



CENTRO DE DOCUMENTACIÓN Biblioteca

INFORMATIVO CEDOC

No. 1 – Febrero 2007

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**



**XXXIV Reunión Ordinaria de la Comisión Sudamericana para la
Lucha contra la Fiebre Aftosa**

**Caracas, Venezuela
15 al 16 de marzo de 2007**

AGENDA TENTATIVA

<http://www.panaftosa.org.br/inst/cosalfa/pro34esp.pdf>



**SEMINARIO INTERNACIONAL
"Nivel Local: Eslabón Crítico en la Gerencia de los Programas de
Sanidad Animal"**

**Caracas, Venezuela
12 al 13 de marzo de 2007**

PROGRAMA PRELIMINAR

<http://www.panaftosa.org.br/inst/cosalfa/sEMINARIO34.pdf>

Informaciones disponibles en formato electrónico

Se puede tener acceso a las publicaciones en el link citado bajo los resúmenes presentados o solicitarlas a nuestro Centro de Documentación a través del correo electrónico apimente@panaftosa.ops-oms.org

Atención Veterinaria a Nivel Local: bibliografía

Atención veterinaria local

Serrão UM, Dora JFP, Muzio F, Tamayo H, Astudillo VM, Zottele A
Bol Cent Panamerican Fiebre Aftosa 2001;(57): 60-73.
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Atención veterinaria a nivel local. La planificación en un Municipio Piloto

Cotrina N, Zottele A, Pereira JC
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Aspectos intersectoriales e interdisciplinarios en los sistemas de atención veterinaria local

Astudillo VM, Zottele A
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Aseguramiento de la calidad de atención sanitaria en servicios veterinarios que cuentan con participación social

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Seminario Internacional sobre Aspectos de la Vigilancia Aplicado a la Gestión Sanitaria en Áreas con Diferentes Status de la Fiebre Aftosa. Porto Alegre, RS, 15-17 marzo 1999.
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Contribuciones del médico veterinario al desarrollo local

Málaga H
Bol Cent Panamerican Fiebre Aftosa 1995; (61):14-21.
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Fortalecimiento de los sistemas de información geográfica y vigilancia epidemiológica de la salud animal a nivel local

Astudillo VM
Seminario Internacional sobre Sistemas de Vigilancia Epidemiológica con Especial Referencia para la Prevención de las Enfermedades Exóticas. Río de Janeiro, 18-20 marzo 1991.
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La organización de los Servicios Veterinarios en Latinoamérica y su evolución

Gimeno E
Rev sci tech Off int Epiz. 2003; 22 (4):449-61.
http://www.oie.int/eng/publicat/rt/2202/9_GIMENOesp.pdf

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<http://bvs.panaftosa.org.br/textoc/Astudillo-participacion-social-ConfMilenio.pdf>

Servicios Veterinarios: cómo establecer el aseguramiento de la calidad en países en desarrollo

Astudillo V, Vargas IN
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Astudillo VM, Zottele A, Serrão UM
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Brucellosis



Programa Nacional de Controle e Erradicação da Brucelose e da Tuberculose Animal (PNCEBT): manual técnico

Brasil. Ministério da Agricultura,

Pecuária e Abastecimento

Brasília: MAPA/DAS/DAS, 2006

http://www.spcib.gov.br/2006/03/06/PAGE=MAPA/PROGRAMAS/UEEA_ANIMAL/PNCEBT/MANUAL_TECNICO/UEEA/COMPLETO.PDF

Encefalopatías Espongiformes Transmisibles



Advanced survival models for risk-factor analysis in scrapie

Corbière F, Barillet F, Andréoletti O, Fidelle F, Laphitz-Bordet N, Schelcher F, Joly P

