



VII Conference of the European Wildlife Diseases Association

27th-30th September 2006
Aosta Valley, ITALY



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Welcome!

On behalf of the Wildlife Diseases Association, the National Reference Centre for Wildlife Diseases (Ce.R.M.A.S.) and the Italian Society of Ecopathology (SIEF) we are happy to welcome you to S.Vincent and the 7th Conference of the European section of the Wildlife Diseases Association.

The scientific programme is really varied and ranges from invertebrate to mammals. We have chosen some topics that are of great concern among professional and ordinary people, such as wildlife and emerging diseases, wildlife diseases and conservation, wildlife diseases monitoring and risk of disease transmission between wildlife and domestic animals. Data exchange and discussion are the goal of every scientific meeting. We hope our organization efforts will create a friendly and stimulating environment and allow all of us to increase not only our culture, but also our friendship.

The front line of wildlife diseases research in Europe, but also from other continents, is presented in the more than 120, oral or poster, presentations. We can learn from them and increase our ability to preserve both wildlife and public health.

We hope you will enjoy the conference and your stay in Italy!

Ezio Ferroglio
SIEF

Riccardo Orusa
Ce.R.M.A.S

Conference Programme



Conference Programme

Wednesday 27th September 2006

14:30-15:30	Registration
15:30-18:00	Opening Ceremony
18:00	Welcome cocktail

Thursday 28th September 2006

8:00-9:00	Registration	
9:00-10:00	“Wildlife Disease surveillance in Europe“.	Key Note Speaker M. ARTOIS Moderator: P. Duff
10:00-11:30	Session: Wild boar	Chair: C. Gortazar, J. Hars
	Estimation of European wild boar relative abundance and aggregation: a novel method in epidemiological risk assessment	<i>Acevedo P, Vicente J, Höfle U, Cassinello J, Ruiz-Fons F and Gortazar C</i>
	Serological survey of 3 pathogens in free ranging wild boar (<i>Sus scrofa</i>) in France in the 2000's and evaluation of the risk of inter-transmission from wild boar populations to open air piggeries, dogs, and humans.	Rossi S, Hars J, Garin-Bastuji B, Lepotier MF, Boireau P, Toma B, Boue F, Terrier ME
	<i>Erysipelothrix rhusiopathiae</i> in wild boar (<i>Sus scrofa</i>) in an area of south-central Spain	Vidal D, Ruiz-Fons F, Martin MP, Larrasa J, Gortazar C
	Epidemiological interactions on Aujeszky's disease virus between domestic pig and European wild boar in Castilla-La Mancha, Spain	Ruiz-Fons F, Vidal D, Vicente J, Acevedo P, Fernandez-de-Mera I, Montoro V, Gortazar C
	Quantitative approach on classical swine fever management in wild boar (<i>Sus scrofa</i>) population	Fenati M, Guberti V
	Pseudorabies virus in wild boar (<i>Sus scrofa</i>) from central Italy.	Verin R, Ressel L, Nigrelli D, Brocchi E, Faccini S, Varuzza P, Poli A
11:30-11:45	Coffee break	
11:45-13:00	Session: wildlife management: overall view and the tb debate.	Chair: D. Gavier-Widen, R. Delahay
	Moving towards sustainable co-ordinated wildlife disease surveillance in the UK.	Tomlinson AJ, Zimmer IA, Huntley SJ, Jackson V, Morgan C, Hunter S, Grant R, Taylor MA
	The wildlife health and welfare strategy– a framework for the future	Hartley MP
	A cost-benefit analysis of culling badgers to control bovine tuberculosis	Smith GC, Bennet R, Wilkinson D, Cook R

	Social organisation and movement influence the incidence of bovine tuberculosis in an undisturbed high density badger (<i>Meles meles</i>) population	Vicente J, Delahay RJ, Walker N Cheeseman, CL
	Tuberculosis in wild boar in the Marche region, Italy (part i): 2003-2006, a four years survey	Gavaudan S, Bartolini C, DeCurtis M, Duranti A, Crotti S, Cagiola M, Baroni C, Tomarelli R, Micci E, Perugini G, Mattozzi C, Severi G, Fiorelli S, Mazzone P, Foglini A
13:00-14:30	Lunch	
14:30-15:30	“Wildlife diseases, zoonotic and conservation issues”.	Key Note Speaker D. KNOBEL Moderator: A. Sainsbury
	Session: diseases and conservation	Chair: Sainsbury A, Aguirre A
	Mortality of wintering monarch butterflies: are emerging pathogens the cause of declining populations?	Aguirre A, Sandoval AL, Ramirez D, Jimenez G, Soriano D, Rodriguez S, Mondragon R, Bernal M, Rendon E, Zepeda H
	Pattern and trends in the distribution of squirrel poxvirus disease in the UK	Sainsbury AW, Deaville R, Lawson B, Stack M, Duff P, McInnes CJ, Gurnell J, Pfeiffer D, Nettleton P, Lurz PWW
15:30-16:30	Identification and partial characterisation of <i>Hepatozoon</i> sp. in red squirrels (<i>Sciurus vulgaris</i>) and grey squirrels (<i>S. carolinensis</i>) in England	Simpson V, Birtles R, Bown K, Panciera R, Butler H
	Causes of mortality in a European mink eep breeding colony	Wibbelt G, Speck S, Frölich K, Peters E, Seebass C
16:30-16:45	Coffee break	
	Session: avian diseases	Chair: M. Ignasi, K. Erdelyi
16:45-17:30	Atoxoplasmosis associated with morbidity and mortality in captive and translocated ciril buntings (<i>Emberiza cirilus</i>)	McGill I, Sainsbury AW, MacGregor S, Pocknell A, Sayers G, Jeffs C, Marshall R, Peirce M
	Mortality factors of white-tailed sea eagles	Krone O, Kenntner N, Tataruch F
	Blood parasites in birds from Burkina Faso	Giammarino M, Vaschetti G, Boano G
18:00	Visit to Bard Fortress, Vin d’Honneur and EWDA Auction	

Friday 29th September 2006

9:00-10:00	“Wildlife and EID”	Key Note Speaker A. OSTERHAUS Moderator: T. Kuiken
10:00-11:40	Session: avian flu	Chair: T. Kuiken, V. Guberti
	Role played by the mute swan (<i>Cygnus olor</i>) and other <i>Anatidae</i> in the epidemiology of avian flu within the Dombes region (Ain “ <i>département</i> ”, France)	Hars J, Ruette S, Benmergui M, Fouque C, Lebret V, Legouge A, Dupuy C, Terrier ME, Baroux D, Jestin V
	Descriptive epidemiology of Avian Influenza virus amongst ducks of the Dombes area, in winter 2005-2006.	Durand I, Doctrinal D, Aubin JT, Ming C, Baroux D, Darbon F, Ruette S, Dupuy C, Bureau E, Castanier B, Mas JP, Simon A, Van der Werf S, Artois M
	Modelling the introduction of an Influenza virus in a wildfowl population in the Dombes region	Doctrinal D, Artois M, Bicout D
	Highly pathogenic influenza virus - H5N1 infection in Swedish wildlife: clinical findings and epidemiology	Mörner T, Ågren E, Bernodt K, Bröjer C, Jansson DS, Uhlhorn H, Mattsson R, Gavier-Widén D
	Highly pathogenic avian influenza in wild birds in Sweden: characterization of lesions in the central nervous system	Gavier-Widén D, Ågren E, Uhlhorn H, Bröjer C, Bernodt K, Zohari S, Thoren P, Mörner T
	Highly pathogenic avian influenza virus H5N1 infection in Swedish wildlife: preliminary pathology findings.	Ågren E, Bernodt K, Bröjer C, Jansson D, Uhlhorn H, Mörner T, Mattsson R, Gavier-Widén D
	Avian Influenza surveillance in wild birds in the UK – integrating diagnostic procedure during an urgent surveillance response	Duff P
Surveillance of avian influenza in wild birds in North America: forecasting the potential spread of emergent diseases	Alonso A, Deliberto T, Leighton F	
11:40-11:55	Coffee break	
11:55-13:00	Session: vector borne diseases	Chair: E. Ferroglio, L. Reperant
	The wall lizard (<i>Podarcis muralis</i>) as a major host for <i>Ixodes ricinus</i> ticks and as a reservoir for <i>Borrelia lusitaniae</i> in Tuscany, central Italy.	Bertolotti L, Amore G, Tomassone L, Ragagli C, Grego E, Nebbia P, Mannelli A
	Molecular evidence of <i>Anaplasma phagocytophilum</i> infection in <i>Ixodes ricinus</i> larvae collected from roe deer (<i>Capreolus capreolus</i>) in North-eastern Italy	Carpi G, Pecchioli E, Cagnacci F, Rizzoli A
	Lineage 2 West-Nile virus infections in birds of prey in Hungary	Erdélyi K, Ursu K, Ferenczi E, Szeredi L, Bakonyi T
Tick-borne encephalitis (TBE): fundamental ecology and epidemiological patterns recorded in Trentino	Rizzoli A, Rosà R, Neteler M, Perkins SE, Gould EA, Hudson P	

	Modeling tick-borne encephalitis in Trentino (northern Italy)	Rosà R, Pugliese A, Hudson P, Rizzoli A
13:00-14:30	Lunch	
14:30-15:30	“Diseases shared with wildlife: an European perspective”.	Key Note Speakers C. GORTAZAR AND K. FROELICH Moderator: D. Gavier-Widen
	Session: carnivores	Chair: M. Artois, R. Orusa
	<i>Echinococcus multilocularis</i> : a zoonosis in the city	Reperant L, Hegglin D, Fischer C, Deplazes P
15:30-16:15	<i>Trichinella</i> sp. in the black bear (<i>Ursus americanus</i>) south of the 50th parallel in Quebec, Canada: distribution, prevalence, intensity of infection and genotype	Côté N, Villeneuve A, Bélanger D
	Salmonella infections in foxes (<i>Vulpes vulpes</i>)	Handeland K, Bergsjø B, Djønnø B, Lillehaug A, Nesse L, Vikøren T
	Session: diagnosis	Chair : V. Simpson, K. Handeland
16:15-16:45	Pathological patterns in wild fauna of North-Western Alps with some histological and bacteriological investigations	Domenis L, Orusa R, Robetto S
	Development of an ELISA for the detection of Interferon-gamma (IFN- γ) as a diagnostic tool for tuberculosis in elephants	Morar D, Tijhaar E, Negrea A, Klos H, Hendriks J, Van Rijhn I, Godfroid J, Michel A, Rutten V PMG
16:45-17:00	Coffee break	
	Session: ungulates	Chair: K. Froelich, B. Bassano,
	Sero-epidemiological survey on bovine respiratory syncytial virus in a wild roe deer (<i>Capreolus capreolus</i>) population in demographic decrease in the Northern Apennines, Italy (1995-2004).	Armaroli E, Corrain R, Guberti V
	Evidence of Respiratory Syncytial Virus infection in a chamois (<i>Rupicapra r. rupicapra</i>) population in the Italian Central Alps	Gaffuri A, Magnino S, Pelliccioli L, Vicari N, Bertolotti I, Gelmetti D
17:00-18:30	Long term study on <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> in free ranging alpine wildlife in north-eastern Italy	Bregoli M, Cova M, Debiasi K, Pozzato, Pasolli C
	Description of an outbreak of pestivirus infection in chamois (<i>Rupicapra pyrenaica</i>) in the Pyrenees during 2005 and 2006	Marco I, Rosell R, Mentaberre G, Casas E, Cabezón O, Velarde R, Lavín S
	Do abortive infections decrease survival in Pyrenean chamois (<i>Rupicapra pyrenaica pyrenaica</i>)?	Pioz M, Loison A, Gibert P, Artois M, Gilot-Fromont E
	Evidence of sheep and goat associated malignant catarrhal fever in free-ranging cervids	Turid Vikøren T, Hong Li H, Lillehaug A, Monceyron C, Jonassen, Böckerman I, Handeland K
18:30-19:30	EWDA business meeting	
20:00	Social Dinner	

Saturday 30th September 2006

9:30-18:00	Guided excursion to the Gran Paradiso National Park
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**Posters will be displayed from 27th to 29th
near the Congress hall**



Abstracts

Oral Presentation



ESTIMATION OF EUROPEAN WILD BOAR RELATIVE ABUNDANCE AND AGGREGATION: A NOVEL METHOD IN EPIDEMIOLOGICAL RISK ASSESSMENT.

Acevedo P, Vicente J, Höfle U, Cassinello J, Ruiz-Fons F and Gortazar C

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AIM OF THE STUDY: The first aims of this study are to evaluate abundance estimates based on the frequency of faecal droppings, and refine the method in order to calculate a spatial aggregation index. We secondly aimed to compare the data with hunting bag results across a number of hunting estates, and test the estimates (abundance and aggregation indexes) for relationships with the prevalence of four direct and indirect transmitted diseases.

MATERIALS & METHODS: We evaluated a simple method based on the frequency of faecal droppings found on transects (FBII), and developed a spatial aggregation index, based on the runs test statistic. Estimates were compared with hunting data, and with porcine circovirus (PCV2) and Aujeszky's disease virus seroprevalences and *Mycobacterium tuberculosis* complex and *Metastrongylus* spp. prevalences.

RESULTS: The FBII and the aggregation index were correlated with the hunting effort index, but both of the former estimates correlated better than the latter with the disease prevalences. In addition, management differences between study sites (open, fenced, intensively managed) in September were clearly reflected both in differences in FBII and in the aggregation index.

CONCLUSIONS: At least in habitats with high wild boar densities, the dropping FBII combined with the aggregation index constitute a cheap and reliable alternative for wild boar abundance estimation that can be used for epidemiological risk assessment, even outside the hunting season and in areas with no available data on hunting effort.

SEROLOGICAL SURVEY OF THREE PATHOGENS IN FREE RANGING WILD BOAR (*Sus scrofa*) IN FRANCE (2000-2004) AND EVALUATION OF THE RISK OF TRANSMISSION FROM WILD BOAR POPULATIONS TO OPEN AIR PIGGERIES, DOGS, AND HUMANS.

Rossi S., Hars J, Garin-Bastuji B, Lepotier M-F, Boireau P, Toma B, Boue F, Terrier ME

In France, a serological survey was implemented at a national level in free ranging wild boar regarding three diseases that were suspected to be transmitted from wildlife to pigs (brucellosis, Aujeszky's disease), dogs (Aujeszky's disease), or humans (trichinellosis). Sampling was performed from 2000/2001 to 2004 on shot wild boar under the coordination of the Game Wildlife Agency and the local vet services. Diagnosis by ELISA tests were performed by various research units of the Agency for Food Safety. Serological data were first analyzed in order to provide maps of seroprevalence for each pathogen, taking into account the quality of tests. Then a particular analysis was performed in order to determine the spatial structure and risk factors for diseases. Finally, we analyzed the risk of transmission from wild boar to other species using hunting bags and domestic pig census data collected in the 2000's. More than 6000 sera from 75 departements were analysed regarding each pathogen. Seroprevalence of *Brucella* sp. was high (up to 20%) in many departements, only Corsica seems free from brucellosis. Thus the risk of infection for open air pigs is high in continental France; and the number of outbreaks is particularly high in the center-ouest where the number of open air piggeries is highest. Seroprevalence of Aujeszky's disease is much more aggregated in the North-East, in the Center, Corsica and two departements in the West. We predicted a highest risk of transmission to dogs in the North-East and Corsica, while the risk of outbreaks in pigs seems highest in the Center and Corsica. Seroprevalence of trichinellosis is highly aggregated, (up to 5% only in the mediterranean coast and Corsica). Perspectives for future surveys are discussed.

***Erysipelothrix rhusiopathiae* IN WILD BOAR (*Sus scrofa*) IN AN AREA OF SOUTH-CENTRAL SPAIN**

Vidal D¹, Ruiz-Fons F¹, Martin MP¹, Larrasa J¹, Gortazar C¹

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AIM OF THE STUDY:

Description of *E. rhusiopathiae* infection in wild boars in an area of South-Central Spain.

MATERIALS & METHODS:

In July 2005, a wild boar was found moribund in an hunting estate from south-central Spain. In October 2005, another animal was found death in the same estate. We investigated the prevalence and the seroprevalence of *E. rhusiopathiae* by microbiological and serological analyses in this estate and in other 3 neighbouring estates. A total of 178 sera collected from wild boars in different years (1999-2006) were analysed by a commercial ELISA test. Moreover, 36 animal samples were collected in the 2005-2006 hunting season in the study area and spleens and tonsils were cultured in order to isolate *E. rhusiopathiae*.

RESULTS:

Erysipelothrix rhusiopathiae was isolated from spleen in both moribund/dead animals. Seroprevalence was 7.7 % for all analysed sera. Nevertheless, seroprevalence reached 21.6 % in the estate where infected animals were found. Microbiological analyses revealed that *E. rhusiopathiae* positive animals were present in two of the sampled hunting estates.

