

**Leishmaniasis in Albania**

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**Background:** Different aspects of Leishmaniasis in Albania has been described in different research papers. Leishmaniasis is mandatory notified near public health services. From 1960-2001 an average of 80 cases per year has been described in the literature. Also other studies of vectors as well as studies of seroprevalence in dogs has been performed recently. Data from ecological survey, reservoirs and vectors were analysed in different geographical areas.

**Methods:** A retrospective analysis of cases admitted in district and tertiary care hospitals from 1997-2008

Also such analysis has included confirmed Visceral Leishmaniasis (VL) cases notified to the the national surveillance center

VL cases were reported from 35 out 36 districts, characterised by different levels of morbidity. Mortality and co infection data were also analysed.

ELISA and IFAT were use dfor diagnosis.

**Results:** A total of 1439 cases of Visceral Leishmaniasis cases were analysed. The incidence rate ranked from 3.4 - 4.3 cases/10000 population.

About 89% percent of the districts are infected with VL. The most affected areas are: Shkodra 1.4, Lezha 1.6, Berat, 1.1, Elbasan 0.7, Tirana 0.3 and. Vlora 0.4cases/10.000population.

A high proportion of cases occurred among infantile population: especially children below 5 years, and 79.6% below 10 years of age.

*P.neglectus* and *P. papatasi* are the common while *P.tobi* is concentrated only in one geographic area.

The seroprevalence in 340 dogs collected from 7 regions show a rate of 5.8%.

**Conclusion:** VL in Albania represents a serious health problem. Paediatric cases are exceeding 80%. It is present all over the country. A control program needs to be established.

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34.030

**Prevalence of HPAI in live-bird markets in the Jabodatabek region of west Java, Indonesia in 2009**C. Lockhart<sup>1,\*</sup>, E. Wuryaninggih<sup>2</sup>, E. Brum<sup>1</sup>, P.R. Barrios<sup>1</sup><sup>1</sup> *Avian Influenza Control Programme, Indonesia, Jakarta, Indonesia*<sup>2</sup> *Campaign Management Unit, Jakarta, Indonesia*

**Background:** Outbreaks of highly pathogenic avian influenza (HPAI) due to H5N1 began in October 2003 and have affected poultry in 31 of 33 provinces in Indonesia. Very little is known about the HPAI in commercial poultry. The objectives of this study were to determine the prevalence of HPAI due to H5 avian influenza viruses in live-bird markets that trade in commercial poultry located in the greater Jakarta metropolitan area on Java Island, Indonesia. Secondary objectives were to identify geographic origin

**Methods:** Pooled environmental swabs were taken from a random sample of live-bird markets in 12 districts and subjected to H5 testing over a period of six months to determine the presence of HPAI. Data on type of birds as well as origin of birds were gathered in order to assess risk associated with HPAI infection in markets.

**Results:** Our results show that markets were continuously infected with HPAI, with 33.3% of market samples testing positive over the study period. HPAI infection was concentrated in markets in the northeast and central regions of the study area where more than 60% of markets tested positive.

**Conclusion:** HPAI due to H5 avian influenza appears to be widespread within markets and concentrated in the northeast and central areas of the study region. Knowledge about marketlevel prevalence in each district provides indication of the level of HPAI circulating within the commercial poultry industry, information that is currently not available from other sources.

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34.031

***Ancylostoma* spp. on beaches of Elota, Sinaloa, México**

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**Background:** Eggs and larvae of *Ancylostoma* spp. can disseminated in the soil of public areas, and resist to adverse environment conditions, capable of surviving for many months. Humans and pets can infect that have contact with contaminated soil of parks and sand of beaches. Ancylostomiasis can be a zoonotic infection with hookworm species that do not use humans as a definitive host, the most common being *A. braziliense* and *A. caninum*. The normal definitive hosts for these species are dogs and cats; humans may also become infected when filariform larvae penetrate the skin. With most species, the larvae cannot mature further in the human host, and migrate aimlessly within the epidermis, causing cutaneous larva migrans (also known as creeping eruption), sometimes as much as several centimeters a day. Some larvae may persist in deeper tissue after finishing their skin migration. Occasionally *A. caninum* larvae may migrate to the human intestine, causing eosinophilic enteritis. *Ancylostoma caninum* larvae have also been implicated as a cause of diffuse unilateral subacute neuroretinitis. The objective was determine the presence of *Ancylostoma* spp in sand of beaches of Elota municipality of Sinaloa, México.