J Gen Virol. 2007; 88: 696-705

Because of the confounding effects of long incubation duration and flock management, accurate epidemiological studies of scrapie outbreaks are difficult to carry out. In this study, 641 Manech red-faced sheep from six scrapie-affected field flocks in Pyrénées Atlantiques, France, were monitored for clinical scrapie over a 6–9 year period. Over this period, 170 scrapie clinical cases were recorded and half of the culled animals were submitted for post-mortem transmissible spongiform encephalopathy diagnosis to assess their infectious status. Collected data were analysed using a 'mixture cure model' approach, which allowed for the discriminating effect of PrP genotype and flock origin on incidence and incubation period. Simulations were performed to evaluate the applicability of such a statistical model to the collected data. As expected, ARR heterozygote sheep were less at risk of becoming infected than ARQ/ARQ individuals and had a greater age at clinical onset. Conversely, when compared with ARQ/ARQ, the VRQ haplotype was associated with an increased infection risk, but not a shorter incubation period. Considering the flock effect, we observed that a high incidence rate was not associated with shorter incubation periods and that the incubation period could be significantly different in flocks harbouring similar infection risks. These results strongly support the conclusion that other parameters, such as the nature of the agent or flock management, could interfere with epidemiological dynamics of the infection in scrapie-affected flocks.



Efficient dissemination of prions through preferential transmission to nearby cells

Paquet S, Langevin C, Chapuis J, Jackson GS, Laude H, Vilette D
J Gen Virol. 2007; 88: 706-13.

Despite circumstantial evidence that prions can be found extracellularly or at the surface of infected cells, little is known about how these infectious agents spread from cell to cell. In order to gain better insight into this critical issue, this study used two different cell lines (neuroglial MovS and epithelial Rov cells) that have previously been shown to be permissive for ovine prion multiplication. Co-culture of infected cells and uninfected target cells at a ratio of 1 : 9 resulted in total infection of MovS cells within 10 days but not of Rov cell cultures, suggesting that the efficiency of prion dissemination may vary greatly depending on the type of permissive cell. Analysis of the spatial distribution of the newly infected cells revealed that, although long-range spread could also occur, cells proximal to the infected donor cells consistently accumulated more abnormal PrP, consistent with preferential infection of nearby cells. This experimental approach, focused on dissemination among living cells, could help in the analysis of mechanisms involved in the cell-to-cell spread of prion infections.

Epidemiología



An event-based model of superspreading in epidemics

James A, Pitchford JW, Plank MJ
Proc Biol Sci. 2007 Mar; 274 (1610): 741-7

Many recent disease outbreaks (e.g. SARS, foot-and-mouth disease) exhibit superspreading, where relatively few individuals cause a large number of secondary cases. Epidemic models have previously treated this as a demographic phenomenon where each individual has an infectivity allocated at random from some distribution. Here, it is shown that superspreading can also be regarded as being caused by environmental variability, where superspreading events (SSEs) occur as a stochastic consequence of the complex network of interactions made by individuals. This interpretation based on SSEs is compared with data and its efficacy in evaluating epidemic control strategies is discussed.

<http://www.math.canterbury.ac.nz/~m.plank/papers/prsb07.pdf>

Fiebre Aftosa



Genetic variation of foot-and-mouth disease virus isolates recovered from persistently infected water buffalo (*Bubalus bubalis*)

Barros JJF, Malirat V, Rebello MA, Costa EC, Bergmann E

Vet Microb. 2007; 120 (1-2):50-62

Genetic variation of foot-and-mouth disease virus (FMDV) isolates, serotype O, recovered serially over a 1-year period from persistently infected buffalos was assessed. The persistent state was established experimentally with plaque-purified FMDV, strain O₁Campos, in five buffalos (*Bubalus bubalis*). Viral isolates collected from esophageal-pharyngeal (EP) fluids for up to 71 weeks after infection were analyzed at different times by nucleotide sequencing and T₁ RNase oligonucleotide fingerprinting to assess variability in the VP1-coding region and in the complete genome, respectively. Genetic variation increased, although irregularly, with time after infection. The highest values observed for the VP1-coding region and for the whole genome were 2.5% and 1.8%, respectively. High rates of fixation of mutations were observed using both methodologies, reaching values of 0.65 substitutions per nucleotide per year (s/nt/y) and 0.44 s/nt/y for nucleotide sequencing and oligonucleotide fingerprinting, respectively, when selected samples recovered at close time periods were analyzed.