CONCLUSIONS:

This is to our knowledge the first report of *E. rhusiopathiae* infection in wild boars from Spain. Swine erysipelas should be considered in wild boar populations in Spain as an important problem for Animal and Public Health authorities.

EPIDEMIOLOGICAL INTERACTIONS ON AUJESZKY'S DISEASE VIRUS BETWEEN DOMESTIC PIG AND EUROPEAN WILD BOAR IN CASTILLA-LA MANCHA, SPAIN

Ruiz-Fons F¹, Vidal D¹, Vicente J¹, Acevedo P¹, Fernandez-de-Mera I¹, Montoro V¹, Gortazar C¹

¹Instituto de Investigación en Recursos Cinegéticos IREC (CSIC-UCLM-JCCM)

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AIM OF THE STUDY:

By exploratory analyses, the objective of this study was to investigate associations between the patterns of ADV seroprevalence at municipal level in the wild boar and the domestic pig populations in a region of south-central Spain.

MATERIALS & METHODS:

Epidemiological analyses of risk factors of ADV serostatus in wild boar and domestic pig were carried out in the study region. Factors such as management, wild boar abundance index and aggregation, as well as habitat use and structure among others were tested for their influence on ADV epidemiology in wild boar populations. Number of pigs, pig farm density and production type were tested for their influence on ADV in domestic pigs. The influence of ADV seroprevalences between wild boar and domestic pig at the municipal level were also analysed. Spatial analyses of ADV seroprevalences at municipal level were tested for both the wild boar and the domestic pig in the study region.

RESULTS:

No evidence of interaction in the epidemiology of ADV disease between the domestic pig and the wild boar was found. The spatial autocorrelation for the domestic pig ADV seroprevalence had a distance range not more distant than 10 km. In the case of the wild boar, the spatial autocorrelation pattern for the wild boar showed a distance of 25 km.

CONCLUSIONS:

At large scale, no signs of any associations between wild boar and domestic pig ADV seroprevalence were evidenced in this study. As seroprevalence could not be indicative of wild boar/domestic pig interaction at the interface, more research should focus in the used molecular and finer scales, taking special attention to open-air Iberian pig systems to definitively elucidate the epidemiological role of both groups of suids.

QUANTITATIVE APPROACH ON CLASSICAL SWINE FEVER MANAGEMENT IN WILD BOAR (*Sus scrofa*) POPULATION

Massimo Fenati¹, Vittorio Guberti

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AIM OF THE STUDY: Assessing some control measures for managing classical swine fever (CSF) in wild boar populations.

MATERIALS & METHODS: A simple SIR (Susceptible, Infected and Removed) differential compartmental model is performed to simulate the dynamic of CSF infection in a small wild boar population. The model is compared with field data from the Varese (Italy) outbreak where self-limiting CSF infection was observed in the wild boar population. Several management strategies, in particular vaccination and hunting, are applied on the calibrated model and they are analyzed by deterministic and stochastic (Montecarlo analysis) approaches.

RESULTS: The model explains about 90% of the data variability ($R^2 = 0.88$, $p < 0.05$) and shows the same natural trend observed in the Varese CSF outbreak with natural extinction of the virus. The interaction between control measures (effort, time, etc.) and virus dynamics in the wild boar population produces different and unexpected results such as (1) long time persistence of the virus in the environment or (2) slight effects on the epidemic curve.

CONCLUSIONS: Vaccination campaigns and hunting policy measures have often been applied on CSF outbreak in wild boar population but their efficacy is not yet demonstrated. The presented model shows that the natural course of wild boar CSF outbreak could be modified by policy control measures even with negative consequences, when a self-limiting infection is expected. Management has to be assessed

PSEUDORABIES VIRUS IN WILD BOAR (*Sus scrofa*) FROM CENTRAL ITALY

Verin Ranieri 1, Ressel Lorenzo 1, Nigrelli Daniele 2, Brocchi Emiliana 3, Faccini Silvia 2, Varuzza Paolo 4, and Poli Alessandro . 1 Dipartimento di patologia Animale, Profilassi ed Igiene degli Alimenti, Università di Pisa (Italy); 2 Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna – Sezione di mantova; 3 Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna – Sezione di Brescia; ATC 14 Pisa (Italy). Corresponding author (email: apoli@vet.unipi.it)

The aim of the study was to further investigate the distribution of pseudorabies virus (PRV) in wild boars living in Tuscany (Central Italy) and to study the distribution of viral antigen in lymphoid tissues by immunohistochemistry and molecular biology.

During the hunting season 2002-2003 and 2005-2006, 245 tissue and blood samples were collected from wild boars (*Sus scrofa*) from two distinct Tuscany areas in Central Italy. The presence of PRV antibodies, antigen and DNA were confirmed by enzyme-linked immunosorbent assay (ELISA) immunohistochemistry, and PCR respectively. Only 139 of 245 sera collected were suitable for serological studies: of these 49.6% (69/139) was positive for specific anti-PRV antibodies with two similar relative prevalences from the districts under study: 51% (41/80) from the Province of Grosseto and 47.4% (28/59) from the Province of Pisa. Analysis of host age, sex of the animals and spatial factors showed significantly higher presence of PRV antigen and seroprevalence in older animals than in younger individuals. No difference were detected between males and females or for animals coming from different areas sampled. Of the wild boar tested, 38.8% (95/245) were positive for viral antigen in tonsillar tissue, and positive immunohistochemical results were confirmed by PCR analysis. The results of our study confirm that PRV infection is endemic in wild boar population in Central Italy with a high prevalence. The results of immunohistochemical investigations demonstrated that a large part of examined wild boars harbours PRV in tonsillar tissue, wild boars should be therefore considered as an important reservoir of PRV.

MOVING TOWARDS SUSTAINABLE CO-ORDINATED WILDLIFE DISEASE SURVEILLANCE IN THE UK.

Tomlinson, A.J., Zimmer, I.A, Huntley, S.J., Jackson, V., Morgan, C., Hunter, S., Grant, R. and Taylor, M.A. Central Science Laboratory, Sand Hutton, York, UK.

Alexandra.Tomlinson@csl.gov.uk

AIM OF THE STUDY: One of the goals of our work in the Veterinary Surveillance Team at CSL (Central Science Laboratory) is to establish a UK network of organisations involved in wildlife pathology/wildlife management and within that a centralised database of wildlife tissue/samples.

MATERIALS & METHODS: The foundations for this work have been laid with projects on parasites of the fox (*Vulpes vulpes*), our primary predator, already underway. An EU requirement for the UK to demonstrate that native wildlife species do not carry *Trichinella spiralis* has focussed on the fox. To date over 2800 foxes have been collected and examined with negative findings. In addition, in-house and collaborative studies (Bristol University and Royal Veterinary College) are underway to determine the parasite burden, prevalence and geographical distribution of cardio-respiratory nematodes in foxes. Parasite species of interest include *Capillaria aerophila* (*Eucoleus aerophilus*), *Crenosoma vulpis*, *Angiostrongylus vasorum* and *Dirofilaria immitis*. *A. vasorum* appears to be an increasingly significant pathogen in domestic dogs in the UK and rising levels of international pet travel increase the probability of *D. immitis* introduction to the UK. Our aim will be to target surveillance for *D. immitis* in foxes from geographical areas where the establishment of competent vector populations is most likely. Further potential projects include sample examination for *Thelazia* species, *Echinococcus multilocularis*, *Pneumonyssoides caninum*, *Pseudamphistomum truncatum* and *Hepatozoon canis* among others.

CONCLUSIONS: Once this multidisciplinary network has been established, we will be in a strong position to react to exotic disease outbreaks, to apply for funding for collaborative projects, and ultimately to link with other national and international networks.

THE WILDLIFE HEALTH AND WELFARE STRATEGY– A FRAMEWORK FOR THE FUTURE

HARTLEY MP¹

¹ Surveillance, Zoonoses and Emerging Issues Division, Defra, matthew.hartley@defra.gsi.gov.uk

Diseases of wildlife are increasingly recognised as having a significant role in the epidemiology of new and emerging diseases that pose risks to human health, animal health, wildlife conservation and economic productivity. In order to assess and respond to this potential risk in an effective and appropriate way the UK government has initiated development of the Wildlife Health and Welfare Strategy.

The strategy will direct a full review of policy, funding and activity for wildlife health and welfare across the UK government and agencies.

Stakeholders have been engaged so that the Wildlife Health and Welfare Strategy is based on sound scientific principles across the spectrum of interests in wildlife disease and is widely accepted by those in the field. Identifying practical implementation methods and applying these will occur during and after development of the strategy. In order to do this a series of stakeholder workshops will be held. This process will culminate in a full government public consultation. The first of these workshops

The initial stakeholder meeting took place on 1st June 2006 and was the largest and most comprehensive meeting of the wildlife community, including government departments, agencies, ngo's, universities, research institutions and zoological institutions, ever held. Break out groups discussed the nine key strategic focuses, 1. Wildlife disease surveillance, 2. Research training and education, 3. Cross governmental working, 4. Rehabilitation and re-introductions, 5. Imports, exports and movements, 6. Partnership working, 7. Disease management and control, 8. Human health and zoonoses and 9. Wildlife welfare.

This workshop developed suggested outcomes for the strategy and identified the policy and resource considerations. Publication of the finalised strategy should occur in Autumn 2007. This is an opportunity to develop wildlife disease management in the UK in a novel and progressive manner. We hope that the UK strategy provides an impetus for development of similar approaches in other countries.

A COST-BENEFIT ANALYSIS OF CULLING BADGERS TO CONTROL BOVINE TUBERCULOSIS

Smith, G.C.¹ Bennet, R.², Wilkinson, D.¹ & Cooke, R.². ¹ CSL, York, UK ²University of Reading, UK.:
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AIM OF THE STUDY: The incidence of bovine tuberculosis (TB) in cattle herds has steadily risen in the UK, and badgers are strongly implicated in spreading disease. Since the mid-1970s the UK government has adopted a number of badger culling strategies to attempt to reduce infection in cattle. Recent experimental work in the Randomised Badger Culling Trial (RBCT) in the UK has shown no real benefit for culling badgers to control cattle TB, and this is hypothesised to be due to social perturbation in the badger. This paper reports on an investigation of the economic benefits of culling badgers to reduce bovine TB incidence in cattle, and the effects of social perturbation.

MATERIALS & METHODS: We used an established computer model to simulate TB in badgers, transmission to cattle, and control by badger culling. The culling strategies simulated were badger trapping or gassing, carried out by Defra (Department for Environment Food and Rural Affairs). Costs were supplied by Defra for badger trapping (based on the RBCT) and gassing (based on historical information).

RESULTS: In the absence of social perturbation, regardless of culling intensity or area simulated, an overall reduction in the cattle herd breakdown rate was seen. With a high culling efficacy and no social perturbation, the economic mean Net Present Value of a few simulated culling strategies in an “ideal world” was positive, meaning the economic benefits outweighed the costs. However, the introduction of social perturbation of the badger after culling removed any economic benefits from culling badgers.

CONCLUSIONS: This is the first attempt to model the true costs and benefits of badger culling to reduce bovine TB in cattle. Unless the refinement of uncertainty changes the relative order of the above badger culling strategies, it appears that small scale, repeated reactive culling is less likely to be of economic benefit than larger scale culls targeted in the worst affected areas.

SOCIAL ORGANISATION AND MOVEMENT INFLUENCE THE INCIDENCE OF BOVINE TUBERCULOSIS IN AN UNDISTURBED HIGH DENSITY BADGER (*Meles meles*) POPULATION.

Vicente, J., Delahay, R. J., Walker, N. & Cheeseman, C. L.

Culling of European badgers (*Meles meles*) has been used to attempt to control bovine tuberculosis (TB) in UK cattle for many years. Recent results, however, suggest that culling may enhance disease spread. We examined the relationships between TB incidence and badger ecology in a high density population in South West England which has been the subject of a long-term intensive study. We related the probability of TB incidence (detected by culture of clinical samples) at the level of the individual and the social group, to demography, movement, social organisation and prevalence. The probability of an individual being an incident case was greater in groups where TB was already present, but this was less influential in groups experiencing instability in numbers. Individuals and groups were more likely to be incident cases where the social group was diminishing in size, although no relationship was observed with group size itself. This suggests that the process of group size reduction, rather than group size per se, has most influence on disease dynamics. The likelihood that either an individual or a group was an incident case was positively correlated with inter-group movements, and was also influenced by the proportion of females in a group. These relationships highlight the importance of social structure in driving TB transmission dynamics in this population, and support the idea that a stable social structure mitigates against the spread of TB. The results cast further doubt over the value of culling as a disease control measure.

TUBERCULOSIS IN WILD BOAR IN THE MARCHE REGION, ITALY: 2003-2006, A FOUR YEAR SURVEY

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AIM OF THE STUDY: In 2002 a wild boar with tuberculosis caused by *Mycobacterium bovis* was found in the Marche region of Italy and since then an eradication plan for bovine tuberculosis (TB) has provided active surveillance for infection in wildlife.

MATERIALS & METHODS: During 2003-2006, post-mortem specimens were collected by veterinarians of the regional meat inspection service at the slaughterhouse. The sampling included animals with no visible lesions (NVL) if aged 2 years and over, and animals of any age if visible lesions (VL) were found. Lymph nodes of the head and neck and tonsils from 406 animals were examined.

Specimens with NVL were screened by histological examination and, if granulomatous lesions were found, fresh tissues were submitted to seminested-PCR procedure for TB complex mycobacteria and culture.

If VL were found, affected organs were simultaneously processed by all the tests.

Identification of isolates was carried out both by biochemical properties and DNA analysis techniques.

RESULTS: Ten isolates of *M bovis* were obtained by culture. Genetic fingerprinting characterised all the strains as *M. bovis* BCG-like and VNTR 33432 profile. All affected wild boars had been hunted in the same area.

CONCLUSIONS: *M. bovis* infects wild boar in the Marche Region. The genetic fingerprinting allows comparison of the isolated strains to a bovine strain isolated from an outbreak in the same area.

The occurrence of tuberculosis in wild boars could invalidate the eradication programme for TB, if specific livestock/wildlife interface control is not also carried out.

MORTALITY OF WINTERING MONARCH BUTTERFLIES: ARE EMERGING PATHOGENS THE CAUSE OF DECLINING POPULATIONS?

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The monarch butterfly (*Danaus plexippus*) is one of the best known North American butterflies, because of its annual migration. Unable to withstand freezing weather in the northern range, in autumn, tens of millions fly south, roosting in huge numbers in oyamel fir (*Abies religiosa*) forest fragments in Mexico. Mortality of monarch butterflies on the wintering grounds may be due to effects of global climate change, deforestation, starvation, desiccation, freezing, and predation. Recent studies indicate that infection with the protozoan parasite *Ophryocystis elektroscirrha* may be related to low survival of infected larval and adult butterflies, induced by the sporozoite, which potentially causes severe damage to the gut, and mortality. During winters 2004-2006, we sampled four sites in the Monarch Butterfly Biosphere Reserve. Live and moribund butterflies and samples of abdominal scales from 500 live butterflies per site were collected for bacteriology, virology, mycology and parasitology. Oocysts of *O. elektroscirrha* were documented at all sites during two sampling episodes. Prevalence ranged from 0-7% depending of the site. Bacterial and fungal isolations were similar at all sites, *Corynebacterium* spp., *Bacillus* spp., zygomycetes and slow-growth fungi predominating. We currently are attempting to characterize a fungus found in the abdominal scales of live butterflies. A baculovirus was also isolated. Strong synergism between infection with *O. elektroscirrha* and the fungus that penetrates wing scales may contribute to severe mortality, perhaps abetted by other potential pathogens, including the virus isolated.

PATTERNS AND TRENDS IN THE DISTRIBUTION OF SQUIRREL POXVIRUS DISEASE IN THE UK

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AIM OF THE STUDY: To investigate the temporal and spatial trends of squirrel poxvirus infection in free-living populations of red squirrels.

MATERIALS & METHODS: Red squirrels found dead in England, Scotland and Wales between 1993 and 2005 were examined post mortem. Transmission electron microscopy was used to detect poxvirus in cases of skin disease. The location of deceased red squirrels was plotted on maps using Arcview together with the geographical range of grey squirrels.

RESULTS: Fifty-four cases of poxvirus disease were detected in red squirrels from England. The distribution of cases was patchy and cases occurred where the density of greys squirrels was predicted to be high.

CONCLUSIONS: Our empirical findings show that epidemics do not occur until several years after the invasion of grey squirrels into an area inhabited by red squirrels, supporting the models of this viral disease.

IDENTIFICATION AND PARTIAL CHARACTERISATION OF *Hepatozoon* Sp. IN RED SQUIRRELS (*Sciurus vulgaris*) AND GREY SQUIRRELS (*S. carolinensis*) IN ENGLAND

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AIM OF THE STUDY: Identify and characterise protozoan parasites in lungs of red and grey squirrels in UK

MATERIALS & METHODS: Necropsies performed on a) red squirrels found dead on Isle of Wight and mainland England, b) on grey squirrels from mainland England. Examine lungs by histopathology for parasites, apply immunoperoxidase staining, extract and amplify parasite DNA, characterise using nucleotide base sequence.

