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INFORMATIVO CEDOC

No. 5 – Agosto 2006

CEDOC	
Misión	Objetivo
Mantener informados a los profesionales del Centro Panamericano de Fiebre Aftosa – OPS/OMS (PANAFTOSA-OPS/OMS) como proceso de educación continuada en Salud Pública Veterinaria a través del suministro de información técnico-científica.	Ofrecer subsidios bibliográficos técnico-científicos, suministrando información a los usuarios de PANAFTOSA-OPS/OMS en salud pública veterinaria, incluida las zoonosis, fiebre aftosa, enfermedades vesiculares y la inocuidad de alimentos.



**Organización
Panamericana
de la Salud**



Oficina Regional de la
Organización Mundial de la Salud

**CENTRO PANAMERICANO DE FIEBRE AFTOSA
Unidad de Salud Pública Veterinaria – OPS/OMS**

Temas de interés general

Pesquisa estuda a especiação de vetores da leishmaniose visceral

Com abordagem pioneira, uma pesquisa do Instituto Oswaldo Cruz (IOC), uma unidade da Fiocruz, trouxe a mais recente resposta para a seguinte pergunta: se o *Lutzomyia longipalpis*, principal vetor da *Leishmania chagasi*, agente etiológico causador da leishmaniose visceral americana no Brasil, constitui uma única espécie ou não. A pesquisa agregou à análise do som que os machos produzem durante a cópula a observação do comportamento desses vetores e a utilização de marcadores moleculares, evidenciando a existência de pelo menos quatro espécies diferentes no país.

http://www.fiocruz.br/ccs/novidades/ago06/leishmanioses_ioc.htm



Em roxo, protozoários causadores da leishmaniose visceral

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Encefalopatía Espongiforme Bovina

The human prion disease hypothesis does not justify the origin of bovine spongiform encephalopathy

Chatterjee Shyama, Van Marck E

J Postgrad Med. 2006 Jul-Sep; 52 (3): 223-5

The human prion disease hypothesis is based on the authors' declaration that the large-scale import by UK of crushed/whole bones and carcass parts containing soft tissue of mammalian origin, from India, Pakistan and Bangladesh, in the 1960s, ended up under poor control and regulatory conditions as animal feed. The authors declare that the half-burnt bodies of deceased Hindus that floated down the river Ganges were a source of human remains that were utilized together with animal bones by the processing mills for animal feed in the UK. According to Colchesters, these partly cremated bodies were infected with the human transmissible spongiform encephalopathy (TSE) called Creutzfeldt-Jacob disease (CJD), thereby becoming the root cause of the BSE epidemic in the UK. The Colchester hypothesis is partly based on the book by Dr. Alley, a physical anthropologist, who has in the meanwhile disassociated himself with this hypothesis, categorically mentioning that the information in his book and some of the personal discussion Colchesters had with him had been misquoted. In our view, the human prion disease hypothesis is implausible since no cases of bovine spongiform encephalopathy (BSE) have been reported in India to date, this indicating a low level of TSE in the region. Even suspecting that surveillance for BSE in India may not be perfect, BSE epidemics have only occurred in those countries where there has been intensive farming with recycling of waste cattle tissue back to cattle in meat and bone meal. Such a practice is uncommon in India, if it occurs at all.

<http://www.jpqmonline.com/article.asp?issn=0022-3859;year=2006;volume=52;issue=3;spage=223;epage=225;aulast=Chatterjee>

Fiebre Aftosa



Enhanced immune response with foot and mouth disease virus VP1 and interleukin-1 fusion genes

Jong Hyeon Park, Sun Jin Kim, Jae Ku Oem, Kwang Nyeong Lee, Yong Joo Kim, Soo Jeong Kye, Jee Yong Park, Yi Seok Joo

J Vet Sci. 2006 Sep;7(3):257-262

The capsid of the foot and mouth disease (FMD) virus carries the epitopes that are critical for inducing the immune response. In an attempt to enhance the specific immune response, plasmid DNA was constructed to express VP1/interleukin-1 α (IL-1 α) and precursor capsid (P1) in combination with 2A (P1-2A)/IL-1 α under the control of the human cytomegalovirus (HCMV) immediate early promoter and intron. After DNA transfection into MA104 (monkey kidney) cells, Western blotting and an immunofluorescence assay were used to confirm the expression of VP1 or P1-2A and IL-1 α . Mice were inoculated with the encoding plasmids via the intradermal route, and the IgG1 and IgG2a levels were used to determine the immune responses. These results show that although the immunized groups did not carry a high level of neutralizing antibodies, the plasmids encoding the VP1/IL-1 α , and P1-2A/IL-1 α fused genes were effective in inducing an enhanced immune response.