The data herein indicate that complex mixtures of genotypes may arise during FMDV type O persistent infection in water buffalos, which can act as viral reservoirs and also represent a potential source of viral variants. These results fit within the quasi-species dynamics described for FMDV, in which viral populations are constituted by related, non-identical genomes that evolve independently from each other, and may predominate at a given time.



Mosaic structure of foot-and-mouth disease virus genomes

Jackson AL, O'Neill H, Maree F, Blignaut B, Carrillo C, Rodriguez L, Haydon DT

J Gen Virol. 2007; 88: 487-92

The results of a simple pairwise-scanning analysis designed to identify inter-serotype recombination fragments, applied to genome data from 156 isolates of *Foot-and-mouth disease virus* (FMDV) representing all seven serotypes, are reported. Large numbers of candidate recombinant fragments were identified from all parts of the FMDV genome, with the exception of the capsid

genes, within which such fragments are infrequent. As expected, intertypic fragment exchange is most common between geographically sympatric FMDV serotypes. After accounting for the likelihood of intertypic convergence in highly conserved parts of the FMDV genome, it is concluded that intertypic recombination is probably widespread throughout the non-structural genes, but that recombination over the 2B/C and 3B/C gene boundaries appears to be less frequent than expected, given the large numbers of recombinant gene fragments arising in these genes.



Veterinary epidemiology: vaccination strategies for foot-and-mouth disease

Kitching RP, Taylor NM, Thrusfield MV.

Nature 2007 Feb;445(7128):E12;

discussion

E12-3

When foot-and-mouth disease struck the United Kingdom in 2001, the traditional 'stamping out' policy of 1967-68 was supplemented by the pre-emptive culling of animals in premises contiguous to infected premises. A model proposed by Tildesley et al. indicates that the introduction of vaccination should at least halve the number of premises that would need to be subjected to culling in the event of another outbreak. We contest, however, that the overlapping confidence intervals of the outputs of their model, and the inconsistency of their results compared with those from previous models, call into question the model's value as a decision tool, while adding little to the recognized tenet of ring vaccination.

Veterinary epidemiology: Vaccination strategies for foot-and-mouth disease (reply)

Tildesley MJ, Savill NJ, Shaw DJ, Deardon R, Brooks SP, Woolhouse ME, Grenfell BT, Keeling MJ

Nature. 2007 Feb 8;445(7128):E12-3

Kitching express concerns about our mathematical models of reactive vaccination strategies for the control of foot-and-mouth disease epidemics. However, in our view, these concerns are misplaced.

Influenza Aviar



Avian and swine influenza viruses: our current understanding of the zoonotic risk

Van Reeth K
Vet Res. 2007 Mar-Apr; 38 (2): 243-60

The introduction of swine or avian influenza (AI) viruses in the human population can set the stage for a pandemic, and many fear that the Asian H5N1 AI virus will become the next pandemic virus. This article first compares the pathogenesis of avian, swine and human influenza viruses in their natural hosts. The major aim was to evaluate the zoonotic potential of swine and avian viruses, and the possible role of pigs in the transmission of AI viruses to humans. Cross-species transfers of swine and avian influenza to humans have been documented on several occasions, but all these viruses lacked the critical capacity to spread from human-to-human. The extreme virulence of H5N1 in humans has been associated with excessive virus replication in the lungs and a prolonged overproduction of cytokines by the host, but there remain many questions about the exact viral cell and tissue tropism. Though pigs are susceptible to several AI subtypes, including H5N1, there is clearly a serious barrier to infection of pigs with such viruses. AI viruses frequently undergo reassortment in pigs, but there is no proof for a role of pigs in the generation of the 1957 or 1968 pandemic reassortants, or in the transmission of H5N1 or other wholly avian viruses to humans. The major conclusion is that cross-species transmission of influenza viruses per se is insufficient to start a human influenza pandemic and that animal influenza viruses must undergo dramatic but largely unknown genetic changes to become established in the human population.