RESULTS: a) Protozoal schizonts typical of *Hepatozoon* sp were demonstrated by histopathology in lungs of 18/49 (37%) red squirrels from Isle of Wight. Immunoperoxidase staining confirmed the identity of schizonts and a polymerase chain reaction-based assay identified the presence of *Hepatozoon* DNA in lung. The prevalence of infection was higher in squirrels dying from natural causes (9/12, 75%) than in road accidents (7/27, 26%). The weight of infection varied and heavy infections were seen in squirrels dying from concurrent toxoplasmosis and bacterial pneumonia. b) *Hepatozoon* DNA was also recovered from lungs of two apparently healthy red squirrels and two grey squirrels killed in mainland England. Schizonts typical of *Hepatozoon* sp were seen in lungs of one of the grey squirrels only. The nucleotide base sequence of the PCR products from the red squirrels on the Isle of Wight and mainland England were identical but differed from that recovered from the grey squirrels.

CONCLUSIONS: Red squirrels on the Isle of Wight and in mainland England are infected with a common *Hepatozoon* sp. This is demonstrably different from the *Hepatozoon* species seen in grey squirrels and which is presumed to be *Hepatozoon griseisciuri*, a common parasite of grey squirrels in the USA. The significance of *Hepatozoon* sp. infection in red squirrels is uncertain but may predispose to secondary infections.

CAUSES OF MORTALITY IN A EUROPEAN MINK EEP BREEDING COLONY

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AIM OF THE STUDY: As a part of the EEP conservation program, the German NGO EuroNerz e.V. maintains a breeding stock of the highly endangered European mink (*Mustela lutreola*) as a founder-pool for reintroduction projects. Another stock of animals is kept by the Department of Ethology, Osnabrück University, Germany, for behavioural research. Together, both stocks comprise about 120 individuals, which - due to cooperation between the two institutions - are partly kept at the same location during mating season. Despite good reproductive success a number of animals died between 2003 and 2006. It was noted that there was a particular increase of fatalities at the beginning of early winter, which prompted the search for a seasonal background. From May 2004 carcasses were submitted to the IZW for further investigations.

MATERIALS & METHODS: Twenty four deceased animals (11 male, 13 female) of all age groups were necropsied and patho-histological, bacteriological and virological examinations were performed. The carcasses were either fresh or had been stored at -20°C before arriving at the IZW. Standard routine protocols were used for histology and bacteriology. Additionally, the occurrence of clostridial toxins was investigated by a commercial lab (Ripac Labor[®], Germany). PCR was used for the detection of nucleic acids of parvovirus and canine distemper virus.

RESULTS: More than half of the investigated cases revealed hemorrhagic enteritis, most of these associated with isolation of *Clostridium perfringens*, a few others were positive for nucleic acids of parvovirus in spleen and mesenteric lymph nodes. Other individuals died of bacterial pneumonia e.g. due to *Pasteurella multocida* or *Nocardia* spp., a few animals also died of predation or hypoglycemia (newborns). One animal had a subcutaneous fibrosarcoma on the dorsal aspect of its foot.

CONCLUSIONS: Hemorrhagic enteritis and pulmonary disease are the main causes of death in this European mink breeding stock. To counter the clostridial infections a type specific vaccine against the isolated *Clostridium perfringens* was developed (Ripac Labor[®]).

A TOXOPLASMOSIS ASSOCIATED WITH MORBIDITY AND MORTALITY IN CAPTIVE AND TRANSLOCATED CIRL BUNTINGS (*Emberiza circlus*)

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AIM OF THE STUDY: During health surveillance of captive and translocated ciril buntings involved in a reintroduction programme, initial post mortem findings supported a diagnosis of coccidial disease. The aim of this study was to diagnose the cause of the disease in these and other cases and develop a plan to monitor, and prevent further disease.

MATERIALS & METHODS: 4 of 17 ciril bunting chicks taken from the nest in the wild for translocation and reintroduction died during rearing, as did one adult ciril bunting kept for captive breeding. Standard avian post mortem examinations were carried out, including the making of impression smears from the liver and spleen, heart blood smears, and direct wet mounts of intestinal contents and faeces. Group faecal samples from the aviaries housing the ciril buntings were collected and coccidial oocysts recovered. These were then sporulated to aid identification of the coccidial species.

RESULTS: Post mortem results in three of the chicks and the adult were consistent with coccidial disease, including necrotising enteritis of variable severity, coccidial oocysts and systemic schizonts and trophozoites

of *Atoxoplasma* spp. Sporulation of oocysts from the faeces demonstrated spherical oocysts of measurement 24µm x 24µm, with sporocysts of approximately 15.2µm x 11.36µm. Each sporulated oocyst contained 2 sporocysts, suggesting that they may be either *Isospora* or *Atoxoplasma* species.

CONCLUSIONS: The finding of systemic forms of coccidia confirms the diagnosis of toxoplasmosis. However, it has not been possible to rule out a concurrent infection with *Isospora* spp. Methods put in place to control toxoplasmosis include strict hygiene and quarantine, prophylactic treatment with toltrazuril and ongoing health surveillance.

MORTALITY FACTORS OF WHITE-TAILED SEA EAGLES

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Diseases and causes of death in white-tailed sea eagles (*Haliaeetus albicilla*) are examined by several veterinary disciplines (pathology, parasitology, bacteriology, virology), as well as governmental nature conservation agencies, eagle protection groups, and ornithological stations. Remarkable are the high numbers of deaths caused by anthropogenic factors. The most important mortality factors are lead intoxication due to ingestion of lead particles and collisions with trains. Among the “natural” causes of death intraspecific conflicts (territorial fights) and infections are predominant. Lesions of the liver, bile ducts and gall bladder were at first attributed to infections with the liver fluke (*Metorchis bilis*). Therefore, the biology (life-cycle) of this parasite was investigated. Based on increasing findings of lead particles in the stomach of the white-tailed sea eagles it turned out that the liver lesions were mainly caused by lead intoxications. Lead intoxication is responsible for the death in 1/3 of the sea eagles found dead. In contrast to the lead intoxications, pesticides play a minor role nowadays. New threats such as collisions with wind power plants may become of increasing importance. Investigations on the mortality factors of white-tailed sea eagles from Greenland and Finland point to the significance of anthropogenic caused deaths, especially lead intoxications.

BLOOD PARASITES IN BIRDS FROM BURKINA FASO

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AIM OF THE STUDY: This study aims to evaluate the prevalence and density of haemoparasites in a native population of immature and adult male and female birds of Burkina Faso.

MATERIALS & METHODS: In the protected area “Foret de Diefoula” (south-western Burkina Faso) we collected samples of blood smears from wild birds captured in the dry savannah along the Comoé river, near the Village of Folonzo (N 09° 57'49"; W 004° 40'56"), at an elevation of 298 m above sea level. We trapped 110 birds with mist nets, scattered in the low vegetation and near water point and opened from 27th to 29th of November 2003. Each bird captured was immediately identified, measured (wing chord, tarsus), weighed, sexed and assigned to age categories according to Borrow and Demey (2001). We obtained blood samples from 101 birds, using a drop of blood taken by venipuncture of the brachial vein. Blood smears were made, air dried and fixed in 100% methanol on the same collection day and then returned to the laboratory in Italy to be stained with Dip-Quickly Stain for processing.

RESULTS: On 101 sampled birds, 47 harboured blood parasites, with an overall prevalence of infection of 46,5%. 15 birds (14,8%) harboured mixed infections. *Haemoproteus* (the prevalence of infection is 30,7%), *Plasmodium* (13,9%), *Trypanosoma* (10,9%), microfilaria (8,9%) and *Leucocytozoon* (5,9%) were most frequently recorded.

CONCLUSIONS: This study is the first monitoring of blood parasite infections in wild birds (mainly passerines) in Burkina Faso, in sub-Saharan regions. The high prevalence of blood parasites (46,5%) recorded here was typical for the sub-Saharan area and was well within the range reported for the resident birds in other African regions. According to Bennet et al. (1978) the presence of a large biomass in a colony may exercise a stronger attraction for vectors than an isolated bird. In this study, in fact, the gregarious species (*Ploceus cucullatus*, *Euplectes hordeaceus*, *Uraeginthus bengalus*, *Turtur abyssinicus*) resulted more frequently parasitized than species with isolated behavioural patterns (*Turdus pelios*, *Pycnonotus barbatus*) ($\chi^2 = 4.5$, $P = 0.03$).

ROLE PLAYED BY THE MUTE SWAN (*Cygnus olor*) AND OTHER ANATIDAE IN THE EPIDEMIOLOGY OF AVIAN FLU WITHIN THE DOMBES REGION (AIN “DÉPARTEMENT”, FRANCE)

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In France, influenza viruses have been monitored in wild birds, since September 2005, by sampling on one hand dead and “potentially sick” birds (so called passive survey) and on the other hand “healthy” birds that were captured or hunter-killed (so called active survey). The Dead bird collection was based on a national network dedicated to the survey of wildlife mortality “SAGIR” and coordinated by the National Game and Wildlife Agency (ONCFS). Viral diagnosis has been performed using both tracheal and cloacal swabs. First a screening by M-PCR test was employed in six local authorized laboratories. Then, positive M-PCR samples were tested for H5-PCR, pathogenicity and neuraminidase-type by the national reference laboratory of the French agency for food safety (AFSSA, Ploufragan).

The first HP H5N1 sample had been detected in February the 13th of 2006 from three common pochard (*Aythya ferina*) that have been found dead in the Dombes wetland region (Ain “département”). A few days after this first case was detected in wildlife, a turkey facility located in the Dombes became infected. This was the only domestic outbreak in France. In the Dombes region, from February until to June 2006, 727 dead birds were collected from which 277 pools of swabs were analysed for avian flu. HP H5N1 was isolated from 42 pools corresponding to 65 dead birds. 83% of the infected birds were mute swans (*Cygnus olor*). A retrospective analysis suggests that the HP H5N1 virus was introduced by common pochard or other *Anatidae* from East-Europe, due to hard cold meteorological conditions encouraging bird movements. Mute swan then played the role of a good “sentinelle” in the wetlands.

Concerning the active survey, all over France, more than 4000 captured or hunter-killed birds were analysed from which no HP H5N1 was isolated.

DESCRIPTIVE EPIDEMIOLOGY OF AVIAN INFLUENZA VIRUS AMONGST DUCKS OF THE DOMBES AREA, IN WINTER 2005-2006.

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AIM OF THE STUDY: In February 2006, a highly pathogenic Avian Influenza appeared in the Dombes area and affected wild waterfowl. The Dombes is a humid area, 50 km north east away from the city of Lyon. This area is famous for traditional free ranging poultry farming then at risk for the circulation of AI virus emerging from wildlife. In addition the Dombes is characterized as a very important nesting and migrating area for wildfowl.

MATERIALS & METHODS: To investigate the ecology of Avian Influenza virus in the Dombes area, hunted and captured wild ducks were sampled for virological and serological analysis in order to test the circulation of AI virus between wild and domestic birds. Concurrently, captive “sentinel” ducks, potentially exposed to infected wild waterfowl, have been sampled for virological and serological analysis every fortnight.

RESULTS: Since September 2005 onward, up to February 2006, 837 fecal samples, and 441 blood samples were analysed respectively by Pasteur Institute and Veterinary laboratory of the Ain “département”. Seventy eight cloacal swabs and 21 blood samples reacted positively for influenza A viruses.

CONCLUSIONS: We will try to quantitatively assess the epidemiological threat posed by the prevalence of AI in wild birds in the Dombes area.

MODELLING THE INTRODUCTION OF AN INFLUENZA VIRUS IN A WILDFOWL POPULATION IN THE DOMBES REGION

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Wild waterfowl is considered as the main reservoir of influenza A viruses in nature. All the 16 hemagglutinin and 9 neuraminidase subtypes have been found in the wild avian population. Among the avian species, ducks are often found to be of paramount importance for the understanding of the epidemiology of this infection. Because of this central role in the ecology of influenza viruses, it is important to better understand the dynamics of infection in the duck population.

We propose here a risk assessment of avian influenza outbreak based on the epidemiological processes theory. In this context, we develop a SEIR compartmental model to study the circulation of influenza strains in wild waterfowl. Moreover, we compute the probability of a highly pathogenic avian influenza outbreak (occurrence probability) as a function of the basic reproduction rate R_0 in a population of ducks. As the reproduction rate depends on epidemiological and demographical parameters, we study the effect of changing those parameters on the occurrence probability.

HIGHLY PATHOGENIC INFLUENZA VIRUS - H5N1 INFECTION IN SWEDISH WILDLIFE: CLINICAL FINDINGS AND EPIDEMIOLOGY

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The first cases of HPAI H5N1 in Swedish wildlife were diagnosed on February 28 in two Tufted ducks (*Aythya fuligula*) found dead in waters adjacent to Oskarshamn nuclear power plant, approximately 400 km north of Rügen. Since then the disease has been diagnosed in Mute swan, Scaup (*Aythya marila*), Goosander (*Mergus merganser*), Smew (*Mergus albellus*), Canada goose (*Branta canadensis*), and Herring gull (*Larus argentatus*). The disease has also been observed in predators of waterfowl; Common buzzard (*Buteo buteo*), European eagle owl (*Bubo bubo*), and in a wild Mink (*Mustela vison*). Neurological signs dominated the clinical picture, the affected waterfowl were observed compulsively swimming around in circles. The majority of the HPAI positive birds were in good body condition, indicating that the highly pathogenic H5 infection is an acute disease. Up to May 15th, 536 tracheal/cloacal swabs, mainly from birds, have been examined virologically with PCR. 64 of them were positive. Conclusions drawn from the outbreak indicate that the transmission rate of this H5N1 virus seems to be low and only very few individuals out of big flocks of many thousand wild birds, were found to be affected. By the middle of May the disease had spread along the Swedish eastern coast, northwards up to the Stockholm area (400 km north of the first found positive cases). By mid-May, and with the arrival of warmer weather, the number of found dead birds positive for HPAI dropped dramatically, indicating that the avian influenza outbreak in Swedish wild birds had waned. Extensive AI testing of avian wildlife will continue, in order to monitor the further occurrence of HPAI and LPAI in Sweden.

HIGHLY PATHOGENIC AVIAN INFLUENZA IN WILD BIRDS IN SWEDEN: CHARACTERIZATION OF LESIONS IN THE CENTRAL NERVOUS SYSTEM

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Encephalitis was a characteristic lesion caused by highly pathogenic avian influenza (HPAI), H5N1 in the various wild avian species affected during an outbreak in Sweden in 2006. This study describes the neuropathology associated with the infection in 45 birds: 22 tufted ducks (*Aythya fuligula*), 5 mute swans (*Cygnus olor*), 5 goosander (*Mergus merganser*), 4 scaups (*Aythya marila*), 2 Canada geese (*Branta Canadensis*), and a few other species. Sections representative of the major brain areas were stained with H&E and with special stains. Immunohistochemistry (IHC) applied pre-treatment with proteinase K and mAbs AI-84 (EVL, The Netherlands). Multifocal areas of gliosis and inflammatory infiltrate, with a predominance of macrophages/activated microglial cells in the grey matter were consistently observed. Neuronal degeneration, neuronophagia, vacuolation of the neuropil, and in some cases focal necrosis was observed in these areas. There were abundant perivascular cuffs of mononuclear cells. Vasculitis with degenerative changes (vacuolation and presence of acidophilic debris) was present in the cases with severe encephalitis. Endothelial-cell hypertrophy occurred frequently. Milder, and probably earlier lesions, were represented by small foci of gliosis and inflammatory infiltrate including occasional heterophils and thin perivascular cuffs with a few macrophages and heterophils. Viral antigen, as demonstrated by IHC, was present in the nucleus and cytoplasm of neurons, in macrophages and in glial cells. The lesions had a random distribution affecting any areas of the brain, but occurred more frequently in the cerebrum than in the midbrain, medulla oblongata and cerebellum; the spinal cord was less affected. The severity of the encephalitis varied among the tufted ducks, but it was severe in more than 30% of the cases. The brain lesions were particularly severe in the swans and the geese. An eagle owl (*Bubo bubo*) had focal necroses, vasculitis and cuffs, all rich in heterophils. Some of the birds with encephalitis had tested negative at a PCR analysis of the tracheal swab. Approximately 10% of the birds had minimal lesions in the brain. In conclusion, the HPAI virus in Sweden appeared to be highly neurotropic in a range of avian species, resulting in encephalitis as a main lesion.

