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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

Plano de Ação para Febre Aftosa

Volume I: Atendimento à Notificação de Suspeita de Doença Vesicular

Brasil. Ministério da Agricultura, Pecuária e Abastecimento
2009

<http://www.panaftosa.org.br/Comp/MAPA/ManuaisTecnicos/PlanoAcaoFebreAftosa/PlanoAcaoFebreAftosa.zip>

O presente documento elaborado pelo Ministério de Agricultura, Pecuária e Abastecimento (MAPA) refere-se ao Plano de Ação para Febre Aftosa, que agrupa o conhecimento e os procedimentos básicos referentes ao atendimento de suspeitas de doenças vesiculares e à atuação em ações de emergência veterinária para eliminação de focos de febre aftosa. As fases de Investigação e de Alerta constituem o Volume I do Plano de Ação.



Coletânea de Imagens: Lesões de Febre Aftosa e de Outras Doenças Incluídas no Sistema Nacional de Vigilância de Doenças Vesiculares

Brasil. Ministério da Agricultura, Pecuária e Abastecimento
2009

<http://www.panaftosa.org.br/Comp/MAPA/ManuaisTecnicos/ColetaneaImagens/ColetaneaImagens.zip>

Como parte do Plano de Ação para Febre Aftosa - Volume I, o Departamento de Saúde Animal (DSA) do Ministério de Agricultura, Pecuária e Abastecimento (MAPA) publica a presente coletânea de fotos de lesões de febre aftosa e de outras enfermidades envolvidas na vigilância de doenças vesiculares.



Informaciones disponibles en formato electrónico / Information available in electronic format

Brucelosis / Brucellosis



The genus *Brucella* and clinical manifestations of brucellosis

Xavier MN, Paixão TA, Costa EA, Santos RL

Cienc Rural Oct 2009; 39, (7): 2252-2260

Infection with bacteria of the genus *Brucella* results in major economic and political impact by causing reproductive diseases in a significant number of domestic animal species. Moreover, it has a great social significance, since many species are capable of causing human infection, with severe consequences. Dissemination of knowledge on a specific disease is an essential step for its control. Considering that brucellosis is still the most prevalent zoonosis in the world, information about taxonomy, clinical signs in domestic animals and humans are crucial for attempting to reduce the prevalence of this disease. The recent isolation and characterization of non-classical species of *Brucella* indicates that a lot remains to be discovered about this genus. Nevertheless, due to the social-economic importance of brucellosis, this review aims to clarify points related to taxonomy of the genus and describe the clinical relevance of infection in humans and domestic animals.

Text in English

<http://www.scielo.br/pdf/cr/v39n7/a268cr1542.pdf>

Febre Aftosa / Foot-and-Mouth Disease



Expression and purification of an anti-Foot-and-mouth disease virus single chain variable antibody fragment in tobacco plants

Joensuu JJ, Brown KD, Conley AJ, Clavijo A, Menassa R, Brandle JE

Transgenic Res. 2009 Oct; 18 (5): 685-96

Low-cost recombinant antibodies could provide a new strategy to control Foot-and-mouth disease virus (FMDV) outbreaks by passive immunization of susceptible animals. In this study, a single chain variable

antibody fragment (scFv) recognizing FMDV coat protein VP1 was expressed in transgenic tobacco plants. To enhance the accumulation of scFv protein, the codon-usage of a murine hybridoma-derived scFv gene was adjusted to mimic highly expressed tobacco genes and fused to an elastin-like polypeptide (ELP) tag. This scFv-ELP fusion accumulated up to 0.8% of total soluble leaf protein in transgenic tobacco. To recover scFv-ELP protein from the leaf extract, a simple and scalable purification strategy was established. Purified scFv-ELP fusion was cleaved to separate the scFv portion. Finally, it was shown that the purified scFv proteins retained their capacity to bind the FMDV in the absence or presence of ELP fusion.