<http://www.edpsciences.org/articles/vetres/pdf/2007/02/v07011.pdf?access-ok>



Deadly H5N1 may be brewing in cats

Vet Sci Tomorrow 2007

Bird flu hasn't gone away. The discovery, announced last week, that the H5N1 bird flu virus is widespread in cats in locations across Indonesia has refocused attention on the danger that the deadly virus could be mutating into a form that can infect humans far more easily.

<http://www.vetscite.org/publish/items/003469/index.html>



Design of a single tube RT-PCR assay for the diagnosis of human infection with highly pathogenic influenza A(H5) viruses

Yea C, Adachi D, Johnson G, Nagy E, Gharabaghi F, Petric M,

Richardson SE, Tellier R

J Virol Meth. 2007; 139 (2): 220-6

Concerns about emergence of a pandemic strain of influenza have been increasing. The strains of highly pathogenic influenza A(H5N1) currently circulating are considered among the most

plausible candidates for giving rise to a pandemic strain. In this study the design and development of a RT-PCR assay specific for these highly pathogenic influenza A(H5) strains is presented. This is achieved in part by the design of a primer targeting the coding region for the protease cleavage site of the hemagglutinin, and another primer derived from a pan-hemagglutinin RT-PCR assay also presented in this study. It is shown that the HPAI A(H5) specific assay amplifies only the nucleic acids of highly pathogenic A(H5), with a high sensitivity.

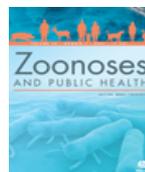


Hampered foraging and migratory performance in swans infected with low-pathogenic avian influenza a virus

van Gils JA, Munster VJ, Radersma R, Liefhebber D, Fouchier RA, Klaassen M
PLoS ONE 2007 Jan 31;2:e184

It is increasingly acknowledged that migratory birds, notably waterfowl, play a critical role in the maintenance and spread of influenza A viruses. In order to elucidate the epidemiology of influenza A viruses in their natural hosts, a better understanding of the pathological effects in these hosts is required. Here we report on the feeding and migratory performance of wild migratory Bewick's swans (*Cygnus columbianus bewickii* Yarrell) naturally infected with low-pathogenic avian influenza (LPAI) A viruses of subtypes H6N2 and H6N8. Using information on geolocation data collected from Global Positioning Systems fitted to neck-collars, we show that infected swans experienced delayed migration, leaving their wintering site more than a month after uninfected animals. This was correlated with infected birds travelling shorter distances and fuelling and feeding at reduced rates. The data suggest that LPAI virus infections in wild migratory birds may have higher clinical and ecological impacts than previously recognised.

<http://www.pubmedcentral.nih.gov/picrender.fcgi?artid=1773019&blobtype=pdf>



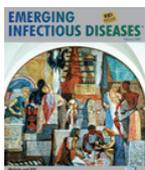
Rapid and Simultaneous Detection of Avian Influenza and Newcastle Disease Viruses by Duplex Polymerase Chain Reaction Assay

Farkas T, Antal M, Sami L, German P, Kecskemeti S, Kardos G, Belak S, Kiss I

Zoonoses and Public Health 2007; 54 (1): 38-43

A duplex reverse transcription-polymerase chain reaction (dRT-PCR) assay has been developed for the simultaneous, rapid and specific detection/discrimination of avian influenza virus (AIV) and Newcastle disease virus (NDV). Primers targeting the matrix protein gene (M) of AIV and the fusion protein gene (F) of NDV were evaluated

experimentally with 13 AIV and 19 NDV strains. PCR products of the expected size of 144 bp and 316 bp were amplified from AIV/NDV samples, respectively, while no cross-reaction was observed with negative controls or with 16 other avian pathogens. The endpoint of detection was defined as approximately $10^{+0.5}$ 50% egg infectious dose (EID₅₀)/0.2 ml for AIV and $10^{+2.2}$ EID₅₀/0.2 ml for NDV. The assay was able to detect AIV/NDV with similar sensitivity in spiked stool samples and in specimens from vaccinated birds. The developed dRT-PCR assay is a rapid, cost-effective tool, which provides powerful novel means for the early diagnosis of avian influenza and Newcastle disease.