HIGHLY PATHOGENIC INFLUENZA VIRUS-H5N1 INFECTION IN SWEDISH WILDLIFE: PRELIMINARY PATHOLOGY FINDINGS

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An outbreak of highly pathogenic avian influenza-H5N1 was detected for the first time in Sweden in two Tufted ducks (*Aythya fuligula*) in February 2006. Since then, a number of wild avian species, including ducks, geese, swans, gulls and raptors, as well as a wild mink (*Mustela vison*) have died of H5N1 infection. A few birds and the mink were observed with signs of neurologic dysfunction. Most birds were in good body condition. Gross lesions, when present, consisted most frequently of necrosis and haemorrhages in the pancreas, and sometimes severely congested lungs. Histologically, preliminary observations indicate that the most frequently observed lesions were non-suppurative meningo-encephalitis and necrosis in the pancreas. Lung congestion and pneumonitis, and inflammation in the upper respiratory tract were observed less frequently. Multifocal necrosis with infiltration of heterophils and macrophages and perivascular inflammatory infiltrates were observed less regularly in several organs, such as liver and adrenal glands. Immunohistochemistry was conducted on formalin fixed tissues, 0.1% protease treated sections, and applying monoclonal antibodies to Influenza A (EVL Hb65 www.evlonline.nl). Disease specific antigen in association to the lesions, with both nuclear and cytoplasmic localization was observed in the brain, lungs, pancreas, adrenal glands and other organs. Additionally, some of the birds that had encephalitis tested negative on the PCR-analysis of the tracheal swab, but were positive on PCR-analysis of brain tissue. The affected mink showed pulmonary consolidation with areas of hyperaemia and haemorrhages mostly in apical lobes and caudal parts of diaphragmatic lobes. Severe exudative pneumonia with presence of viral antigen was observed.

AVIAN INFLUENZA SURVEILLANCE IN WILD BIRDS IN THE UK – INTEGRATING DIAGNOSTIC PROCEDURE DURING AN URGENT SURVEILLANCE RESPONSE

Duff P.

AIM OF THE STUDY: To collect disease data during the UK's 'urgent' AIV surveillance response.

MATERIALS & METHODS: Diagnostic examinations on wild birds submitted for Avian Influenza surveillance. Posting results on the internet.

RESULTS: Wild bird surveillance for AIV at VLA resulted in the submission of 6100 wild birds in the first 6 months of 2006. At its peak 1000 birds were submitted in one week. The VLA Diseases of Wildlife Scheme (VLADoWs) rationalised this work and examined a percentage of the submissions diagnostically. The diagnoses reached were posted on the internet by Defra on a weekly basis for public access.

CONCLUSIONS: The emergency response to AIV surveillance in wild birds in the UK had several noteworthy features. It was the first national surveillance for a specified disease in wildlife. It involved reporting by the public, and collaboration between government and non-government agencies on a large scale. It is unlikely that as many wild birds will be examined again in this time scale.

Based on the government supported Diseases of Wildlife scheme set up in 1998, a percentage of the birds submitted were examined diagnostically from this unique sampling opportunity. How this was achieved, and the diseases and disease trends observed are described in this presentation.

SURVEILLANCE OF AVIAN INFLUENZA IN WILD BIRDS IN NORTH AMERICA: FORECASTING THE POTENTIAL SPREAD OF EMERGENT DISEASES

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Avian influenza viruses are known to infect birds, providing an extensive reservoir from which highly pathogenic strains (HPAI) can evolve. To date, all outbreaks of HPAI have been caused by influenza A viruses of subtypes H5 and H7. In some instances, direct or indirect contact of domestic flocks with wild migratory waterfowl has been implicated as a frequent cause of epidemics. No HPAI H5N1 virus has been detected in North America. Some questions to answer include which wild birds will be involved in carrying AI in North America? What are the potential movements along the North American flyways? Are there seasonal patterns to the spread of influenza in birds? Can we predict the spread of HPAI in both the breeding and wintering grounds if it emerges? In addition to the increase in morbidity and mortality in wild bird populations, these species may serve as a source of virus to humans and domestic animal populations. Following the XI Meeting of the Canada/Mexico/US Trilateral Committee for Wildlife & Ecosystem Conservation and Management, the three countries agreed to collaborate in surveillance of avian influenza. We will participate in supporting response and surveillance protocols, assist in live bird surveillance in all shared flyways, develop waterbird/waterfowl and wetland risk assessment maps and conduct complementary population delineation studies. The rationale of an early detection system for surveillance of all avian influenza viruses includes protection of export trade in poultry and poultry products, early detection of strains, maintenance and improvement of national laboratory and surveillance capacity for AI viruses and information in support of risk analysis and risk communication including information for human health.

THE WALL LIZARD (*Podarcis muralis*) AS A MAJOR HOST FOR *Ixodes ricinus* TICKS AND AS A RESERVOIR FOR *Borrelia lusitaniae* IN TUSCANY, CENTRAL ITALY.

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AIM OF THE STUDY: In this study we evaluated the role of wildlife, including mice (*Apodemus* spp) and wall lizards (*Podarcis muralis*), in the transmission cycle of *Borrelia lusitaniae*, which is one of the agents of Lyme borreliosis and is mostly found in southern Europe and the Mediterranean.

MATERIALS & METHODS: Wild animals were live-captured in Le Cerbaie Hills in the province of Pisa, in 2004 and 2005. Attached ticks and tissue samples were collected and processed by Polymerase Chain Reaction (PCR) targeted to a 225-bp intergenic spacer region included between genes codifying for 5S and 23S ribosomal RNA. PCR products were sequenced and submitted to BLAST to identify similarities to known sequences, and therefore to classify *B. burgdorferi*-positive samples by genospecies.

RESULTS: Prevalence of infestation by larval *Ixodes ricinus* (the tick vector of *B. burgdorferi*) and counts of larvae per individual host were similar in mice and lizards. Conversely, *I. ricinus* nymphs were much more common on lizards than on mice. Prevalence of *B. lusitaniae* in larvae feeding on lizards was 19.8% (95% confidence interval: 14.4; 26.0), and the infection was also detected in tissues and blood from *P. muralis*. *Borrelia lusitaniae* was not found in 111 larvae and 68 tissue samples that were collected from mice.

CONCLUSIONS: *Podarcis muralis* lizards satisfied important criteria for reservoir competence for *B. lusitaniae*: a) lizards are a major component of wildlife populations in certain geographic areas; b) they serve as major hosts for the tick vectors; c) the infection was demonstrated in lizards' tissues; d) a relatively high proportion of larvae feeding on lizards was infected with *B. lusitaniae*; considering that larvae are very rarely infected transovarially, this can be considered as evidence of pathogen's transmission from lizards to ticks.

MOLECULAR EVIDENCE OF *Anaplasma phagocytophilum* INFECTION IN *Ixodes ricinus* LARVAE COLLECTED FROM ROE DEER (*Capreolus capreolus*) IN NORTH-EASTERN ITALY.

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AIM OF THE STUDY: Human Granulocytic Ehrlichiosis (HGE) is of growing concern in human and veterinary medicine as an emerging tick-borne disease in Europe and in the North America. Ruminants and rodents have been suggested to maintain in nature the HGE agent. Nevertheless, the role played by wild ungulate is still matter of study. The aim of this study was to investigate the potential role of roe deer (*Capreolus capreolus*) as a natural reservoir for strains of *Anaplasma phagocytophilum* that cause human infection.

MATERIALS & METHODS: Feeding *Ixodes ricinus* ticks, at the larval stage, were collected by screening legs of shot roe deer during 2004 hunting season in the Province of Trento (North-Eastern Italian Alps). DNA extraction was carried out on a total of 78 pool of larvae collected from the same number of forelegs. PCR amplification of the tick mitochondrial gene cytochrome *b* gene was performed as a quality control for tick DNA extraction. Only positive samples were further processed for the presence of *Anaplasma phagocytophilum* by mean of nested PCR.

RESULTS: Out of the 78 pool collected from the same number of roe deer legs, 18 (21,3%) were found infected. Further phylogenetic analysis on positive samples were carried out through partial sequence analysis of the 16S rRNA gene and *groESL* heat shock operon, in order to evaluate homology of strains isolated from different hosts in Europe.

CONCLUSIONS: These results highlight the ability of roe deer to infect various *I. ricinus* stages with the pathogen *Anaplasma phagocytophilum*. Results will be presented and implication for human health discussed.

LINEAGE 2 WEST-NILE VIRUS INFECTIONS IN BIRDS OF PREY IN HUNGARY

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In the Southeast of Hungary several goshawks (*Accipiter gentilis*) and one sparrowhawk (*Accipiter nisus*) developed acute neurological disease during the summers of 2004 and 2005. One goshawk fledgling died, two were euthanized. Three goshawks (one adult) and one sparrowhawk recovered from the disease as the result of force-feeding and supportive therapy. No specific macroscopic lesions could be found on post-mortem examination of three dead goshawks. Organ samples were taken for histology and were also submitted for bacteriological and virological examinations. Bacteriological culture of brain, liver and intestinal samples yielded negative results in all cases. Histopathological examinations revealed multi-focal, lymphocytic panencephalitis with marked gliosis, neuronal degeneration comprising chromatolysis, necrosis and neuronocytophagia, multi-focal proliferation of reticulocytes and lymphoid depletion in spleens, multi-focal lympho-histiocytic myocarditis, mild lymphocytic enteritis and proventriculitis in all cases. Additionally, demyelination of the cerebellar white matter and lymphocytic meningitis were detected in two cases. The presence of WNV antigen in pathological lesions was confirmed in all three cases by immunohistochemistry. A Japanese encephalitis virus complex-specific RT-PCR test was performed from all three post-mortem cases and from the buffy-coat of two clinical blood samples. All samples tested positive and the products were sequenced. Sequences were identified by BLAST search against the GenBank database. They have shown the highest (<97%) identity with lineage 2 WNV strains. The WNV strain was isolated from brain and blood samples by intracerebral inoculation of suckling mice.

Since other species (e.g. peregrine falcon, common buzzard, domestic fowl) living at the temporary rehabilitation center were not clinically unaffected by the disease, we must assume that goshawks and sparrowhawks are more susceptible to WNV infection and might be used as indicator species. Both years the causative agent was identified as a lineage 2 West Nile virus and this is the first evidence of lineage 2 West Nile virus circulation outside the African continent.

TICK-BORNE ENCEPHALITIS (TBE): FUNDAMENTAL ECOLOGY AND EPIDEMIOLOGICAL PATTERNS RECORDED IN TRENTO

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AIM OF THE STUDY: Tick-borne encephalitis (TBE) is an emerging viral infection transmitted in Europe by the tick *Ixodes ricinus*. The virus persists only in those geographic areas where a combination of biotic and abiotic factors favours co-feeding of larvae and nymphs on rodent hosts permitting the non-systemic transmission of the virus. In Trentino (northern Italy), infection in humans was recorded since 1992. The aim of our work was to assess the spatial distribution of TBE foci in this area and activate a surveillance system on the temporal distribution of the rodent infectious status and the climatic variability.

MATERIALS & METHODS: Longitudinal and cross-sectional serological and entomological studies have been carried out on rodents and domesticated goats. Sera samples were tested with ELISA and PRNT. Moderate Resolution Imaging Spectroradiometer (MODIS) Land Surface Temperature (LST) data were used to evaluate cooling rate. Statistical analysis were performed with GLM

RESULTS: The circulation of TBEv, as predicted by serological data, was wide but with significant variation in spatial distribution. In the case of goats sera, a significant correlation with the cooling rate recorded per site was obtained. Fluctuation in *A. flavicollis* abundance was observed, with two major population peak at a 5 years interval. Interannual variation in TBE seroprevalence and infestation with *I. ricinus* were also recorded.

CONCLUSIONS: Tick borne encephalitis virus persists and appear to be widespread in this area but the transmission potential of the infection appear to varies temporally and spatially in relation to local climatic condition and host densities. Project supported by the research fund of the Autonomous Province of Trento, under grant 1060 ECODIS and 3479 MOSTWIN.

MODELING TICK-BORNE ENCEPHALITIS IN TRENTO (NORTHERN ITALY)

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AIM OF THE STUDY: In this study we explore, through the analysis and simulation of models that include constant or fluctuating mice populations, how changes in the relative host densities, in particular small rodents and deer, affects the persistence and the dynamics of tick-borne encephalitis virus (TBEv). The findings from these models are then compared with temporal variations of TBEv sero-prevalence in an endemic hot spot of TBE in Trentino (northern Italy).

MATERIALS & METHODS: The dynamics of TBEv is explored through the analysis and simulation of models that include different assumptions on tick-host dynamics and consider different routes of infection transmission. Ticks are assumed to feed on two types of host species (mice and deer) which vary in their reservoir competence.

RESULTS: The relative ratio of host densities determines whether the disease can persist or not. An increase in deer density has a positive effect on tick abundance but causes a dilution effect through “wasted bites”. In some cases, also mice, at extremely high densities, cause a negative effect, as a consequence of the pattern of tick distribution among mice. In fluctuating populations the model may predict that peaks of mouse densities coincide with highs or lows of TBEv prevalence, according to the mean value of density. With our parameter set TBEv cannot persist if only systemic transmission is included in the model but, in accordance with the general view of TBEv, co-feeding transmission is required for virus persistence.

CONCLUSIONS: These results show that variations in relative densities of both mice and deer would have a profound influence on persistence and prevalence of TBEv in Trentino. Project supported by the research fund of the Autonomous Province of Trento, under grant 3479 MOSTWIN

Echinococcus multilocularis: A ZOOZONOSIS IN THE CITY

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The urban fox phenomenon that was first described in a number of British cities in the 1940's reached continental Europe twenty-five years ago. Urban red foxes (*Vulpes vulpes*) are now commonly sighted in most of the European metropolises. The red fox is the main definitive host of *Echinococcus multilocularis* (*E. m.*) in Europe. *E. m.* is highly pathogenic in humans causing alveolar echinococcosis, which is lethal if left untreated. The canton of Geneva, Switzerland is located in the core of the endemic range of the parasite, and 47% of its red foxes were found infected. Although the prevalence of *E. m.* in foxes decreased with the level of urbanization of the habitat, 31% of Geneva urban foxes harboured the parasite, resulting in serious public health concerns. *E. m.* is a dioxenous cestode and requires a rodent intermediate host to complete its life cycle. Despite the presence of infected urban foxes, it remained unclear whether urban foxes were infected after preying in rural surroundings or whether an established urban life cycle of *E. m.* occurred within the city. We captured and necropsied 466 water voles (*Arvicola terrestris scherman*), which is one of the main intermediate hosts of *E. m.* in Switzerland. The prevalence of *E. m.* did not vary with the level of urbanization of the habitat; 6.0% (N=184) and 5.4% (N=129) of the trapped water voles were infected in the rural and urban areas respectively. One urban trapping site was highly contaminated with a prevalence of 20% in water voles (N=35), indicating the establishment of an urban cycle of *E. m.* in the city of Geneva. A cluster of alveolar echinococcosis in water voles trapped along the right bank of Lake Geneva (prevalence of 22%, N=97) revealed a significant risk of exposure for humans in the north-western residential area.

***Trichinella* Sp. IN THE BLACK BEAR (*Ursus americanus*) SOUTH OF THE 50TH PARALLEL IN QUEBEC, CANADA: DISTRIBUTION, PREVALENCE, INTENSITY OF INFECTION AND GENOTYPE**

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The black bear (*Ursus americanus*) was the source of the last episodes of human trichinellosis in Quebec: 25 cases were reported from 2003 to 2005. In 2004, 659 tongues of black bears were collected in Quebec south of the 50th parallel, in order to determine the distribution, prevalence, intensity of infection and genotypes of *Trichinella* in black bear. The tongues were analyzed by peptic digestion: six black bears were infected. The positive bears were distributed north of the St-Laurent river, from the west to the east of the Quebec province. We estimate, that the prevalence of *Trichinella* sp. in the black bear in Quebec, south of the 50th parallel, is 0,91% (95% CI: 0,33 to 1,97%). The intensity of infection varied between 0,01 and 4,15 larvae per gram. The identification by multiplex PCR revealed that the six bears were infected by a new genotype of *Trichinella* (Pozio, E. *International Trichinella Reference Centre*, Laboratory of Parasitology, Istituto Superiore di Sanita viale Regina, Rome, Italy). Even if the prevalence and the intensity of infection to *Trichinella* sp. in black bear on this territory are relatively low, all the hunters and trappers should be informed of the precautions to take to avoid being infected by consuming meat of black bear containing a new genotype of which we do not know the pathogenicity for human.

SALMONELLA INFECTIONS IN FOXES (*Vulpes vulpes*)

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AIM OF THE STUDY: 1) To study the prevalence of salmonella infections in free-ranging red foxes (*Vulpes vulpes*) in Norway, and 2) to study experimental infections in farmed silver foxes (*Vulpes vulpes*) using two different PFGE profiles of *S. Typhimurium* 4,12: i: 1,2 isolated from small passerine birds.

MATERIALS AND METHODS: The prevalence study included bacteriological examination of faecal samples from 215 red foxes shot during November to April 2002-2004. In the experimental study, six silver foxes were divided into two equal groups, and inoculated with either *S. Typhimurium* 4,12: i: 1,2 PFGE profile A2 or X201. A2 is a common and X201 a rare PFGE profile associated with disease outbreaks in stationary small passerines during the winter in Norway.