<http://www.vetsci.org/2006/pdf/257.pdf>



Predictions for the timing and use of culling or vaccination during a foot-and-mouth disease epidemic

Hutber AM, Kitching RP, Pilipcinec E.

Res Vet Sci. 2006 Aug; 81(1):31-6.

First-fortnight incidence (FFI) is a modelling parameter that can be used to predict both the prevalence and duration of a foot-and-mouth disease (FMD) epidemic at regional and national levels. With an indication of how long an epidemic may last by the end of week two, it becomes possible to estimate whether vaccination would be economically viable from the start of an epidemic. Where FFI indicates that an epidemic is unlikely to last for as long as an export ban on agricultural produce, it may be inappropriate to implement a policy of 'vaccination to live'. Alternatively where FFI indicates that an epidemic will equal or exceed the ban length, then the benefits of vaccination should be considered at an early stage, during or after the first fortnight. Since blanket vaccination of the national or regional herds and flocks would be both costly and heighten the risk of producing carrier animals, targeting vaccination through risk assessment becomes useful.



Presence of antibodies to non-structural proteins of foot-and-mouth disease virus in repeatedly vaccinated cattle

Lee F, Jong MH, Yang DW.

Vet Microbiol. 2006 Jun 15;115 (1-3):14-20

For the purpose of removing infected animals by detecting humoral immune responses to non-structural proteins of the foot-and-mouth disease (FMD) virus, antibodies induced by contaminated residual non-structural proteins contained in less pure FMD vaccine can be problematic for serological screening. The aim of the present study was to measure the possible presence of antibodies against these non-structural proteins in repeatedly vaccinated calves and beef cattle. Five imported FMD vaccines were examined using two commercial ELISA kits, UBI FMDV NS EIA and Ceditest FMDV-NS, for serological testing. After five doses of vaccination, the serum of one calf tested positive, and two vaccines induced a significant increase in anti-3ABC antibodies in calves. This finding demonstrated that a positive reaction to non-structural proteins due to impurities in the FMD vaccine was detectable using commercial tests. A low percentage of field sera sampled from beef cattle in Kinmen also tested positive, but the key factor resulting in the positive reactions could not be positively identified based on our data.



Sequence analysis of the non-structural 3A and 3C protein-coding regions of foot-and-mouth disease virus serotype Asia1 field isolates from an endemic country

Biswas S, Sanyal A, Hemadri D, Tosh C, Mohapatra JK, Manoj Kumar R, Bandyopadhyay SK.

Vet Microbiol. 2006 Aug 25;116 (1-3): 187-93

A total of 18 foot-and-mouth disease virus (FMDV) serotype Asia1 field isolates belonging to two different lineages (including the divergent group) as delineated earlier in VP1-based phylogeny were sequenced in the non-structural 3A and 3C protein-coding regions. The phylogenetic trees representing the regions coding for the non-structural proteins were very similar to that of the structural VP1 protein-coding region. Phylogenetic comparison at 3C region revealed clustering of Asia1 viruses with the isolates of serotypes O, A and C in the

previously identified clade. Comparison of amino acid sequences identified lineage-specific signature residues in both the non-structural proteins. Overall analysis of the amino acid substitutions revealed that the 3A coding region was more prone to amino acid alterations than 3C region.

Influenza Aviar



Lack of transmission of H5N1 avian-human reassortant influenza viruses in a ferret model

Maines TR, Chen LM, Matsuoka Y, Chen H, Rowe T, Ortin J, Falcon A, Hien NT, Mai le Q, Sedyaningsih ER, Harun S, Tumpey TM, Donis RO, Cox NJ, Subbarao K, Katz JM.
Proc Natl Acad Sci U S A. 2006 Aug 8;103 (32):12121-6

Avian influenza A H5N1 viruses continue to spread globally among birds, resulting in occasional transmission of virus from infected poultry to humans. Probable human-to-human transmission has been documented rarely, but H5N1 viruses have not yet acquired the ability to transmit efficiently among humans, an essential property of a pandemic virus. The pandemics of 1957 and 1968 were caused by avian-human reassortant influenza viruses that had acquired human virus-like receptor binding properties. However, the relative contribution of human internal protein genes or other molecular changes to the efficient transmission of influenza viruses among humans remains poorly understood. Here, we report on a comparative ferret model that parallels the efficient transmission of H3N2 human viruses and the poor transmission of H5N1 avian viruses in humans. In this model, an H3N2 reassortant virus with avian virus internal protein genes exhibited efficient replication but inefficient transmission, whereas H5N1 reassortant viruses with four or six human virus internal protein genes exhibited reduced replication and no transmission. These findings indicate that the human virus H3N2 surface protein genes alone did not confer efficient transmissibility and that acquisition of human virus internal protein genes alone was insufficient for this 1997 H5N1 virus to develop pandemic capabilities, even after serial passages in a mammalian host. These results highlight the complexity of the genetic basis of influenza virus transmissibility and suggest that H5N1 viruses may require further adaptation to acquire this essential pandemic trait.