Subclinical Infection with Avian Influenza A (H5N1) Virus in Cats

Leschnik M, Weikel J, Möstl K, Revilla-Fernández S, Wodak E, Bagó Z, Vanek E, Benetka V, Hess M, Thalhammer JG
Emerg Infect Dis. 2007 Feb; 13 (2): 243-7.

Avian influenza A virus subtype H5N1 was transmitted to domestic cats by close contact with infected birds. Virus-specific nucleic acids were detected in pharyngeal swabs from 3 of 40 randomly sampled cats from a group of 194 animals (day 8 after contact with an infected swan). All cats were transferred to a quarantine station and monitored for clinical signs, virus shedding, and antibody production until day 50. Despite unfamiliar handling, social distress, and the presence of other viral and nonviral pathogens that caused illness and poor health and compromised the immune systems, clinical signs of influenza did not develop in any of the cats. There was no evidence of horizontal transmission to other cats because antibodies against H5N1 virus developed in only 2 cats.

<http://www.cdc.gov/eid/content/13/2/pdfs/243.pdf>

Inocuidad de los Alimentos

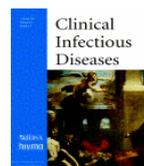


La calidad de los alimentos ecológicos

Rodríguez Perez JJ
Consumaseguridad.com 2007 Feb

Un alimento ecológico posee, como cualquier otro, ventajas y riesgos, y ha de ser tratado en condiciones adecuadas para evitar enfermedades de transmisión alimentaria. En los últimos años se ha producido en la Unión Europea un incremento espectacular de la producción y consumo de alimentos ecológicos. Aunque el sector ecológico de la alimentación todavía tiene una cuota pequeña de mercado, todos los estudios y proyecciones de futuro auguran un fuerte crecimiento del sector a corto y

medio plazo. De hecho, y teniendo en cuenta la evolución en países como EEUU, las expectativas de crecimiento son muy importantes, motivada sobre todo por la aceptación de los consumidores, que están dispuestos a pagar más por alimentos considerados más sanos y nutritivos. Pese a todo, debe tenerse en cuenta que un alimento ecológico posee, como cualquier otro, ventajas y riesgos, y ha de ser tratado y manipulado en condiciones adecuadas.



Activities, achievements, and lessons learned during the first 10 years of the Foodborne Diseases Active Surveillance Network: 1996-2005

Scallan E.
Clin Infect Dis. 2007 Mar 1;44(5):718-25

Since the establishment of the Foodborne Diseases Active Surveillance Network (FoodNet) in 1996, it has been an essential resource for the surveillance and investigation of foodborne disease in the United States. FoodNet has had a major impact on food safety because it conducts population-based, active surveillance for laboratory-confirmed infections from 9 pathogens commonly transmitted through food. Each year, FoodNet publishes the National Report Card on Food Safety, which is used by regulatory agencies, industry and consumer groups, and public health personnel to prioritize and evaluate food safety interventions and monitor progress toward national health objectives. FoodNet also determines the human-health impact of foodborne illness by conducting related epidemiological studies that contribute to the estimates of the overall burden of foodborne illness, attribute the burden of foodborne illness to specific foods and settings, and address important foodborne disease-related issues, such as antimicrobial resistance and sequelae from foodborne infections. This article summarizes the activities, achievements, and lessons learned during the first 10 years of FoodNet.