RESULTS: None of the 63 foxes shot in November and December were found to be positive for salmonella, whereas 9% (14/152) of those shot during the period January to April carried salmonella bacteria. The foxes shot in January-April 2004 showed a significantly higher carrier rate (12/74; 16%), compared to those shot during the same period in 2003 (2/78; 3%). The majority of the isolates belonged to the serovar *S. Typhimurium* 4,12: i: 1,2. All of the three experimental foxes inoculated with the PFGE profile A2 shed the bacteria in their faeces from day 1 to days 13-15, whereas no salmonella bacteria were found during the remaining four weeks of the experimental period. One of the three foxes inoculated with the PFGE profile X201 shed the bacteria in its faeces at day 1 post inoculation, all other samples were negative. No clinical signs of disease were observed in any of the foxes.

CONCLUSIONS: The present study found that the red fox is commonly infected with *S. Typhimurium* 4,12: i: 1,2 during the winter. The infections presumably reflect fox predation on small passerines with concomitant *S. Typhimurium* 4,12: i: 1,2 disease. The study also showed that the common PFGE profile A2 associated with disease outbreaks in passerines can establish a clinically silent infection in foxes, of two weeks duration, suggesting that the fox could play a role in the ecology of this bacterium in nature.

PATHOLOGICAL PATTERNS IN WILD FAUNA OF NORTH-WESTERN ALPS WITH SOME HISTOLOGICAL AND BACTERIOLOGICAL INVESTIGATIONS

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AIM OF THE STUDY: Aim of the study is to show some case reports observed during necroscopic activity on different wild animals of Northern Western Alps. We'll describe various expressions of some more common pathological lesions or single case reports which are particularly typical or have different reasons for debating

MATERIALS & METHODS: In order to define the etiology of lesions we have applied, depending on the circumstances, visual exam, bacteriological exam (using common media as Blood Agar and Mc Conkey Agar or, for differential diagnosis with tuberculosis, selective media as Stonebrink, L.J., L.J. w/o glicerine), histological exam (with Haematoxylin-Eosin stain), special stains such as Ziehl-Neelsen, modified Ziehl-Neelsen and Gram and finally, only for the case of nocardiosis, genotypization with Mycroseq ID-16S rDNA 500 (applied Biosystem). **RESULTS:** With regard to the features, the cases are grouped as follows: 1)injuries/starvation 2) metabolic disturbances 3) parasitic diseases 4) infectious diseases 5) neoplastic diseases. Most important cases reports described are: a) hepatic fat degeneration in deer b) tuberculosis in roe deer c) nocardiosis in chamois d) staphylococcosis in eagle e) squamous carcinoma in deer 5) renal cystic adenoma in beech marten 6) nasal papilloma in chamois. About infectious diseases, we describe the lesions by corynebacteria, that can be more or less severe according to the species of *Corynebacterium* involved (*C. pseudotuberculosis*, *C. striatum*, *C. ulcerans*) and the various histological features of retropharyngeal lymph node lesions of wild boar with differential diagnosis against tuberculosis.

CONCLUSIONS: Injuries and starvation are the most common fatal lesions we can see on wild animals taken to the laboratory. Parasitic diseases are also very frequent and contribute to the decline and the death of the animal arising in addition to infectious or other pathological process. At the end neoplastic diseases seems unusual, perhaps because wild fauna doesn't reach an age fit for the development of this type of disorder.

DEVELOPMENT OF AN ELISA FOR THE DETECTION OF INTERFERON-GAMMA (IFN- γ) AS A DIAGNOSTIC TOOL FOR TUBERCULOSIS IN ELEPHANTS

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AIM OF THE STUDY: To develop reagents to set up an elephant IFN- γ (EpIFN- γ) assay that can be used as a routine diagnostic tool for *Mycobacterium bovis* and or *Mycobacterium tuberculosis* infection in elephants. This is of importance in breeding and relocation projects aiming at the conservation of biodiversity and for addressing the zoonotic concerns in zoo's and circuses.

MATERIALS & METHODS: The Asian elephant IFN- γ (EpIFN- γ) gene was cloned, sequenced and expressed as a mature protein. The hexa-histidine tagged recombinant elephant IFN- γ was purified by immobilized metal chromatography and mouse monoclonal, as well as polyclonal chicken antibodies (IgY) with specificity for recombinant EpIFN- γ were produced. These antibodies were used to setup a capture ELISA for the detection of native EpIFN- γ .

RESULTS: Sequence analysis of the cloned EpIFN- γ gene demonstrated the highest homology with equine IFN- γ , i.e. 82% and 75% identity on the nucleotide and amino acid level, respectively. Using the developed mouse monoclonal antibodies and polyclonal IgY a capture ELISA could be developed that was able to detect recombinant EpIFN- γ as well as native EpIFN- γ .

CONCLUSIONS: An EpIFN- γ specific capture ELISA has been produced with the potential to be developed into a diagnostic assay for *M.bovis* and *M. tuberculosis* infection in elephants.

SERO-EPIDEMIOLOGICAL SURVEY ON BOVINE RESPIRATORY SYNCYTIAL VIRUS IN A WILD ROE DEER (*Capreolus capreolus*) POPULATION IN DEMOGRAPHIC DECREASE IN THE NORTHERN APPENNINES, ITALY (1995-2004).

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AIM OF THE STUDY: The aim of the investigation was to verify the prevalence of BRSV in a wild roe deer population of the northern Appennines (Italy) which presented a rapid decline of density, and evaluate the associations between the transmission of BRSV, demographic parameters, and density decrease.

MATERIALS & METHODS: Within the period 1995-2004, 244 blood samples collected from roe deer of known age and sex were investigated by virus-neutralization tests. A multiple logistic regression was performed to identify independent predictors of seropositivity among demographic variables (age classes, density, sex). A SIRS model of BRSV transmission was also prepared. In the model, individuals acquired immunity gradually after repeated exposure to reinfection. To incorporate more of the characteristic features of BRSV a latency period and the presence of persistently infected individuals were included. In order to understand if wild roe deer population was able to maintain the virus, the model was fitted simulating sporadic or absent contacts with domestic ruminants.

RESULTS: We found a seroprevalence of 14.8% (I.C. 95% 10.5-19.8) with log-transformed antibody titres ranging between 1.39 and 4.17 (median 1.61). Logistic regression demonstrated a significant association between population density variations and virus prevalence (O.R.=1.170-2.367, p=0.005). Model fitting allowed for estimation of parameters of infection, indicated a strong influence of variations of roe deers density and of duration of humoral immunity on BRSV transmission dynamics, and confirmed the possibility of virus persistence independently from contacts with domestics.

CONCLUSIONS: According to virus transmission features, BRSV persisted in wild roe deer populations with an endemic pattern, showing a correlation with host population density variations.

EVIDENCE OF RESPIRATORY SYNCYTIAL VIRUS INFECTION IN A CHAMOIS (*Rupicapra r. rupicapra*) POPULATION IN THE ITALIAN CENTRAL ALPS.

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AIM OF THE STUDY: Since 1999 a high seroprevalence against Respiratory Syncytial Virus (RSV) has been demonstrated in a chamois population of the Orobic Alps (Central Alps, Italy), and during 2000-2001 an outbreak of severe respiratory disease with high mortality was observed among the chamois. The aim of this study is to investigate the aetiology of pulmonary distress and the relationship with the evidence of circulation of RSV.

MATERIALS & METHODS: From Autumn 2000 to Autumn 2005, 29 carcasses and 99 lungs of hunted chamois were necropsied. Most of the lung samples were submitted for bacteriological and virological examinations, and 22 were fixed in formalin. Serial sections of 4mm were stained with HE and incubated with mAb 1G3 raised against bovine RSV (BRSV); 11 were analysed by PCR with a protocol aimed at the detection of both BRSV and ovine respiratory syncytial virus (ORSV).

RESULTS: Macroscopically, intralobular haemorrhages, red areas of consolidation and bronchopneumonia were observed in the lung samples. Histologically, verminous pneumonia, catarrhal bronchopneumonia and bronchiolitis were detected in all samples. Occasionally, syncytial giant cells were present in the respiratory epithelium. Fifteen out of 22 samples were positive by immunohistochemistry (IHC) for RSV. The positive reaction was mainly localised in the cytoplasm of bronchial epithelial cells and in the macrophages. All samples were negative by the PCR test.

CONCLUSIONS: In the study area, RSV is involved in the acute and fatal respiratory disease of the chamois and in the chronic lesions as well. As the chamois and sheep flocks (where a seroprevalence of 82% against RSV has been found) share the same habitats during summer pasturing, an interspecies transmission of RSV can be speculated. The negative results of the PCR test could be due to the presence of a virus different from BRSV and ORSV and/or to the prolonged storage of the samples (> 3 years) before testing

LONG TERM STUDY ON *Mycobacterium avium* subsp. *paratuberculosis* IN FREE RANGING ALPINE WILDLIFE IN NORTH-EASTERN ITALY

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AIM OF THE STUDY: The purpose of this survey was to assess the prevalence of *Mycobacterium avium* subsp. *paratuberculosis* (MAP) infection and its effects in red deer (*Cervus elaphus*) populations in north-eastern Italy, and to study the epidemiology of paratuberculosis (Johne's disease) including other ruminant and non-ruminant wild populations. MATERIALS & METHODS: During the period 1998-2005 a sample of 630 red deer, structured in terms of age and gender classes, was obtained from western and eastern districts of the Trento province. A total of 910 samples were collected from other species: 487 roe deer (*Capreolus capreolus*), 194 alpine chamois (*Rupicapra rupicapra*), 13 alpine ibex (*Capra ibex*), 7 moufflons (*Ovis musimon*), 157 red foxes (*Vulpes vulpes*) and 52 brown hares (*Lepus europaeus*). The investigation was based on gross pathological analysis and on culture on Herrold's Yolk Egg Medium from gut and associated lymph nodes. Isolates were identified by an IS-900-based PCR and characterised by means of an IS-1311-based PCR-REA. RESULTS: Johne's disease (Jd) resulted to be widespread in red deer populations. Different geographic distributions were evidenced: the highest prevalence of infection reached 80% (S.E. + 12%) in western districts, 45% (S.E. + 9%) in eastern ones. Paratuberculosis was assessed as a cause of mortality in 16% of found dead red deer. Macroscopic lesions consistent with Jd were constantly observed and classified. MAP was isolated from 75 roe deer (15%), 28 chamois (14%) and 15 foxes (9,5%). Sporadic cases were detected in alpine ibex and in brown hare. The characterisation of isolates revealed the "bovine subtype". Preliminary data indicate that no clinical nor subclinical Jd is present in bovines sharing pastures with red deer and that herd level seroprevalence is very low (<5%). CONCLUSIONS: The results showed the persistence of high rates of infection and disease in red deer populations suggesting this species to be the key in the maintenance of infection in wildlife in the study area. Populations density appears to be a main risk factor. The wide host range encountered evidenced an environmental contamination of MAP. Further research needs to be carried out in order to study the epidemiology of paratuberculosis in alpine pastures.

DESCRIPTION OF AN OUTBREAK OF PESTIVIRUS INFECTION IN CHAMOIS (*Rupicapra pyrenaica*) IN THE PYRENEES DURING 2005 AND 2006

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In January 2005, a high mortality of chamois was observed at the National Hunting Reserve of Cerdanya-Alt Urgell (Catalonia, NE Spain). In June 2005, the disease spread to the National Hunting Reserve of Cadi, an area close to the southern border of the Cerdanya-Alt Urgell Reserve. During the subsequent months and in 2006, a high mortality was also observed. Fifty eight affected chamois were studied. Clinical manifestations included depression, weakness, difficulty to move, different degrees of alopecia and skin hyperpigmentation. At necropsy a marked cachexia was observed in all animals and most of them had different degrees of pneumonia. Microscopic lesions were found in brain, mainly oedema, gliosis, spongiosis and multifocal necrosis. In some of them a perivascular mononuclear inflammatory infiltrate was also present. Skin lesions included marked follicular atrophy, epidermal hyperplasia with orthokeratotic hyperkeratosis, hyperpigmentation and pigmentary incontinence. A pestivirus was isolated from the affected chamois and identified by RT-PCR.

DO ABORTIVE INFECTIONS DECREASE SURVIVAL IN PYRENEAN CHAMOIS (*Rupicapra pyrenaica pyrenaica*)?

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AIM OF THE STUDY: Recently, several populations of Pyrenean chamois experienced either mass mortalities or decrease in population counts. We tested whether *Salmonella* spp., *Chlamydomphila* spp., *Coxiella* spp. and *Pestivirus* were related to variations in yearly survival. We first used results of antibody and antigen detection to analyse the variations of *pestivirus* incidence and prevalence between 1995 and 2004. We then, searched for a relationship between survival of yearling and adult chamois, studied from 1985 to 2004, and the prevalence of immune responses against *pestivirus*, *salmonella*, *chlamydomphila* and *coxiella*. **MATERIALS & METHODS:** We used Generalised Linear Model to analyse factors explaining variations of *pestivirus* antigen and antibody prevalence. We searched for the effects of age, gender, cohort, season, sampling method (hunted vs capture), population size and number of young animals in the population. Then, we used Capture-Mark-Recapture methods to assess variations of chamois survival. We took into account age and gender and assessed if the estimated *pestivirus* antigen prevalence or the sanitary status of the population according to *Salmonella*, *Chlamydomphila* and *Coxiella* could explain survival variations in chamois. **RESULTS:** *Pestivirus* antigen prevalence, estimated from n = 167 individuals, varies seasonally and is related to the number of young animals in the population, thus virus transmission is highly dependent on host population dynamics. Antibody prevalence (n = 323) is related to the same factors and also depends on age, cohort, gender and capture method, which suggests that exposure and / or susceptibility vary within the population. The survival variations of yearling or adult Pyrenean chamois are not correlated with *Pestivirus* incidence. Survival is high both in male (n= 94) and female (n= 252). However, in female, survival is significantly lower in 1998. The variations of survival are correlated to the presence of bacterial infections. **CONCLUSIONS:** The survival of Pyrenean chamois may be related to the sanitary status revealed by the presence of abortive bacterial diseases.

EVIDENCE OF SHEEP AND GOAT ASSOCIATED MALIGNANT CATARRHAL FEVER IN FREE-RANGING CERVIDS

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AIMS OF THE STUDY: To summarize pathological lesions seen in free-ranging Norwegian cervids with the diagnosis malignant catarrhal fever (MCF), and by means of Polymerase Chain Reaction (PCR) to identify the causative MCF-virus in tissues from these cases. Also, the prevalence of antibodies against MCF-viruses in the Norwegian cervid population was studied.

MATERIALS & METHODS: Pathological lesions associated with MCF were summarized in 15 moose (*Alces alces*), two roe deer (*Capreolus capreolus*), and one red deer (*Cervus elaphus*) examined at the National Veterinary Institute, Oslo 1982-2005. PCR was run on samples from 15 of these individuals for evidence of MCF-virus DNA. Sera from 1,000 free-ranging cervids sampled during hunting were tested for specific antibodies to MCF-virus by competitive ELISA.

RESULTS: The most frequent gross findings were eye lesions and multifocal erosive-ulcerative stomatitis and rhinitis of variable severity. No specific gross lesions were found in the two roe deer. The characteristic histopathologic finding was a non-purulent vasculitis and perivasculitis in the central nervous system. PCR detected Ovine herpesvirus-2 (OvHV-2) DNA in seven cervids (all species represented), and Caprine herpesvirus-2 (CpHV-2) DNA in two moose and one roe deer. Antibodies against MCF-viruses were found in 5.2% (13/250) of the red deer, 3.6% (9/250) of the reindeer (*Rangifer tarandus*), 2.0% (5/250) of the roe deer, and 0.4% (1/250) of the moose tested.

CONCLUSIONS: The study indicated that sheep and goat associated MCF-viruses may cause serious disease in wild cervids. The seropositive animals most likely represented individuals infected with either OvHV-2 or CpHV-2, but may also reflect infections with other related MCF-viruses.

Abstracts

Posters



THE DIET OF THE EURASIAN BADGER (*Meles meles*) AND THE RED FOX (*Vulpes vulpes*) IN RELATION TO *Salmonella* INFECTION IN THE WESTERN ITALIAN ALPS.