<http://www.pnas.org/cgi/reprint/103/32/12121>



Planning for Avian Influenza

John G. Bartlett
Ann Intern Med. 2006 Jul 18;145 (2):141-4

Avian influenza, or influenza A (H5N1), has 3 of the 4 properties necessary to cause a serious pandemic: It can infect people, nearly all people are immunologically naive, and it is highly lethal. The Achilles heel of the virus is the lack of sustained human-human transmission. Fortunately, among the 124 cases reported through 30 May 2006, nearly all were acquired by direct contact with poultry. Unfortunately, the capability for efficient human-human transmission requires only a single mutation by a virus that is notoriously genetically unstable, hence the need for a new vaccine each year for seasonal influenza. Influenza A (H5N1) is being compared to another avian strain, the agent of the "Spanish flu" of 1918-1919, which traversed the world in 3 months and caused an estimated 50 million deaths. The question is if we are ready for this type of pandemic, and the answer is probably no. The main problems are the lack of an effective vaccine, very poor surge capacity, a health care system that could not accommodate even a modest pandemic, and erratic regional planning. It's time to get ready, and in the process be ready for bioterrorism, natural disasters, and epidemics of other infectious diseases.

<http://www.annals.org/cgi/reprint/145/2/141.pdf>

EMERGING
INFECTIOUS DISEASES

Biodefense Shield and Avian Influenza

Ken Alibek and Ge Liu
Emerg Infect Dis. 2006 May;12 (5):873-5

In defending against avian influenza virus H5N1, the possibility of adopting treatments being developed for biodefense should not be overlooked. Biodefense medicine primarily concerns respiratory infections because bioweapons in their deadliest form disperse *Bacillus anthracis* and *Yersinia pestis*, the causes of anthrax and plague, and highly contagious viruses like smallpox, Ebola, and Marburg as aerosols. The National Institutes of Health and Department of Defense have funded developing novel biodefense medications designed to stimulate innate mucosal immunity by using interferons (IFNs) and interferon inducers. We suggest that studies begin immediately to explore the potential of IFNs to prevent infections and reduce deaths caused by avian influenza viruses in animal models and humans.

<http://www.cdc.gov/ncidod/EID/vol12no05/pdfs/05-1480.pdf>

Inocuidad de los Alimentos



Minimal processing for healthy traditional foods

Ana Allende, Francisco A. Tomás-Barberán and María I. Gil

Trends in Food Science & Technology 2006 September; 17 (9): 513-519

The industry of fresh-cut fruits and vegetables is constantly growing due to consumers demand. New techniques for maintaining quality and inhibiting undesired microbial growth are demanded in all the steps of the production and distribution chain. In this review, we summarize some of the new processing and preservation techniques that are available in the fresh-cut industry. The combination of sanitizers with other intervention methods is discussed. The use of ultraviolet-C, modified-atmospheres, heat shocks and ozone treatments, alone or in different combinations have proved useful in controlling microbial growth and maintaining quality during storage of fresh-cut produce. In addition, combinations of physical and chemical treatments are also reviewed. The use of acidic or alkaline electrolyzed water (AcEW), chlorine dioxide, power ultrasound and bacteriocins and the potential applications to the fresh-cut products industry to control human microbial pathogens are presented.



Modeling the frequency and duration of microbial contamination events

Mark R. Powell

Intern J Food Microb. 2006 July; 10 (1):93-99

The frequency and duration of microbial contamination events in the environment in which ready-to-eat (RTE) foods are exposed for processing and packaging is subject to uncertainty and variability. Variability, within-model parameter uncertainty, and uncertainty regarding model selection are formally considered in modeling the frequency and duration of such contamination events by *Listeria* species. The estimated duration of contamination events represents a case where variability dominates with relatively little uncertainty about parameter values or model form. The estimated frequency of contamination events represents a case where there is not only substantial variability but also considerable within-model parameter uncertainty, as well as some uncertainty regarding model selection. The Bayesian Information Criterion provides a formal way of taking into account model uncertainty.