Reduction in the incidence of invasive listeriosis in foodborne diseases active surveillance network sites, 1996-2003

Voetsch AC, et al.
Clin Infect Dis. 2007 Feb 15;44(4):513-20
BACKGROUND: Listeriosis is a leading cause of death among patients with foodborne diseases in the United States. Monitoring disease incidence is an important element of listeriosis surveillance and control. METHOD: We conducted population-based surveillance for Listeria monocytogenes isolates obtained from normally sterile sites at all clinical diagnostic laboratories in the Foodborne

Diseases Active Surveillance Network from 1996 through 2003. RESULTS: The incidence of laboratory-confirmed invasive listeriosis decreased by 24% from 1996 through 2003; pregnancy-associated disease decreased by 37%, compared with a decrease of 23% for patients > or =50 years old. The highest incidence was reported among Hispanic persons from 1997 through 2001. Differences in incidence by age group and ethnicity may be explained by dietary preferences. CONCLUSION: The marked decrease in the incidence of listeriosis may be related to the decrease in the prevalence of *L. monocytogenes* contamination of ready-to-eat foods since 1996. The crude incidence in 2003 of 3.1 cases per 1 million population approaches the government's Healthy People objective of 2.5 cases per 1 million population by 2005. Further decreases in listeriosis incidence will require continued efforts of industry and government to reduce contamination of food and continued efforts to educate consumers and clinicians.

Rabia



Bat echolocation calls: adaptation and convergent evolution: review

Jones G, Holderied MW
Proc R Soc B. 2007 Jan

Bat echolocation calls provide remarkable examples of 'good design' through evolution by natural selection. Theory developed from acoustics and sonar engineering permits a strong predictive basis for understanding echolocation performance. Call features, such as frequency, bandwidth, duration and pulse interval are all related to ecological niche. Recent technological breakthroughs have aided our understanding of adaptive aspects of call design in free-living bats. Stereo videogrammetry, laser scanning of habitat features and acoustic flight path tracking permit reconstruction of the flight paths of echolocating bats relative to obstacles and prey in nature. These methods show that echolocation calls are among the most intense airborne vocalizations produced by animals. Acoustic tracking has clarified how and why bats vary call structure in relation to flight speed. Bats

using broadband echolocation calls adjust call design in a range-dependent manner so that nearby obstacles are localized accurately. Recent phylogenetic analyses based on gene sequences show that particular types of echolocation signals have evolved independently in several lineages of bats. Call design is often influenced more by perceptual challenges imposed by the environment than by phylogeny, and provides excellent examples of convergent evolution. Now that whole genome sequences of bats are imminent, understanding the functional genomics of echolocation will become a major challenge.

<http://www.journals.royalsoc.ac.uk/media/mmm8xdt75vmdtxvqbg9d4/contributions/c77/5/5/c7555003n24827.pdf>



Involvement of nucleoprotein phosphoprotein, and matrix protein genes of rabies virus in virulence for adult

mice

Shimizu K, Ito N, Mita T, Yamada K, Hosokawa-Muto J, Sugiyama M, Minamoto N
Virus Res. 2007; 123 (2): 154-60

Rabies virus Ni-CE strain causes nonlethal infection in adult mice after intracerebral inoculation, whereas the parental Nishigahara strain kills mice. In this study, to identify viral gene(s) related to the difference in pathogenicity between Ni-CE and Nishigahara strains, we generated chimeric viruses with respective genes of the virulent Nishigahara strain in the background of the avirulent Ni-CE genome. Since chimeric viruses, which had the N, P, or M genes of the Nishigahara strain, respectively, killed adult mice after intracerebral inoculation, it became evident that the N, P, and M genes are related to the difference in pathogenicity between Ni-CE and Nishigahara strains. Previously, we showed that the G gene is a major contributor to the difference in pathogenicity between another avirulent strain, RC-HL, and the parental Nishigahara strain. These results imply that the attenuation mechanism of the Ni-CE strain is different from that of the RC-HL strain, thus suggesting that rabies virus can be attenuated by diverse mechanisms. This is the first report of changes in viral genes other than the G gene of rabies virus causing the reversion of pathogenicity of an avirulent strain.

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