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AIM OF THE STUDY: *Salmonella* serotypes have been isolated from a wide variety of mammals, including wild carnivores. Normally infections are acquired by ingestion of contaminated food or water, thence the feeding habits of animals are likely to influence their chance of being infected with the pathogen. To highlight the role played by foraging behaviour in the epidemiology of salmonellosis in alpine carnivores, we compared the diet of the red fox and the Eurasian badger with our data about *Salmonella* prevalence. **MATERIALS & METHODS:** Between 2003 and 2005, 289 fox faeces and 192 badger faeces were collected and analysed. Data were expressed both as frequency of occurrence (%FO=number of faeces containing a specific food items/total number of faeces x 100) and estimated per cent volume (%V=total estimated volume of each food item as ingested/number of faeces containing that item). Diet frequency data according to three height belts (500-999, 1000-1499, 1500-2000 m) were compared using the "chi-square" test (χ^2). Trophic niche breadth was estimated by the Levins' index (B). Pearson's correlation test was used to compare the seasonal prevalence of *Salmonella* with the seasonal %FO and %V of carnivores' main food items. **RESULTS:** Fox diet was more varied (B=0.57), including fruits, rodents, carrions, invertebrates and birds, whilst badgers (B=0.31) consumed mainly invertebrates, *Rosaceae* and amphibians. For both carnivores no significant correlation emerged between seasonal *Salmonella* prevalence and the use of the main diet items. Nonetheless, foxes ate more birds (passerines and pigeons) ($\chi^2=9.29$ p=0.009) and human garbage ($\chi^2=7$, p=0.03) below 1000 m a.s.l., where *Salmonella* prevalence was reported to be higher. **CONCLUSIONS:** Salmonellae being widespread in the environment, generalist carnivores such as the red fox and the badger are likely to acquire the infection from a wide variety of trophic sources, including contaminated water. In this context, environmental contamination from human productive activities could contribute to the occurrence of *Salmonella* in wild carnivores.

SEROLOGICAL SURVEY ON NUTRIA

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AIM OF THE STUDY: The nutria (*myocastor coypus*), a big semi-aquatic rodent originating from South America is present in many regions of Italy and its distribution is expanding. This rodent is considered a pest of agricultural crops. Particularly in Vercelli, nutria cause serious damage to draining systems in rice-fields, they devastate the crops and native plant communities and compete with indigenous and migrating birds. Aim of the study is to provide information about diseases, liable for epizootics, in a population of nutria living in the low land of Vercelli. **MATERIALS & METHODS:** Eighty-seven nutria were trapped or shot in Vercelli around the Sesia river during eradication campaigns from January to December 2005; they were examined for the prevalence for selected serum antibodies (against *Leptospira* and *Brucella*), enteric bacteria (*Salmonella* and *Campylobacter*) and parasites (*Trichinella*). Blood samples were collected by cardiac or abdominal vessel puncture and the animals were necropsied. Fifty-seven sera were examined for *Leptospira* by microscopic agglutination test (minimum significant titer 1:100 final dilution) and *Brucella abortus* by rapid sero-agglutination test. Fifty-five muscle samples (masseter and diaframma) were examined using digestive method to check the presence of *Trichinella spiralis*. Fifty-five fecal samples were examined for *Salmonella* and *Campylobacter*.

RESULTS: Four sera (7.2%) contained antibodies against *L. bratislava*, two sera (3.6%) against *L. icterohaemorrhagiae* and *L. copenhageni*. There was no association between the presence of *Leptospira* antibodies and the renal lesions. All sera were negative for *Brucella abortus*; all fecal sample were negative for *Salmonella* and *Campylobacter*; all muscle samples were negative for *Trichinella spiralis*.

CONCLUSIONS: Healthy condition of nutria population we examined is better than farmed. Therefore continuous surveillance for diseases potentially responsible for epizootic in wild and domestic animals and humans is needed because the epidemiological conditions could be modified by increasing of the non-indigenous population.

A SEROLOGICAL SURVEY ON *Micobacterium avium subsp. paratuberculosis* IN WILD RUMINANTS OF THE PESARO-URBINO DISTRICT (ITALY)

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AIM OF THE STUDY: The aim of the study was to evaluate prevalence of paratuberculosis in wild ruminants of the Pesaro-Urbino district in Marche region. *Micobacterium avium paratuberculosis* (MAP) infects both domestic and wild ruminants. During the period 2003-2005, there has been an increase of diagnosis of paratuberculosis in domestic ruminants of Pesaro-Urbino district. In the same period we had just few evidences of presence of MAP's DNA, detected by PCR procedure performed on ileo-caecal valves, without other clinical signs. In order to carry out an efficient sanitary control plan for paratuberculosis we estimate the serological prevalence in cervids of the district.

MATERIALS & METHODS: The target is the entire population of wild ruminants in the Pesaro-Urbino district which was estimated to be of 17.620 of ungulates among roe deer (*Capreolus capreolus*), fallow deer (*Dama dama*) and deer (*Cervus elaphus*). A random sample of 179 ungulates was selected and 179 samples of serum were collected and analysed both by an ELISA test and an AGID test to detect antibodies against MAP.

RESULTS: No sample resulted positive so estimated prevalence is $\leq 1.65\%$ and the expected maximum number of positive animals in the population is 291.

CONCLUSIONS: This preliminary investigation suggests that during 2003-2005 there wasn't valuable antibodies circulation of MAP in cervids of the Pesaro-Urbino district; however, pasture is the main wildlife/livestock interface in this district and wildlife could have a role as carrier between farms.

CADMIUM CONTAMINATION IN WILD BOAR (*Sus scrofa*) IN THE MARCHE REGION (Italy)

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AIM OF THE STUDY: Cadmium (Cd) bio-accumulation along food chains can lead to dangerous low-level exposure mainly for "extreme-consumers" of some food.

In the Marche Region of Italy the control of cadmium residues includes equine and swine species. During recent years, recommended maximum levels (Reg. 466/2001/CE) have been regularly exceeded in horses living in a mountainous area (where they are free-range and bred for human consumption). To better understand the diffusion of contamination and the potential risk for consumers, a survey was carried out to Cd concentrations in body tissues of a biological indicator occupying the same area.

Wild boar were chosen (*Sus scrofa*) for sampling because they concentrate cadmium in the liver and kidneys, but hunted wild boars are not included in regular surveillance programs for food contaminants.

MATERIALS & METHODS: During 2002-2004 target organs of hunted wild boars from the studied area were sampled. Kidneys and liver of 88 animals were collected; tissue samples were analysed by Atomic absorption spectrometry after microwave mineralisation and data were analysed using Epiinfo 3.3.2 software.

RESULTS: Mean concentrations in target organs confirmed environmental diffusion of cadmium in the studied area and the exceeding of recommended levels in boar.

CONCLUSIONS: The results suggest that game and other local products should be submitted to careful monitoring because of the potential low-level cadmium exposure of some population groups.

DISEASE SCREENING AND MONITORING IN PHEASANTS (*Phasianus colchicus*) REARED FOR HUNTING

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AIM OF THE STUDY: The pheasant is among the most common intensively reared game birds in Italy, both for shooting and repopulation. Aim of our study is to investigate the major diseases of pheasant (*Phasianus colchicus*), of our regional territory (Umbria). MATERIALS & METHODS: The investigation focused on the main diseases known to play an important role in birds management: Avian Influenza (AI), Newcastle Disease (NDV), Marble Spleen Disease (MSD), Mycoplasmosis and Salmonellosis. A total of 13 local public reservoirs deputed to restocking and capture, 8 game bird farms and one farm runs animals imported from East Europe were investigated for the purpose of this study. A minimum of 28 pheasants from each group was sampled for serological and cloacal swab culturing. Such number was considered statistically significant to a prevalence higher than 10% with confidence limits of 95%. In the farm running imported birds 54 animals were sampled so as to detect the infection with a prevalence equal to or major of 5%, with confidence limits of 95%. RESULTS: All farms investigated resulted seropositive both for NDV and MSD. The results of NDV and MSD prevalence were significant at the level of $p \leq 0,05$ for reared animal and free-living. A high variability both in terms of number of NDV seropositive animals and of antibody titres produced was seen in tested game bird farms. All farms investigated resulted seronegative for AI and *Salmonella pullorum*. Cultures from cloacal samples were negative for *Salmonella* spp., too. Only one farm resulted positive for *Mycoplasma gallisepticum* (2,7%). Pheasants in this farm were kept in strict contact with chicken and turkeys which may have acted as asymptomatic carriers of the Mycoplasma. There is no statistical significance between the two Mycoplasmosis prevalence (reared and free-living animal) in fact $p > 0,05$. CONCLUSIONS: Health control, supportive care, strict sanitation and good management practices may prevent outbreaks of disease in order to limit disease spreading. Quarantine, vaccinations and sanitary controls of birds before release are strongly recommended.

PESTIVIRUSES SEROLOGICAL SURVEY IN WILD RUMINANTS IN NORTH-EASTERN ITALY

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INTRODUCTION : Pestiviruses are considered an emerging concern in wild ruminants (Hurtado *et al.*, 2004; Frolich *et al.*, 2005). Aim of the present study is to assess the sero-prevalence for pestiviruses through a cross sectional study in several selected populations of alpine chamois (*Rupicapra rupicapra*), red deer (*Cervus elaphus*) and roe deer (*Capreolus capreolus*) in the Trento province.

MATERIALS & METHODS: A total of 404 blood samples from 230 alpine chamois, 106 red deer and 68 roe deer were collected during the 2002 and 2003 hunting seasons in Trento province. Sera were analysed using a commercial ELISA (Pourquier®) for the detection of antibodies against BVD/MD and BDV. Statistical analysis were performed using WinEpiscope (2.0). The location of each sample was digitized on-screen as point coverages, using a GIS software (ESRI-ArcGis9).

RESULTS: Seroreactors clustered according to geographical distribution and species. Average seroprevalence in chamois was 21% but all the seropositive animals were found in the eastern side of the province. A lower prevalence (1,8%; PR= 16,160; 95% CL: 6,214-42,020) was found in red deer, while all roe deer were negative (maximum possible prevalence 5,59%; 95%CL). In chamois the highest seroprevalence values were recorded in the Fassa district: 71% (PR= 2,776; 95% CL: 1,197-6,438).

CONCLUSIONS: Since seroprevalence is clustered any management action should consider such a space-species distribution. In the study area no mortality consistent with pestivirus infection was observed, according to the findings described in chamois in Spain (Marco and Lavin, 2002). Further research is needed in order to determine the exact aetiology and the epidemiology of pestiviruses in wild ruminants in the study area.

ANTIBIOTIC RESISTANT *E.coli* IN FREE-RANGING ALPINE WILD RUMINANTS

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AIM OF THE STUDY: Antibiotic resistance is a worldwide-recognized problem. No data was available in the study area (Trentino-north eastern Italy) about the presence of environmental antibiotic resistance. Previous surveys on *E.coli* didn't reveal the presence of EPEC but of VTEC in red deer in the same areas (Conedera et al., 2004). The aim of this survey was to obtain preliminary knowledge about antibiotic resistant *E.coli* in wildlife.

MATERIALS & METHODS: *E.coli* strains were obtained from red deer (*Cervus elaphus*), roe deer (*Capreolus capreolus*) and alpine chamois (*Rupicapra rupicapra*) guts collected during the hunting season. A total of 83 samples were detected and used as indicators of antimicrobial resistance in wildlife (30 from roe deer, 28 from red deer and 25 from chamois).

RESULTS: Evidence of antibiotic resistance was found in 16 (19,3%) of the 83 *E.coli* isolates. Resistant isolates were 30% in roe deer, 14,2% in red deer and 12% in alpine chamois. The proportion of resistant *E.coli* strains appeared higher in roe deer than in other ruminants (PR=2,1, 0,8-8,5 95%CL to red deer; PR=2,5, 0,8-7,7 95%CL to chamois). Intermediate resistance resulted in 53,3% of roe deer, 7% of red deer and 32% of chamois isolates. Resistance was found for the following antimicrobials: ampicillin 3 isolates; cefoperazone 3 isolates; cefalexine 3 isolates; gentamicin 3 isolates; colistin sulfate 1 isolate; cefuroxime 1 isolate; linco-spectin 4 isolates; neomycin 2 isolates; nalidixic acid 2 isolates; streptomycin 5 isolates; trimethoprim sulphonomide 1 isolate; tetracycline 4 isolates; flumequine 1 isolate.

Multiresistant isolates were detected: 16% in roe deer, 3,6% in red deer and 8% in chamois.

CONCLUSIONS: These results suggest different arguments of discussion, such as risk of spill-over and spill-back, the possibility of wild reservoirs of resistant strains, the risk of transfer of resistant normal flora or animal pathogens as a source of resistance, and the arise of resistant/multiresistant zoonotic pathogens.

EPIDEMIOLOGY OF EUROPEAN BROWN HARE SYNDROME (EBHS) IN TRENTO (NORTH-EASTERN ITALY)Bregoli M.¹, Nardelli S.², Luchesa L.³, Cova M.¹, Pasolli C.¹¹Istituto Zooprofilattico Sperimentale delle Venezie AT5 Trento ²Istituto Zooprofilattico Sperimentale delle Venezie-Legnaro(PD), ³Associazione Cacciatori Trentinicontact address: as.fauna.at5@izsvenezie.it

AIM OF THE STUDY: This study focuses on the epidemiology of EBHS in selected populations of free living brown hare (*Lepus europaeus*) after an outbreak occurred at the end of 90's.

MATERIALS & METHODS: During 2004-2005 a total of 124 carcasses were necropsied in order to determine the causes of mortality, including the search for EBHSV-antigen from liver and spleen. During the same period a total of 126 sera and further 192 liver and spleen samples were collected from hunted hares for the search of antibodies against EBHSV and for EBHSV-antigen, respectively. The sample, obtained from different densities populations, was structured in terms of gender and age classes and the geographic positions were digitized on-screen as point coverage, using a Geographic Information System software.

RESULTS: While the virus was not detected in both dead or hunted hares in 2004, an increasing number of dead hares was observed in 2005 when the disease re-emerged resulting the main cause of mortality (60%). Nevertheless the impact on hare populations resulted to be different in relation to the study areas. The mortality for EBHS was lower (30%) where the hunting strategies, in consideration of sanitary results, were directed to preserve high population densities. The results of the serological survey showed an endemic condition of EBHSV since 2004: 64% of seroprevalence with low-medium titres and high number of antibody-positive reactors even in young hares (52%). The re-emerging of the disease in 2005 was also evidenced by an increase of the seroprevalence (up to 93%) and of antibody titres and by the presence of 2,5% EBHSV-antigen positive hunted hares.

CONCLUSIONS: EBHSV resulted to be endemic in brown hares under survey, but 2005 presented a peak of mortality. Our results suggest that the deterministic model explaining the natural diffusion of EBHS (Lavazza et al., 1997) could fit in the alpine study area: where hare densities were higher, the virus could circulate stimulating hares immunity, thus reducing the impact of the disease on hare populations.

Sarcoptes scabiei INFECTION IN DIFFERENT HOST POPULATIONS IN TRENITINO (NORTH-EASTERN ITALY)Bregoli M.¹, Rossi L.², Cova M.¹, Rodas Peralta S., Pasolli C.¹¹Istituto Zooprofilattico Sperimentale delle Venezie AT5 Trento ²Università degli Studi Torino

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AIM OF THE STUDY: *Sarcoptes scabiei* is the most important pathogen that can affect population dynamics of alpine chamois (*Rupicapra rupicapra*), alpine ibex (*Capra ibex*) and red fox (*Vulpes vulpes*) (Pence & Ueckermann, 2002). This report focuses on the epidemiology of sarcoptic mange in these species in Trentino (north-eastern Italy).

MATERIALS & METHODS: During the period 2000-2005, 164 chamois, 17 ibex and 1133 red foxes were examined by skin scraping and mites were detected by microscopic observation subsequent to preparation in 10% KOH. Lesions were classified depending on their extension (Pence *et al.*, 1983; Fernandez-Moran *et al.*, 1997). Moreover a seroepidemiological survey was implemented by means of an ELISA test on 1821 lung tissue extracts collected from chamois during six consecutive hunting seasons. Immunoblot analysis was used to confirm ELISA-positive samples. Body condition was evaluated by measuring the kidney fat index (KFI) (Riney *et al.*, 1955). RESULTS: 59 chamois (35%), 14 ibex (82%) and 142 red foxes (12,5%) were affected by sarcoptic mange with different degrees of hyperkeratosis and alopecia. Prevalence (4.9%) and distribution of seropositive chamois suggested a larger spread of scabies than resulted from passive surveillance. Severe extended lesions were the most frequently observed. KFI in scabietic animals resulted significantly lower than in those dead for other causes or hunted as attended, nevertheless no KFI difference resulted in different lesion categories in chamois, suggesting an early loss of condition, while severely affected red foxes had lower KFI values. One case in moufflon (*Ovis musimon*) representing the first case in Italy, and two human cases were detected in non-target species. CONCLUSIONS: Our results indicated host-related epidemiological differences: a slow epidemic progression of scabies in chamois populations with low mortality rates if compared with other reports (Rossi *et al.*, 1995); severe outbreaks in ibex threatening local populations and an enzootic presence in the vulpine population. Further research is needed in order to understand the host-parasite relationship and evolution in the study area.

DOES THE PARASITE COMMUNITY OF CHAMOIS REFLECT CHANGES OF ENVIRONMENT AND INTERACTIONS BETWEEN UNGULATE SPECIES?