Text in English

Influenza Aviar / Avian Influenza



(Highly pathogenic) avian influenza as a zoonotic agent

Kalthoff D, Globig A, Beer M
Vet Microbiol. 2009 Aug

Zoonotic agents challenging the world every year afresh are influenza A viruses. In the past, human pandemics caused by influenza A viruses had been occurring periodically. Wild aquatic birds are carriers of the full variety of influenza virus A subtypes, and thus, most probably constitute the natural reservoir of all influenza A viruses. Whereas avian influenza viruses in their natural avian reservoir are generally of low pathogenicity (LPAIV), some have gained virulence by mutation after transmission and adaptation to susceptible gallinaceous poultry. Those so-called highly pathogenic avian influenza viruses (HPAIV) then cause mass die-offs in susceptible birds and lead to tremendous economical losses when poultry is affected. Besides a number of avian influenza virus subtypes that have sporadically infected mammals, the HPAIV H5N1 Asia shows strong zoonotic characteristics and it was transmitted from birds to different mammalian species including humans. Theoretically, pandemic viruses might derive directly from avian influenza viruses or arise after genetic reassortment between viruses of avian and mammalian origin. So far, HPAIV H5N1 already meets two conditions for a pandemic virus: as a new subtype it has been hitherto unseen in the human population and it has infected at least 438 people, and caused severe illness and high lethality in 262 humans to date (August 2009). The acquisition of efficient human-to-human transmission would complete the emergence of a new pandemic virus. Therefore, fighting H5N1 at its source is the prerequisite to reduce pandemic risks posed by this virus. Other influenza viruses regarded as pandemic candidates derive from subtypes H2, H7, and H9 all of which have infected humans in the past. Here, we will give a comprehensive overview on avian influenza viruses in concern to their zoonotic potential.

Text in English (article in press)



Sistema AVE de información geográfica para la asistencia en la vigilancia epidemiológica de la influenza aviar, basado en el riesgo

FAO, 2009

Dentro de las actividades principales de asistencia, la FAO mediante un acuerdo de cooperación con el INTA (Instituto de Tecnología Agropecuaria de la Argentina) y la colaboración del Centro de Epidemiología de la Universidad de Massey en Nueva Zelanda, desarrollaron el Sistema **AVE** de Información Geográfica para Asistencia en la Vigilancia Epidemiológica de la Influenza Aviar Altamente Patógena (basado en riesgo). El Sistema AVE considera ocho factores de riesgo por los que la IAAP – H5N1 puede ingresar a los países de ALC (fronteras, aeropuertos, ríos, sitios de asentamiento de aves silvestres, rutas pecuarias terrestres, aves de traspatio, espejos de agua y comercialización de aves) cada uno de estos temas o capas son sobrepuestos en un determinado mapa, de forma sencilla para evaluar el riesgo sobre el posible ingreso de la enfermedad a una área determinada, así como para realizar una vigilancia epidemiológica de la enfermedad dirigida al riesgo, reduciendo los costos de las

operaciones de vigilancia en los servicios veterinarios nacionales de la región.

El presente Manual del Sistema AVE se espera que sea de utilidad para que el personal de los servicios veterinarios nacionales pueda elaborar mapas de riesgo sobre la IAAP – H5N1 u otras enfermedades aviarias, sirviendo también de apoyo para el personal técnico del sector privado y la academia en los países de la región.

Text in Spanish

<ftp://ftp.fao.org/docrep/fao/012/i0943s/i0943s00.pdf>

Leishmanioses / Leishmaniasis



First report of vertical transmission of Leishmania (Leishmania) infantum in a naturally infected bitch from Brazil

Silva SM, Ribeiro VM, Ribeiro RR, Tafuri WL, Melo MN, Michalick MS
Vet Parasitol. 2009 Aug

Dogs are the most important reservoir of *Leishmania (L.) infantum*, the causal agent of visceral leishmaniasis (VL) in Brazil. Vectorial infection is the main route of transmission of the parasites. This paper reports the first case of vertical transmission of *L. infantum* in Brazil, confirmed by PCR and immunohistochemistry techniques in samples from spleen and liver of two stillborn pups from a bitch naturally infected with *L. infantum* in Belo Horizonte city, endemic area of VL. This result confirms the existence of transplacental transmission of *Leishmania* between dogs, and suggests the need for further studies to determine the rate of occurrence of this fact in endemic areas and what is their role in the epidemiology of the disease.