**Methods:** The composite samples of sand of three beaches, were determined for representative samples described by the technique of Thrusfield (2005) was used:  $n = [t \cdot SD / L]^2$ . Where n = sample size, t = value of the normal distribution (Student t) for a 95% confidence level (t = 1.96), L = accepted error or precision (5%), and SD = weighted disease prevalence (%); the total of composite sample of sand determined by the double W samplings was 225, took surface moist sand scraping of 100 grams of sand for each sample

and deposited it in plastic bags; transferred to the laboratory of parasitology of the FMVZ-UAS to be analyzed by the sedimentation technique.

**Results:** 45 (20%) of the 225 composite samples of sand and in two of the three beaches were positive to *Ancylostoma spp.*

**Conclusion:** The contamination with *Ancylostoma spp.* represent risk for the pets and public health, yet residents as visitors ignore about parasitic diseases that dogs can transmit them it is necessary implement control strategies and education for the prevention of the infections.

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### 34.032

#### Characterization of Venezuelan field strains of EEEV by RT-PCR and SSCP

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**Background:** Genetic characterization of three field strains of EEEV, by RT-PCR and SSCP shows difference in virulence, antigenic variation and immune response. Two genetic regions of the virus: No Transducible RNAm 26S and a region of the gen nonstructural protein P4 03 (nsP4) might relate to heterogeneity and behavior of the strains.

**Methods:** EEEV field virulent strains were isolated from epizootic outbreaks in equines and named: Strain 1 or PAO from Cojedes State in 2002. Strain 2 or MERCEDES Guárico State in 1996. Strain 3 or TUCACAS from Falcón State in 1984. Primers from known EEEV were used to copy and to amplify a fragment of 542 pb of the region No Transducible RNAm 03 26S and another 532 pb fragment of the gen nsP4. Once amplified a RT-PCR was run and DNAc of both fragments from each of the three strains were verified and compared by SSCP. The double chains of DNAc obtained were denatured and turned into single chains by quick heat and cold stress to promote in chain reassortments or accessory chains. The end products were separated by low amperage PAGE.

**Results:** SSCP of the three strains of EEEV studied showed a wide range of band patterns with marked difference in the migratory pattern of the reassorted singlets (RSS) revealing and showed difference in the migratory patterns of the denatured singlet (DSS). This results uncovered that insertions or deletions of nucleotides took place in the gen sequence of these strains of EEEV.

**Conclusion:** The three field strains of EEEV showed genetic polymorphisms in the genome regions studied which characterize EEEV variants of South America.

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### 34.033

#### Discovery of reverse zoonotic transmission of pandemic H1N1 influenza virus infection in cats following the initiation of a real time sero-molecular epidemiological study

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**Background:** Influenza viruses remain the most significant infectious disease One Health concern entering into 2010. The highly infectious pH1N1 virus is a human host adapted virus with unknown host susceptibility that remains problematic for pandemic influenza preparedness plans. Atypical hosts provide an opportunity for endemic influenza evolution, a new reservoir host, or a site for future mutational events. Following the discovery of the index case for feline pH1N1 infection, we are employing a sero-molecular epidemiological study to monitor infection rates and evolution of this virus at the human-animal contact interface to advance the understanding of influenza virus evolution in populations and predict, prevent or curtail emergent events.

**Methods:** This study utilizes molecular testing; real time RT-PCR differential pH1N1 detection assays; virus isolation, gene sequence analysis for virus detection, typing and viral genomics. Host immune responses are assessed via differential H1N1 ELISA, and specific hemagglutinin inhibition assays and virus neutralization assays.

**Results:** Our epidemiological study discovered the first two feline cases of pH1N1 infections following apparent reverse zoonosis from humans. Both cases include cats older than 10 yrs, clinical signs include re respiratory disease, lethargy and inappetance, 3-5 days following influenza like illness in humans. One cat was moderately febrile. Both cats developed lower respiratory disease characterized by a bilateral dorsal alveolar pattern on radiography and had lymphopenia. Bronchoalveolar lavage or possibly deep ora-pharyngeal swabs were sufficient for PCR based viral detection. The power of serology in diagnosis will be emphasized. As the study continues, additional cases will be also be presented.

**Conclusion:** Here we report on the discovery and a diagnostic approach of the first pH1N1 virus infection in the atypical domestic cat which was associated with significant lower respiratory disease which is similar to more recent human cases possibly suggesting the discovery of a relevant animal model for future experimental trials with pH1N1 viruses. Moreover these atypical index cases demonstrate the possible development of new endemic infections of influenza virus in close household or community human/animal contacts complicating preparedness plans and reinforcing the need for expanding professionally trained comparative clinical scientists via the One Health initiative.

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