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INTRODUCTION: In 1993 high mortality was observed in roe deer in the Paneveggio Natural Park (Trentino North-East Italy). The necropsy evidenced acute abomasitis with unusual high burdens of nematodes. These findings were associated with changes in environment, density of wild ungulate species and in management practice of alpine summer pasture of sheep flocks. These changes lead to different interactions between ungulate species such as chamois evidenced expansion of habitat and overlap with red deer and sheep. We investigated whether the parasite community of chamois was associated with changes in the community of alpine ungulates and presence of sheep flocks.

MATERIALS & METHODS: Since 1993, over 500 abomasas of chamois, roe deer, red deer and sheep were collected and analysed for their parasite content. The parasite community changes of chamois is analysed through Generalised Linear Models in relation to red deer, roe deer, sheep densities and to their abomasal parasite burden.

RESULTS: Along with ungulates density changes, the parasite community of chamois showed changes in its composition with a reduction of the parasites species richness from 10 in 1993 to 8 species in 2005. In particular in the same years, *Haemonchus contortus* a typical nematode of sheep increased from a mean abundance of 4 to 13 worms/individual and *Ostertagia leptospicularis* specific of cervids has increased from a mean abundance of 8 to 55 worms/individual.

CONCLUSIONS: The observed parasite communities variations of chamois suggest the influence of the change in use of habitat of chamois coupled with more frequent interactions with red deer and sheep. These variations highlight the importance of assessment of sanitary interactions between ungulate species, in particular sheep and red deer. This confirms: the importance of managing parasite infections of domestic flock to prevent spill-over to wildlife, and the necessity of an appropriate hunting management.

***Leucozytozoon* AND *Haemoproteus* Sp. IN INJURED OWLS : EFFECT OF HANDLING STRESS ON THEIR CLINICAL IMPORTANCE (PRELIMINARY RESULTS)**

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Haemoproteus and *Leucozytozoon* sp. are hemoparasites frequently found in peripheric blood of owls and birds of prey. Both are transmitted by mosquitos and are, in general, not considered clinically important. However subclinical effects have been demonstrated and the parasites have recently received attention, due to their effect on fitness traits and sexual selection in different avian species. The aim of this study is to analyse the prevalence and intensity of parasitation of owls from different species from central Spain that are admitted injured to rehabilitation centres. The objective is to evaluate whether stress from handling in the infested owls has an influence on intensity and/or prevalence of the infestation and if hence treatment of the condition would be recomendable even in absence of a pathogenic effect of the parasites. Blood smears from peripheral blood from 297 owls from five species (eagle owl, scops owl, little owl and long eared owl) were obtained upon admission, on some animals during treatment, and prior to release. Stained smears were screened for either of the parasites and intensity of parasitation was recorded. The prevalence and intensity of parasitation were then related to the biological and clinical conditions of each bird. Of the owls examined 56% were parasitised, 49% of them by *Leucozytozoon*, and 21% of them by *Haemoproteus* or both. Parasitation corellated positively with the cause of admission, owls with traumatic lesions or electrountion being more likely to have one of the two or both parasites. Permanence at the rehabilitation centre and handling appear no to affect the degree of parasitation, nor its potential clinical effect. Although more analysis are necessary treatment of owls suffering from haemoparasites appears not to be justified.

SEROLOGICAL MONITORING OF BLUETONGUE VIRUS IN WILD RUMINANTS OF THE PESARO-URBINO DISTRICT (ITALY)

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AIM OF THE STUDY: The aim of the study was to evaluate Bluetongue virus circulation in wild ruminants of the Pesaro-Urbino district, in the Central Italian region Marche. In 2003-2005 this district was characterized by a large circulation of the Bluetongue virus in domestic ruminants, due to vaccine serotype 2. Bluetongue virus infects both domestic and wild ruminants, but the relative epidemiological significance of the latter is still not fully clarified. Viral transmission between wild and domestic animals is an important factor to study, in order to carry out an efficient sanitary control plan.

MATERIALS & METHODS: The target population was represented by the whole population of wild ruminants of the Pesaro-Urbino district, which was estimated to be of 17.620 of ungulates among roe deer (*Capreolus capreolus*), fallow deer (*Dama dama*) and deer (*Cervus elaphus*). A random sample of 206 ungulates was selected and, from this, 206 samples of serum were collected and analysed by an ELISA test to detect antibodies against Bluetongue virus. ELISA positive animals were further investigated for the presence of viral nucleic acid by an RT-PCR procedure performed on spleen and liver tissue samples.

RESULTS: Of 206 samples of serum analysed by the ELISA test, antibodies against Bluetongue virus were only detected in one fallow deer (prevalence 0.5% I. C. 95% 0.12 – 1.77). The RT-PCR procedure employed did not detect viral RNA in the tissue samples examined.

CONCLUSIONS: Prevalence of antibodies against Bluetongue virus in the targeted population of wild ruminants was very low, although the high prevalence found in domestic ruminants in the same area and in the same period. PCR analysis did not detect viral nucleic acid in the only serological positive animal. Wild ruminants did not seem to have a role in Bluetongue viral circulation in the Pesaro-Urbino district.

A RETROSPECTIVE STUDY ON ANATOMO-HISTOPATHOLOGICAL FINDINGS OF THE NEBRODI'S FERAL BLACK PIG

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AIM OF THE STUDY: To describe the macroscopical and histological findings reported in slaughtered Nebrodi's feral black pig bred in the Nebrodi natural Park (Sicily).

MATERIALS & METHODS: Between 2003 and 2005 a total of 1350 Nebrodi's feral pigs, aged from 8 months to 4 years were slaughtered. Macroscopical and histological investigations were performed. This presentation summarizes the data obtained during this period.

RESULTS: The most common pathologies were tuberculosis infection, fascioliasis, dicrocoeliosis and gastric lesions. 7.74% of the feral pigs showed tuberculosis lesions in many organs. 32% of the examined livers showed parasitic infestations by *Fasciola hepatica*, *Dicrocoelium dendriticum*, *Echinococcus granulosus* and *Cysticercus tenuicollis*. 41,30% of examined stomachs showed parasitic lesions. Two species of stomach nematodes were found, *Ascarops strongylina* and *Simonsia paradoxa*.

CONCLUSIONS: Numerous pathologies were found in Nebrodi's feral black pig some of them rarely reported in swine. This study reveals that nematodes are important parasites in Nebrodi's feral black pig causing serious gastric pathologies. The AA. describe for the first time the presence of *Simonsia paradoxa* in Nebrodi's feral black pig. The female of *Simonsia paradoxa* is the most frequent of them associated to severe granulomatous lesions, haemorrhages and lymphoid hyperplasia. The feral black pig could be considered an important model to study different pathologies of swine. Surveillance has to be activated to assure the health of the consumer.

DIAGNOSTIC ASPECTS ON TB-LIKE LESIONS IN LYMPH NODES OF WILD BOAR (*Sus scrofa*)

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AIM OF THE STUDY: In wild boar retropharyngeal lymph nodes it's possible to see different lesions that can be confused with tuberculosis. Aim of this study is showing some pathological patterns of these granulomatous or granulomatous-like disorders with the results of related bacteriological and histological exams.

MATERIALS & METHODS: : We have considered 76 wild boars, of different geographical origin, with retropharyngeal lymph node disorders. In order to explain the pathological lesions, we have applied in all cases histological method with Haematoxylin-Eosin staining, *Mycobacterium* spp. research on conventional solid media and Heminested PCR direct on tissue samples to detect *Mycobacterium* tb complex. Only in 6 cases we have applied bacteriological tests with Blood Agar and Mc Conkey Agar.

RESULTS: Mycobacteria detection procedures led to identify 1 *Mycobacterium* spp., 3 *M. microti*, 5 *M. bovis*, while 67 samples were negative.

Histological patterns vary from hyperplastic lymphadenitis, purulent lesions, necrotic aspects, until typical tubercular granuloma with necrosis, calcification and epithelioid flogosis and giant cells.

On 6 lymph nodes, negative for *Mycobacterium* spp., we have observed the characteristic Splendore-Hoeppl phenomenon, in correlation with *Staphylococcus aureus* presence.

CONCLUSIONS: Diagnosis of mycobacteriosis on wild boar is important in order to explain epidemiological features of the disease and especially the interaction between wild swine and livestock. The work points out the difficulty of evaluation of some macroscopic and microscopic lesions and the importance of further exams (bacteriological, PCR) in order to define the etiology of the process.

PATHOLOGICAL LESIONS BY *Corynebacterium Sp.* IN WILD RUMINANTS OF AOSTA VALLEY REGION.

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AIM OF THE STUDY: Wild ruminants can be affected by different species of *Corynebacteria*, most important of these remaining *C. pseudotuberculosis*, cause of caseous lymphadenitis or pseudotuberculosis. These microorganisms give generally a very similar type of lesion (in other words abscesses with grey-green pus) but with a great difference concerning the spread and diffusion in the body. So, with this study we want to describe the patterns of the lesions we have seen in wild ruminants of Aosta Valley region, related to the isolation of *Corynebacterium sp.*

MATERIALS & METHODS: We have considered 17 cases, 16 chamois (*Rupicapra rupicapra*) and 1 steinbock (*Capra ibex*), which showed caseous lesions on different parts of the body. From the pus we have made a classical bacteriological exam with Blood Agar and Mc Conkey Agar. The corynebacteria isolated have been test with API CORYNE (Biomérieux) for the identification of species.

RESULTS: Chamois (*Rupicapra rupicapra*): 11 *C. pseudotuberculosis*, 2 *C. ulcerans*, 2 *C. striatum*, 1 *C. sp.*
Steinbock (*Capra ibex*): 1 *C. pseudotuberculosis*.

The spread of *C. pseudotuberculosis* was very different, from only one cutaneous lymph node affected until severe, generalized process with involvement of various internal organs. *C. ulcerans* and *striatum* have given always severe, generalized forms. The only case of steinbock by *C. pseudotuberculosis* was very serious, with abdominal and thoracic abscess in addition to involvement of various cutaneous lymph nodes.

CONCLUSIONS: Particular attention has to be given to caseous lesions of wild ruminants, in order to discriminate not only from tuberculosis but also from pseudotuberculosis in the cases where there is an involvement of corynebacteria other than *C. pseudotuberculosis*. Especially *C. striatum* (but with less gravity also *C. pseudotuberculosis* and *ulcerans*) is an important zoonotic agent, reported in some cases of endocarditis and broncopneumonia with septicemia in men.

FIRST REPORT OF *Mycobacterium bovis* ON ROE DEER (*Capreolus capreolus*) IN AOSTA VALLEY REGION

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AIM OF THE STUDY: We want to present a case of tuberculosis in roe deer (*Capreolus capreolus*), pointing out anatomo-pathological characteristics with the results of other related exams.

MATERIALS & METHODS: Case report of *M. bovis* infection in a roe deer (*Capreolus capreolus*) hunted in Aosta Valley region. In order to explain the pathological picture, we have applied bacteriological analysis with Blood Agar (BA) and Mc Conkey Agar (McKA), histological method with Haematoxylin-Eosin staining and *Mycobacteria* detection procedures based on bacteriological tests and molecular methods.

RESULTS: At necropsy multiple nodular lesions on pleural costal surface were observed (apart from the thoracic cage, all the other organs have not been examined because thrown away by the hunter).

Bacteriological tests based on BA and McKA inoculation have given negative results, while *Mycobacteria* detection procedures led to identify *M. bovis*.

Histology: tubercular-like granuloma with necrosis, calcification, epithelioid flogosis with giant cells; aspect of osteolysis on costal side of nodules.

CONCLUSIONS: Wild ruminants can be affected from many caseous lesions like tuberculosis, pseudotuberculosis and other suppurative lesions by various *Corynebacteria* (*C. ulcerans* and *C. striatum*). In front of this type of disorders, it's important the application of a complete diagnostic protocol in order to evaluate the correct etiology. This report underlines that roe deer in Aosta Valley could be considered a potential reservoir of *M. bovis*; therefore opportune control strategies according to different animal species have to be applied.

SARCOPTIC MANGE ON NORTH SPAIN WOLVES

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AIM OF THE STUDY: Description of cases of sarcoptic mange in grey wolf (*Canis lupus*)

MATERIALS & METHODS: Three wolves examined in 2006 were included in the present study. All of them originated from the North of Spain area (Burgos). Two one year old males were hunted on february 2006 and the other, a one year old female, was road killed a few months later. Wolves were weighed and examined for alopecic areas by deep skin scrapings. Necropsies were conducted on all animals according to a standard protocol. Skin scrapings were examined under a dissecting microscope to demonstrate the presence of live mites, placed in a Petri dish at 37°C stimulating mites to migrate or treated with 10% KOH solution. Porcions of affected skin were fixed in 10% formol and histopathologically examined.

RESULTS: The three examined wolves showed sarcoptic mange lesions. The percentage of skin damage varied from 15% to 35% in the most affected wolf. Extensive alopecic areas were observed. The skin in the affected area was thickened. The most affected wolf was extremely malnourished (weight 17 kg) while the others were close to the average body condition (22kg). One and three mites were observed on the two male wolves being identified as *Sarcoptes scabiei*. On the female, despite having typical mange lesions, it was not possible to demonstrate the presence of mites

CONCLUSIONS: In Spain endemic and epidemic *Sarcoptes scabiei* infestations are well documented in some species but poorly documented in wolves. The present study may be one of the few reports on the subject in which mites from mangy wolves in Spain were recovered.

MYCOBACTERIOSIS IN WILD BOAR: RESULTS OF 2000-2005 ACTIVITY IN NORTH-WESTERN ITALY

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AIM OF THE STUDY: Tuberculosis is an infectious disease common to mammalian species, including wildlife. This work reports the investigation results about the presence of mycobacteria in wild boars hunted in Piedmont, Liguria and Aosta Valley during 2000-2005.

MATERIALS & METHODS: 1121 samples of submandibular lymph nodes were collected. The whole material has homogenized, decontaminated and inoculated onto three different types of solid media: Lowenstein Jensen, Stonebrink and Lowenstein Jensen w/o glicerine. Solid media were incubated for 10 days to 37°C with 5% CO₂ and then for 80 days to 37°C. Suspected colonies were identified and typed by molecular methods (Multiplex PCR, RD Region analysis, Variable Number Tandem Repeats, Spoligotyping).

RESULTS: 23 strains of *M. bovis*, 75 strains of *M. microti*, 101 strains of *Mycobacterium* spp., 15 of *M. avium* and 6 *M. tb complex* strains with no conclusive identification.

CONCLUSIONS: The highest number of *M. bovis* strains were isolated in Liguria region, while in Piedmont region *M. bovis* report in wild boar is sporadic. This situation could be explained by livestock tb status in some areas of Liguria. In this region usually cattle graze in areas where there is a high density of wild boar population.

So, it could be assumed that wild boar may be infected by *M. bovis* only indirectly by swallowing cow faeces or while digging earth in contact with grass tainted with their urine or sputum. But, wild boar may be infected by other Mycobacteria, e.g. *M. microti*, probably by swallowing infected dead wild animals, like small rodents. In view of their eating of small animals behaviour, they also carry risk of possible infection with various species of mycobacteria other than *M. tb complex*.

IDENTIFICATION OF A RED DEER (*Cervus elaphus*) PAPILLOMAVIRUS BY MOLECULAR METHODSErdélyi K¹, Ursu K¹, Steineck T²¹ Central Veterinary Institute, Tábornok u. 2., H-1149, Budapest, Hungary² Research Institute of Wildlife Ecology, University of Veterinary Medicine Vienna, A-1160 Vienna, Austria
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A one year old, red deer stag shot in Lower Austria in 2004 was diagnosed with purulent meningo-encephalitis. In addition, multiple tumours, some reaching the size of a fist, were found on the skin of the animal. These lesions were classified as fibropapillomas by histological examination. Hyperkeratosis, parakeratosis, akantosis, with occasional foci of inflammation and marked proliferation of fibroblasts and connective tissue could be identified in the lesion.

DNA was extracted from frozen tissue samples and tested in a PCR assay as reported earlier by Erdélyi and Ursu. The PCR amplified a DNA product of approximately 750bp, which was sequenced in length of 728 bps. The multiple alignment of the obtained nucleotide sequence with the matching regions of the known cervid papillomaviruses showed 84.2% identity with Roedeer papillomavirus (PV); 60,2% with Deer PV; 57,3% with Reindeer PV and 57,0% with European elk PV sequences. A protein BLAST search of the GenBank for the partial L2 minor capsid protein of the Red deer papillomavirus sequence showed the following identities: European elk PV, Deer PV and Reindeer PV 51%; Ovine PV 1 and 2: 49%; Bovine PV type 1 and 2: 33%; Canine oral PV: 28%; Human papillomaviruses: less than 28%.

Papillomatous lesions have been described in several deer species and there are three published cervid papilloma virus genomes available. Cutaneous papillomas of red deer have been described from Scotland, and according to our survey sporadic cases were recorded in Southern Austria and in Western Hungary. Our results, supported by the pathological features of the disease imply that we have identified a Red deer papillomavirus, which is phylogenetically closely related to the recently described Roe deer papillomavirus.