Text in English (article in press)



Ocorrência de leishmaniose tegumentar em cães de área endêmica no Estado do Paraná

[Occurrence of cutaneous leishmaniasis in dogs of endemic area, Paraná State]
Pittner E, Voltarelli E, Perles TF, Arraes SMAA, Silveira TGVW, Lonardoni MVC
Arq Bras Med Vet Zootec. 2009; 61 (3): 561-565

The infection by *Leishmania braziliensis* complex was studied in 50 dogs from Maringá, PR, where American Cutaneous Leishmaniasis (ACL) in humans have been detected. Data were collected from August to December 2006 in an area in which ACL cases in humans were reported from 2003 to 2004. Indirect immunofluorescent test (IIF) and polymerase chain reaction (PCR) were applied. No lesions were found in the animals, although 12 (24.0%) had positive IIF and/or PCR. Positiveness was 14.0% for IIF and PCR. Lab tests showed that eight (22.8%) out of the 35 home animals were ACL positive. The other 15 animals were stray dogs, out of which four (26.7%) were PCR positive. The appearance of asymptomatic *Leishmania*-infected dogs in an ACL endemic area may be an indicator of ACL transmission potential for humans and a reference for the establishment of control measures and disease prevention.

Text in Portuguese

<http://www.scielo.br/pdf/abmvz/v61n3/06.pdf>

Rabia / Rabies



Emerging technologies for the detection of rabies virus: challenges and hopes in the 21st century

Fooks AR, Johnson N, Freuling CM, Wakeley PR, Banyard AC, McElhinney LM, Marston DA, Dastjerdi A, Wright E, Weiss RA, Müller T
PLoS Negl Trop Dis. 2009 Sep; 3 (9): e530

The diagnosis of rabies is routinely based on clinical and epidemiological information, especially when exposures are reported in rabies-endemic countries. Diagnostic tests using conventional assays that appear to be negative, even when undertaken late in the disease and despite the clinical diagnosis, have a tendency, at times, to be unreliable. These tests are rarely optimal and entirely dependent on the nature and quality of the sample supplied. In the course of the past three decades, the application of molecular biology has aided in the development of tests that result in a more rapid detection of rabies virus. These tests enable viral strain identification from clinical specimens. Currently, there are a number of molecular tests that can be used to complement conventional tests in rabies diagnosis. Indeed the challenges in the 21st century for the development of rabies diagnostics are not of a technical nature; these tests are available now. The challenges in the 21st century for diagnostic test developers are two-fold: firstly, to achieve internationally accepted validation of a test that will then lead to its acceptance by organisations globally. Secondly, the areas of the world where such tests are needed are mainly in developing regions where financial and logistical barriers prevent their implementation. Although developing countries with a poor healthcare infrastructure recognise that molecular-based diagnostic assays will be unaffordable for routine use, the cost/benefit ratio should still be measured. Adoption of rapid and affordable rabies diagnostic tests for use in developing countries highlights the importance of sharing and transferring technology through laboratory twinning between the developed and the developing countries. Importantly for developing countries, the benefit of molecular methods as tools is the capability for a differential diagnosis of human diseases that present with similar clinical symptoms. Antemortem testing for human rabies is now possible using molecular techniques. These barriers are not insurmountable and it is our expectation that if such tests are accepted and implemented where they are most needed, they will provide substantial improvements for rabies diagnosis and surveillance. The advent of molecular biology and new technological initiatives that combine advances in biology with other disciplines will support the development of techniques capable of high throughput testing with a low turnaround time for rabies diagnosis.

