardonha MAS, Pinheiro LBC, Ferreira NR, Azevedo PRM, Stamford TLM

Food Control 2009, 20 (9): 807-810

The aim of this study was to assess the hygiene practices of food handlers in municipal schools of Natal, Brazil, where 27 public schools were evaluated, using a checklist and microbiological analysis of hands. It was found that 74.1% of the handlers did not receive periodic training, 51.9% did not undergo annual health examinations and 100% did not practice proper hand hygiene, a situation that reflected significantly ($p < 0.05$) in hand contamination, in which fecal coliforms were detected on 55.6% of the hands analyzed. It was concluded that the schools studied did not have appropriate hygienic conditions, suggesting the need for interventions that ensure the quality of school food served to the children.

Text in English



Comparative evaluation of RTi-PCR and Mini-VIDAS SLM system as predictive tools for the routine detection of *Salmonella* spp. in naturally contaminated food products

Elizaquível P, Gabaldón JA, Aznar R

Food Anal Meth. 2009; 2 (2): 102-109

In the present work, we have evaluated a real-time polymerase chain reaction-based method (RTi-PCR) as a routine laboratory test, by comparing the results obtained in two laboratories with the mini-VIDAS SLM (bioMérieux), a standard accepted immunoenzymatic (enzyme-linked immunosorbent assay) method currently used in the food industry. To that aim, a set of 141 naturally contaminated food samples were analyzed after an enrichment step by conventional PCR and mini-VIDAS and prior to the enrichment by RTi-PCR. Results from both laboratories were statistically analyzed using the kappa coefficients, which indicated a perfect agreement between them. Out of the 141 samples, 11 were positive for *Salmonella* detection by mini-VIDAS, 35 by conventional PCR in Lab1, and 44 in Lab2. Twenty-eight of them tested positive by RTi-PCR in Lab1 and 31 in Lab2. In order to use the evaluated methods as a diagnostic test, their predictive capacity was analyzed on the basis of their positive and negative predictive values, calculated using the result obtained—after enrichment—by conventional PCR as the “gold standard.” Both positive and negative predictive values were higher for RTi-PCR than those obtained for mini-VIDAS, indicating good performance of the RTi-PCR technique—applied without enrichment—in the detection of *Salmonella* in food products. Overall, results obtained in this study on naturally contaminated food products highlighted that RTi-PCR without enrichment is a better predictive tool than mini-VIDAS.

Text in English



Relating microbiological criteria to food safety objectives and performance objectives

van Schothorst M, Zwietering MH, Ross T, Buchanan RL, Cole MB, International Commission on Microbiological Specifications for Foods (ICMSF)

Food Control 2009, 20 (11): 967-979

Microbiological criteria, food safety objectives and performance objectives, and the relationship between them are discussed and described in the context of risk-based food safety management. A modified method to quantify the sensitivity of attributes sampling plans is presented to show how sampling plans can be designed to assess a microbiological criterion. Examples presented show that testing of processed foods for confirmation of safety is often not a practical option, because too many samples would need to be analysed. Nonetheless, in such cases the classical "ICMSF cases" and sampling schemes still offer a risk-based approach for examining food lots for regulatory or trade purposes.

Text in English

Legislación / Legislation



Manual de legislação: programas nacionais de saúde animal do Brasil

Brasil, Ministério de Agricultura, Pecuária e Abastecimento

2009

Este manual reúne os principais atos legais relacionados à Política Nacional de Defesa Agropecuária do Brasil, relativos ao período de 1934 a 2008.

Text in Portuguese

Leishmaniasis



Geographic clustering of leishmaniasis in northeastern Brazil

Schriefer A, Guimarães LH, Machado PR, Lessa M, Lessa HA, Lago E, Ritt G, Góes-Neto A, Schriefer AL, Riley LW, Carvalho EM

Emerg Infect Dis. 2009 Jun; 15 (6): 871-6

To determine whether disease outcomes and clades of *Leishmania braziliensis* genotypes are associated, we studied geographic clustering of clades and most severe disease outcomes for leishmaniasis during 1999-2003 in Corte de Pedra in northeastern Brazil. Highly significant differences were observed in distribution of mucosal leishmaniasis versus disseminated leishmaniasis (DL) ($p < 0.0001$). Concordance was observed between distribution of these disease forms and clades of *L. braziliensis* genotypes shown to be associated with these disease forms. We also detected spread of DL over this region and an inverse correlation between frequency of recent DL diagnoses and distance to a previous DL case. These findings indicate that leishmaniasis outcomes are distributed differently within transmission foci and show that DL is rapidly spreading in northeastern Brazil.

Text in English

<http://www.cdc.gov/eid/content/15/6/pdfs/871.pdf>

Eventos / Events

III Congresso Nacional de Saúde Pública Veterinária e I Encontro Internacional de Saúde Pública Veterinária

25 - 28 Outubro, 2009

Bonito, MS, Brasil

<http://www.portalms.com.br/congressos/sites/particular/saudepublica/index.asp>



Salud Pública Veterinaria
Centro Panamericano de Fiebre Aftosa



Veterinary Public Health
Pan American Foot and Mouth Disease Center

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