Use of epidemiologic data to measure the impact of food safety control programs

International Commission on Microbiological Specifications for Foods (ICMSF)

Food Control 2006 October; 17 (10): 825-837

The purpose of this ICMSF position paper is to describe epidemiologic data that are useful for evaluating the public health impact of food safety control programs, and to identify how epidemiologic data can be used in the evaluative process. The paper describes how epidemiologic data can be focused on food safety and public health targets by measuring process indicators, physical and/or microbiological outcome indicators and public health outcome indicators. ICMSF believes that integration and application of epidemiologic data from appropriate data systems for the evaluation of food safety strategies will justify and/or lead to proper modification of food safety programs and support efforts to determine equivalency in health protection between alternative food safety strategies.

Métodos de Diagnostico



A simple method for preparing synthetic controls for conventional and real-time PCR for the identification of endemic and exotic disease agents.

Smith G, Smith I, Harrower B, Warrilow D, Bletchly C.

J Virol Methods. 2006 Aug;135(2):229-34

Medical and veterinary diagnostic and public health laboratories world-wide are increasingly being called upon to introduce molecular diagnostic tests for both endemic and exotic diseases. This demand has accelerated following increasing terrorism fears. Ironically these same concerns have lead to tightening of both import and export controls preventing many laboratories, particularly those outside of the United States, from gaining access to positive control material. This in turn has prevented many laboratories from introducing much needed molecular diagnostic tests. We describe here a generic approach for preparing synthetic DNA or RNA control material for use in either TaqMan or conventional PCR assays. The production of synthetic controls using this approach does not require cloning or special equipment or facilities beyond that found in any laboratory performing molecular diagnostics. The approach significantly reduces the possibility of

contamination or erroneously reporting false-positive reactions due to contamination from positive control material. Synthetic controls produced using this approach have been employed in all molecular diagnostic tests performed in our laboratory and are used irrespective of whether we possess the organism or not.

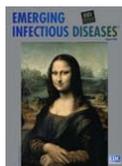
Rabia



Bats: important reservoir hosts of emerging viruses.

Calisher CH, Childs JE, Field HE, Holmes KV, Schountz T.
Clin Microbiol Rev. 2006 Jul;19 (3): 531-45.

Bats (order Chiroptera, suborders Megachiroptera ["flying foxes"] and Microchiroptera) are abundant, diverse, and geographically widespread. These mammals provide us with resources, but their importance is minimized and many of their populations and species are at risk, even threatened or endangered. Some of their characteristics (food choices, colonial or solitary nature, population structure, ability to fly, seasonal migration and daily movement patterns, torpor and hibernation, life span, roosting behaviors, ability to echolocate, virus susceptibility) make them exquisitely suitable hosts of viruses and other disease agents. Bats of certain species are well recognized as being capable of transmitting rabies virus, but recent observations of outbreaks and epidemics of newly recognized human and livestock diseases caused by viruses transmitted by various megachiropteran and microchiropteran bats have drawn attention anew to these remarkable mammals. This paper summarizes information regarding chiropteran characteristics and information regarding 66 viruses that have been isolated from bats. From these summaries, it is clear that we do not know enough about bat biology; we are doing too little in terms of bat conservation; and there remain a multitude of questions regarding the role of bats in disease emergence.



Bat-transmitted Human Rabies Outbreaks, Brazilian Amazon

Elizabeth S.T. da Rosa, Ivanete Kotait, Taciana F.S. Barbosa, Maria L. Carrieri, Paulo E. Brandão, Amiraldo S. Pinheiro, Alberto L. Begot, Marcelo Y. Wada, Rosely C. de Oliveira, Edmundo C. Grisard, Márcia Ferreira, Reynaldo J. da Silva Lima, Lúcia Montebello, Daniele B.A. Medeiros, Rita C.M. Sousa, Gilberta Bensabath, Eduardo H. Carmo, and Pedro F.C. Vasconcelos

Emerging Inf Disease 2006 Aug; 12 (8)

We describe 2 bat-transmitted outbreaks in remote, rural areas of Portel and Viseu Municipalities, Pará State, northern Brazil. Central nervous system specimens were taken after patients' deaths and underwent immunofluorescent assay and histopathologic examination for rabies antigens; also, specimens were injected intracerebrally into suckling mice in an attempt to isolate the virus. Strains obtained were antigenically and genetically characterized. Twenty-one persons died due to paralytic rabies in the 2 municipalities. Ten rabies virus strains were isolated from human specimens; 2 other cases were diagnosed by histopathologic examination. Isolates were antigenically characterized as *Desmodus rotundus* variant 3 (AgV3). DNA sequencing of 6 strains showed that they were genetically close to *D. rotundus*-related strains isolated in Brazil. The genetic results were similar to those obtained by using monoclonal antibodies and support the conclusion that the isolates studied belong to the same rabies cycle, the virus variants found in the vampire bat *D. rotundus*.