Text in English

<http://www.plosntds.org/article/info%3Adoi%2F10.1371%2Fjournal.pntd.0000530>



Novel vaccines to human rabies

Ertl HC

PLoS Negl Trop Dis. 2009 Sep; 3 (9): e515

It is not generally appreciated that descendants of the H1N1 influenza A virus that caused the catastrophic and historic pandemic of 1918–1919 have persisted in humans for more than 90 years and have continued to contribute their genes to new viruses, causing new pandemics, epidemics, and epizootics. The current international pandemic caused by a novel influenza A (H1N1) virus derived from two unrelated swine viruses, one of them a derivative of the 1918 human virus, adds to the complexity surrounding this persistent progenitor virus, its descendants, and its several lineages.

Text in English

<http://content.nejm.org/cgi/content/full/NEJMp0904819?resourcetype=HWCIT>

Reacción en Cadena de la Polimerasa de Transcriptasa Inversa (RT-PCR) / Reverse Transcriptase Polymerase Chain Reaction (RT-PCR)



A review of RT-PCR technologies used in veterinary virology and disease control: sensitive and specific diagnosis of five livestock diseases notifiable to the World Organisation for Animal Health

Hoffmann B, Beer M, Reid SM, Mertens P, Oura CA, van Rijn PA, Slomka MJ, Banks J, Brown IH, Alexander DJ, King DP

Vet Microbiol. 2009 Oct ; 139 (1-2): 1-23

Real-time, reverse transcription polymerase chain reaction (rRT-PCR) has become one of the most

widely used methods in the field of molecular diagnostics and research. The potential of this format to provide sensitive, specific and swift detection and quantification of viral RNAs has made it an indispensable tool for state-of-the-art diagnostics of important human and animal viral pathogens. Integration of these assays into automated liquid handling platforms for nucleic acid extraction increases the rate and standardisation of sample throughput and decreases the potential for cross-contamination. The reliability of these assays can be further enhanced by using internal controls to validate test results. Based on these advantageous characteristics, numerous robust rRT-PCRs systems have been developed and validated for important epizootic diseases of livestock. Here, we review the rRT-PCR assays that have been developed for the detection of five RNA viruses that cause diseases that are notifiable to the World Organisation for Animal Health (OIE), namely: foot-and-mouth disease, classical swine fever, bluetongue disease, avian influenza and Newcastle disease. The performance of these tests for viral diagnostics and disease control and prospects for improved strategies in the future are discussed.

Text in English

Rickettsiosis



Ecology of rickettsia in South America

Labruna MB

Ann N Y Acad Sci. 2009 May; 1166: 156-66

Until the year 2000, only three *Rickettsia* species were known in South America: (i) *Rickettsia rickettsii*, transmitted by the ticks *Amblyomma cajennense*, and *Amblyomma aureolatum*, reported in Colombia, Argentina, and Brazil, where it is the etiological agent of Rocky Mountain spotted fever; (ii) *Rickettsia prowazekii*, transmitted by body lice and causing epidemic typhus in highland areas, mainly in Peru; (iii) *Rickettsia typhi*, transmitted by fleas and causing endemic typhus in many countries. During this new century, at least seven other rickettsiae were reported in South America: *Rickettsia felis* infecting fleas and the tick-associated agents *Rickettsia parkeri*, *Rickettsia massiliae*, *Candidatus*"*Rickettsia amblyommii*," *Rickettsia bellii*, *Rickettsia rhipicephali*, and *Candidatus*"*Rickettsia andeanae*." Among these other rickettsiae, only *R. felis*, *R. parkeri*, and *R. massiliae* are currently recognized as human pathogens. *R. rickettsii* is a rare agent in nature, infecting < or =1% individuals in a few tick populations. Contrastingly, *R. parkeri*, *Candidatus*"*R. amblyommii*," *R. rhipicephali*, and *R. bellii* are usually found infecting 10 to 100% individuals in different tick populations. Despite rickettsiae being transmitted transovarially through tick generations, low infection rates for *R. rickettsii* are possibly related to pathogenic effect of *R. rickettsii* for ticks, as shown for *A. aureolatum* under laboratory conditions. This scenario implies that *R. rickettsii* needs amplifier vertebrate hosts for its perpetuation in nature, in order to create new lines of infected ticks (horizontal transmission). In Brazil, capybaras and opossums are the most probable amplifier hosts for *R. rickettsii*, among *A. cajennense* ticks, and small rodents for *A. aureolatum*.

Text in English

Tuberculosis Bovina / Bovine Tuberculosis



Mycobacterium bovis at the animal-human interface: A problem, or not?

Michel AL, Müller B, van Helden PD

Vet Microbiol. 2009 Sep

Mycobacterium bovis is a pathogen of significant importance in livestock and a wide range of wild animal species worldwide. It is also known to cause tuberculosis disease in humans, a fact which has raised renewed concerns regarding the zoonotic risk for humans, especially those living at the animal-human interface. This review consolidates recent reports in the literature mainly on animal and zoonotic

tuberculosis with an emphasis on evolution, epidemiology, treatment and diagnosis. The information presented reveals the fundamental differences in the complexity and level at which the disease affects the economy, ecosystem and human population of regions where animal tuberculosis control is achieved and regions where little or no control is implemented. In conclusion the review suggests that bovine tuberculosis has essentially been reduced to a disease of economic importance in the developed world, while low-income countries are facing a multifaceted impact which potentially affects the health of livestock, humans and ecosystems and which is likely to increase in the presence of debilitating diseases such as HIV/AIDS and other factors which negatively affect human livelihoods.

Text in English (article in press)

Zoonosis / Zoonoses



Surveillance and Control of Zoonotic Agents Prior to Disease Detection in Humans

Childs JE, Gordon ER

Mt Sinai J Med. 2009 Sep; 76 (5): 421-428

The majority of newly emerging diseases are zoonoses caused by pathogens transmitted directly or indirectly through arthropod vectors to humans. Transmission chains leading to human infection frequently involve intermediate vertebrate hosts, including wildlife and domestic animals. Animal-based surveillance of domestic and wild animals for zoonotic pathogens is a global challenge. Until recently, there has been no scientific, social, or political consensus that animal-based surveillance for zoonotic pathogens merits significant infrastructural investment, other than the fledgling efforts with avian influenza. National institutions charged with strategic planning for emerging diseases or intentional releases of zoonotic agents emphasize improving diagnostic capabilities for detecting human infections, modifying the immune status of human or domestic animals through vaccines, producing better antiviral or antibacterial drugs, and enhancing human-based surveillance as an early warning system. With the exception of human vaccination, these anthropocentric approaches target post-spillover events, and none of these avenues of research will reduce the risk of additional emergences of pathogens from wildlife. Novel schemes for preventing spillover of human pathogens from animal reservoir hosts can spring only from an understanding of the ecological context and biological interactions that result in zoonotic disease emergence. Although the benefits derived from investments to improve surveillance and knowledge of zoonotic pathogens circulating among wildlife reservoir populations are uncertain, our experience with human immunodeficiency virus and the pandemic influenza inform us of the outcomes that we can expect by relying on detection of post-spillover events among sentinel humans.

Text in English

Eventos / Events

36º CONBRAVET. Congresso Brasileiro de Medicina Veterinária

8-12 **Novembro**, 2008

Porto Seguro, Bahia, Brasil

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

16th World Veterinary Poultry Congress

08-11 **November**, 2009

Marrakesh, Morocco

<http://www.wvpc2009.org/>



Salud Pública Veterinaria
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Veterinary Public Health
Pan American Foot and Mouth Disease Center

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apimente@panaftosa.ops-oms.org