<http://www.cdc.gov/ncidod/EID/vol12no08/pdfs/05-0929.pdf>



Studies on an inactivated vaccine against rabies virus in domestic animals

Monaco F, Franchi PM, Lelli R.
Dev Biol (Basel). 2006;125:233-9.

An inactivated vaccine against rabies virus was prepared from the attenuated ATCC PV-12 viral rabbit Pasteur strain. The virus was grown on Baby Hamster Kidney (BHK21) cells, and the supernatant was purified by filtration and inactivated with beta-propiolactone. The inactivated product was checked according to the NHI and European Pharmacopoeia methods. Part of the product was then lyophilised and the other part was adjuvanted with Al(OH)₃. Both parts were used to vaccinate and boost groups of horses, cattle and sheep at different intervals. Their immunogenicity was compared with a similar commercial product. Blood samples were collected on a regular basis and the antibody titre was determined by the Fluorescence Antibody Virus Neutralisation (FAVN) test. No significant differences were found between species after both inoculations even though the immune response increased in intensity and duration after the booster dose in all the animals tested and was stronger and lasted longer with the adjuvanted aliquot.

Reuniones, conferencias, seminarios



BCM 2006 • BIOLOGICAL CRISIS MANAGEMENT IN HUMAN AND VETERINARY MEDICINE EMERGING DISEASES: PREPAREDNESS AND IMPLEMENTATION ISSUES

Ecole Normale Supérieure, Lyon (France), 5-8 November 2006

The meeting aims at increasing preparedness against emerging or re-emerging diseases.

Emerging diseases such as avian influenza and pandemic risk are never far from the headlines. **BCM 2006** will provide a unique forum for scientists, industry and regulatory body representatives to meet and discuss the issues of biological crisis management.

<http://www.bcm2006.org/>



First International Conference of OIE Reference Laboratories and Collaborating Centres

Florianopolis (Brasil), 3-5 de diciembre de 2006

The purpose of the Conference is to provide a multidisciplinary forum for strengthening scientific cooperation within the Network of OIE Reference Laboratories and Collaborating Centres as well as Veterinary Services. The Conference will further promote the updating and setting of standards for methodologies in the fields of diagnostics, vaccine quality and biosecurity; the improvement of links between existing Reference Laboratories, Collaborating Centres and national official and private laboratories; and discuss methods to support developing and in-transition countries through capacity building and training programmes.

<http://www.oie.int/eng/Brazil/home.htm>



1st OIE International Conference of GIS Veterinary Activities

Silvi Marina (TE) Abruzzo (Italia), 8-11 de octubre de 2006

Objectives: To provide a forum for the exchange of the latest information and application of Geographic Information System (GIS) in veterinary activities; To identify GIS tools for animal diseases and zoonoses monitoring; To identify priority needs for the development of GIS tools in animal diseases and zoonoses surveillance; To discuss a proposal for the implementation of a GIS portal for veterinary activities.

<http://www.gisconference.it/>

Tránsito de los animales



A description of cattle movements in two departments of Buenos Aires province, Argentina.

Leon EA, Stevenson MA, Duffy SJ, Ledesma M, Morris RS

Prev Vet Med. 2006 Sep 15;76 (1-2):109-20

We present a descriptive analysis of cattle movement information retrieved from the Argentinean animal movement database for two departments in the province of Buenos Aires during 2004. For each quarter of the year (January to March, April to June, July to September, and October to December) we report the number of on- and off-farm movement events for the purpose of finishing. Our analyses show that the distribution of the number of finishing-related movement events per farm was skewed, with the majority of farms reporting at least 1 and less than 5% of farms of reporting greater than 15 finishing related movement events throughout the year. The frequency of finishing-related movement events varied over time, with a 1.2-1.8-fold increase in reported movement events from April to September, compared with the rest of the year. These analyses indicate that cattle movement patterns in these departments are dependent on the relative mix of constituent cattle enterprise types. Departments with a mixture of breeding and finishing enterprises behave as potential recipients and distributors of infectious disease, whereas departments comprised of primarily finishing enterprises are predominantly recipients of infectious disease, rather than distributors. Data integrity audits of the Argentinean animal movement database, on a regular or intermittent basis, should allow the presence of bias in these data to be quantified in greater detail.

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