NATURAL INFECTION OF IBEX (*Capra ibex*) BY A CAPRINE ARTHRITIS ENCEPHALITIS VIRUS-LIKE.

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AIM OF THE STUDY: Small ruminant lentiviruses : Caprine Arthritis Encephalitis Virus (CAEV) and Visna/Maedi (VMV) cause persistent infections in domestic goats and sheep worldwide. In the context of researches on transmission of pathogenic germs between domestic small ruminants and wild ungulate, the aim of this work was to study lentiviral infection of ibexes (*Capra ibex*) closely interacting with local goat herds in french Alps. **MATERIALS & METHODS:** Blood samples were taken from domestic goats and captured ibex living in cohabitation in three sites in french Alps. Sera were tested for presence of specific antibodies against small ruminant lentiviruses, using a commercially available ELISA based on detection of the recombinant p28-gag protein. Peripheral blood mononuclear cells (PBMC) isolated on Ficoll gradient were cultured in macrophage differentiation medium to obtain monocyte-derived macrophage (MDM) monolayers for virus isolation. DNAs from non cultured PBMC were used as templates for PCR amplification of proviral genome with primer sets chosen in a conserved region of gag gene sequences from published CAEV genomes. PCR products (512 nt) were cloned and sequenced. Sequences were analysed using Clustal software. **RESULTS:** Since 1994, among all tested ibexes from french Alps, four animals (1%) were found positive for CAEV. In Valbonnais, wild ibex closely interact with local goat herds and, in fact, the males interbreed with domestic nannies, producing viable hybrid offspring. Gag PCR(+) was found from PBMC DA of a seropositive male ibex. Furthermore supernatant from seropositive ibex MDM culture induced typical cytopathic effects in goat MDM monolayer and was gag PCR(+). PCR amplification and sequencing of a portion of gag gene of ibex proviruses compared to the sequence of prototypic CAEV-CO strain showed clear differences (8%) but these sequences were closer to CAEV prototype than MVV prototype. Proviral sequences from ibex, hybrids and some goats living in cohabitation with ibex clustered in group which individual sequences differed only by 1-2 %. **CONCLUSIONS:** These findings present for the first time direct evidence of virus isolation and sequence data of natural CAEV-like infection of wild ibex. Epidemiological conditions and phylogenetic analysis suggest a possible transmission of CAEV from domestic goats to ibex.

PARASITOSIS AND FITNESS IN WILD BIRDS: IS A CASE REGARDING SUSCETIBILITY TO COLLISIONS?

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AIM OF THE STUDY: This study aims to describe a clinical case about a parasitological study on a Kestrel *Falco tinnunculus*, brought to the Racconigi Recover Centre for wild birds after traumatism, showed a presence of enteric parasites and, mainly, *Haemoproteus* sp. in the peripheral blood.

MATERIALS & METHODS: A young (1st calendar year) female Kestrel, *Falco tinnunculus*, was brought to the Racconigi Recover Centre after traumatism. We obtained a blood sample, using a drop of blood taken by venipuncture of the brachial vein. Blood smear was made, air dried and fixed in 100% methanol and stained with Dip-Quickly Stain for processing. The bird died after 2 days and so it was processed to anatomopathological analysis.

RESULTS: From blood smear it was possible to identify many erythrocytes with *Haemoproteus* sp. at different stages develop. The infection intensity was very high (3,03%) and we found erythrocytes super-infected.

The anatomopathological analysis showed, in the small intestine, sixteen parasites belonging to the Cestoda.

CONCLUSIONS: Authors think that this blood infection should have been the cause of weakness that, reducing the flight efficiency, could favour the traumatic impact.

PHYLOGENETIC ANALYSIS OF AVIAN POXVIRUS ISOLATES FROM HUNGARIAN AND SPANISH WILD BIRDS

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As the potential impact of avian pox on endangered wild bird species can be substantial, it is essential to clarify the question of diversification, host specificity and pathogenicity of Avian poxviruses.

We have developed a new PCR system for the detection of Avian poxviruses, based on polymerase gene sequences available from GenBank. With this method we have determined nucleotide sequences of 13 Poxvirus isolates originating from Spanish and Hungarian wild bird species, mainly raptors (Booted eagle, Imperial eagle Goshawk, Common buzzard, Red kite, Red-legged partridge, Great bustard, Peacock). A PCR method used for the amplification of a fragment of the 4b core protein gene was adapted from Adams et al. 2005. Two additional sequences were obtained with this method from our samples. Partial polymerase and 4b core protein sequences were subjected to phylogenetic analysis by the Distance Matrix followed by Fitch method (Phylip programme package) together with corresponding gene sequences available from GenBank. Alignments were created using the web based Multalin software.

The analysis of the 4b core protein sequences confirmed the results of Adams et al. defining 5 distinct clades of Avian poxviruses. However, the diversity demonstrated within clade 4. supports the suggestion of Lüschof et al. 2004 dividing this group further into three distinct clades. This distinction was supported by the results of the analysis of polymerase gene sequences. The validity of clade III. defined by Lüschof was independently reinforced by the topology of a branch formed by three raptor derived pox polymerase sequences. A further distinct divergence was detected within clade II. confirmed by the topology of both 4b core and polymerase sequences from the same great bustard and booted eagle viruses. We conclude, that the polymerase gene based approach gives good results both in phylogenetical analysis and the detection of Avian poxviruses by PCR.

SURVEY OF EUROPEAN BROWN HARE SYNDROME (EBHS) IN FRIULI VENEZIA GIULIA (NORT-EASTERN ITALY) - PRELIMINARY REPORT

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The European Brown Hare Syndrome (EBHS) was first described in Italy in 1989 and is now endemic in most of the Regions. In Friuli Venezia Giulia (North-Eastern Italy) the appearance of sporadic yet periodic outbreaks seems to recall the epidemiological deterministic model of the disease based on the equilibrium between the active immunity acquired thanks to free virus circulation in brown hare offspring and the natural density of the population. EBHS outbreaks trigger the Public authority to prohibit hunting for at least one season, but an improved management procedure should be developed relating the likelihood of outbreak appearance to specific antibody levels. A project aimed to monitor the presence of EBHS virus and the natural specific immunity was set up over a wide territory where at least three different managing systems and brown hare density areas are recognizable.

The project is an observational study between the 2005/2006 and incoming 2006/2007 hunting period. During the first hunting season 273 samples were collected. A sandwich ELISA system to detect EBHS virus and a competitive ELISA to detect specific antibodies were used. Preliminary data report that no outbreaks were registered in hunted or found dead hares. The serological results show a variable antibody titre in the population. The development of the situation in the next hunting season will allow us to relate the antibody titres to EBHS protection in order to technically support the decision making process of the hunting management system.

SARCOPTIC MANGE SURVEY IN WILD BOARS FROM LIGURIA (NORTH-WEST ITALY)

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AIM OF THE STUDY: Sarcoptic mange has been rarely reported in wild boars free-ranging populations. Reports usually refer to single cases and surveys at population level have been rarely done. To evaluate the prevalence and diffusion of *Sarcoptes scabiei* in a wild boar population in an area (Imperia Province, Italy), where clinical cases were observed in 2001, a survey was carried out in 2002 and 2003 on wild boars culled during hunting seasons.

MATERIALS & METHODS: the right ear was collected from wild boar hunted in the province of Imperia (North West Italy), 552 during the 2002 hunting season from the whole province and 57 during the 2003 hunting season from the areas where cases were observed in 2002 in order to evaluate if infestation persists in the same area also in absence of clinical cases. The internal part of the ear was scraped with a scalpel blade and detritus were put in a tube and digested over night in 10% NaOH. Tubes were centrifuged and sediment was observed at microscope.

RESULTS: 8 out of 552 (1.5%) ears collected from wild boars in 2002 and 5 out of 57 (8.8%) ears collected in 2003 were positive for the presence of *S. scabiei* mites. Positive wild boars were found in the same area from 2001 to 2003, but a lot of new cases in 2002 and 2003 came from areas where clinical cases have never been reported.

CONCLUSIONS: sarcoptic mange has usually a severe impact on wild mammals population due to its high mortality. Wild boar seems to be a specie resistant to this mite because there is no evidence of an impact of this parasite on population dynamic. Also in our study area reports of mange in wild boars are rare, however our data show that the parasite is diffused in the population from the whole province, and also can persist from one year to the other. It should be very interesting to study wild boar- *S. scabiei* interactions in order to evaluate which are the factors that allow the presence of the mite without clinical signs and why sometimes infestation coincides with disease.

HELMINTHOLOGICAL SURVEY ON WILD BOARS FROM ELBA ISLAND (PARCO NAZIONALE ARCIPELAGO TOSCANO, ITALY)

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AIM OF THE STUDY: The wild boar (*Sus scrofa*) population of the Elba island originates from reintroductions done in the '60 after specie extinction in the XIX sec. Actually the population of the island (23.780 ha) is estimated to be of about 2.500 wild boars. To date no data are available on gastro-intestinal (g-i) helminth in this wild boar population. We deemed it interesting to do a survey in order to evaluate species and abundance of g-i helminths.

MATERIALS & METHODS: g-i tracts were obtained during necropsy from 45 wild boar less than 1 yr old found dead due to road accident, capture accident or other causes. G-i tracts were examined for the presence of helminths according to routinely parasitological methods and collected parasites were classified according to the usual keys.

RESULTS: Five species of helminths have been found : *Globocephalus urosubulatus*, *Physocephalus sexalatus*, *Trichuris suis*, *Ascaris suum* and *Macracanthorhynchus hirudinaceus*. Prevalence was 38%, 11% 53%, 7% and 20% respectively. While intensity was of 12.4, 16.6, 3.9, 1 and 4.4 respectively.

CONCLUSION: While a lot of g-i helminths species, both with direct and indirect cycle, has been maintained in the island, some species usually found in wild boars from Eurasia and North-America such as *Ascaropsis strongylina* and *Oesophagostomum dentatum* have not be found in our samples. This is quite common in reintroduced population and can be done to founder effect or to environmental and climatic condition of the new area. In spite of the high density of wild boars on the island (10.5 head/100 ha) intensity of parasite is low and prevalence of parasite species is in the range reported from other areas. Only *Trichuris suis* prevalence seems to be higher than the one usually reported by other environments.

Neospora caninum: RESULTS OF A SURVEY ON MICROMAMMALS

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AIM OF THE STUDY: The possibility that small mammals act as a potential reservoir of infection has been suggested and recently demonstrated in rats in China and in mice and rats in U.K. Considering that no data are available on the presence of *N. caninum* in small mammals in Italy, we deemed it interesting to evaluate, by PCR, the presence of infection in house mice (*Mus musculus*), wood mice (*Apodemus sylvaticus*), cotton-tail rabbit (*Sylvilagus floridanus*) and rats (*Rattus norvegicus*) in areas with a previous history of *N. caninum* infection.

MATERIALS & METHODS: Forty-nine house mice, 34 rats, 49 wood mice and 40 cotton-tail rabbit were captured with snap traps or shotted (cotton-tail rabbit) in, or near, dairy cattle farms in the province of Turin (North West Italy, 44.5° N; 7.5° E). DNA was extracted from animals brain and tested by PCR using the *N. caninum*-specific primer pair Np6 and Np21. After amplification, 20 µl aliquots from each reaction were analyzed by electrophoresis on 7% polyacrylamide mini gels, in comparison with molecular weight markers (V and VI weight Markers, Roche Diagnostics, Mannheim, Germany). Gels were silver stained and photographed.

RESULTS: None of the brain samples tested was positive at PCR. However our data evidence a 95% CI interval ranging from 0.0 to 12.6% for rats, 0.0 to 9.0% for house and wood mice and 0.0 to 10.9% for cotton-tail rabbit. These data are within the prevalence found in other areas in rats (4.4-5.8%) and mice (0.0-3%)

CONCLUSIONS: Unfortunately no positive micromammals has been found our results are within the range from other authors. Further studies are needed to clarify the epidemiological role of wild rodents in the *N. caninum* cycle in Italy.

SERUM BIOCHEMICAL VALUES OF FREE RANGING RED DEER (*Cervus elaphus*) FROM PARCO DI PANEVEGGIO-PALE DI S. MARTINO (ITALY) CAPTURED BY BOX-TRAP.

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AIM OF THE STUDY: The evaluation of blood parameters of wild animal can provide useful information on health status of the population, possible nutritional deficiency and habitat quality, but reference intervals are required to compare the results obtained. The influence on serum chemical values of capture and handling of animals, environmental or physiological factors such as age, sex etc, should be considered. Most blood chemical values reported in the literature regard captive deer or free ranging deer from outside of Italy. Aim of this work is to define the hematological patterns and the possible seasonal changes in free ranging red deer living on Alps (Trentino). MATERIALS & METHODS: red deer were captured by box-trap baited with vegetables, and with a radio transmitter alerting the capture team as soon as an animal entered the trap. Red deer were chemically sedated (xylazine-ketamine) before blood was collected. Blood sera, obtained by centrifugation, were frozen at -30°C . Haemolytic sera were discarded and 28 non haemolytic samples were analysed for total and fractionated protein, urea, creatinine, cholesterol, triglycerides, CK, calcium, phosphate, sodium, potassium. RESULTS: significant differences were observed for age class, sex and season. Young deers (<1 year) showed higher values of calcium and cholesterol, and lower values of total protein and gamma globulin. Serum creatinine, that is correlated to muscle mass, was higher in male. Red deer in February-April had lower values of serum albumin and sodium, and higher values of serum alpha globulin and creatinine than deer in October-December. CONCLUSIONS: Most serum values were in the ranges previously reported for red deer, but individual variability was higher than in domestic animals. Higher calcium levels in young animals are related to rapid bone increase; low antibody levels may predispose to infectious diseases. Decreased serum albumin, associated to increased creatinine values at the end of winter, suggest poor protein nutrition and muscle protein catabolism. Even if these results must be considered as preliminary, due to small sample size, they confirm that blood serum analysis can be useful to assess metabolic changes and health status of free ranging deer.

SEROLOGICAL SURVEILLANCE FOR SELECTED VIRAL AGENTS IN CAPTIVE AND FREE-RANGING POPULATIONS OF ARABIAN ORYX (*Oryx leucoryx*) FROM SAUDI ARABIA AND THE UNITED ARAB EMIRATES

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ABSTRACT: A total of 294 sera collected between 1999 and 2001 from eight captive and one free-ranging herds of Arabian oryx (*Oryx leucoryx*) distributed in Saudi Arabia (SA) and the United Arab Emirates (UAE) were assayed for antibodies against thirteen selected viral agents. Arabian oryx have been exposed to bluetongue virus (BTV), epizootic hemorrhagic disease virus (EHDV), rinderpest virus (RPV), bovine respiratory syncytial virus (BRSV), bovine adenovirus-3 (BAV-3), cervid herpesvirus-1, foot-and-mouth disease virus, equine herpesvirus-9 and bovine viral diarrhoea virus (BVDV). The high seroprevalence detected against BTV and EHDV in both UAE and SA indicates that Arabian oryx are likely to be susceptible to infection by these viruses and therefore could act as a source of virus to vectors during the infective stage of infection. Moreover, antibodies were detected against RPV and BRSV in sera from SA and against BAV-3 in sera from UAE. No antibodies were found against bovine herpesvirus-1, caprine herpesvirus-1, enzootic bovine leucosis virus, and peste des petits ruminants virus. Based on these results, caution should be applied when considering translocation of Arabian oryx and only those proven to be free of infectious agents that might present a risk to other species should be moved.

HEALTH SCREENING OF SOME WILD FAUNA SPECIES IN CASTELPORZIANO, (THE ITALIAN PRESIDENTIAL ESTATE). CORRELATION OF POSSIBLE ZOOSES (BRUCELLOSIS, TUBERCULOSIS, TRICHINOSIS.) BETWEEN DOMESTIC AND WILD ANIMAL POPULATION I.

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This work shows the results of a screening activity carried out in the years 2005-2006 targeted to assess the presence of zoonotic bacterial and parasite infections among the wild ruminants and wild boar populations of a naturalistic area in the province of Rome this area, about 10,000 ha wide, hosts cattle (291 heads of Maremmana breed), are from brucellosis, tuberculosis and bovine leukemia, along with subpopulations of fallow-deer (N=2043), red deer (N=600) and roe deer (N=600). The following biological samples were collected from 1001 wild boars and 122 fallow-deer during the hunting campaign aimed at reducing the density of the respective subpopulations in the last 12 months: i) cardiac clot and lung extract for the serological diagnosis of brucellosis; ii) lymph nodes from both the respiratory and the intestinal districts and the spleen for the Brucella spp. and Mycobacterium spp. detection and identification; iii) wild boar diaphragmatic tissues for the Trichinella spp. detection and identification. A PCR was then performed on all the organs obtained from the 2 species for the bio-molecular diagnosis of Brucella spp., Mycobacterium spp. and Trichinella spp. All the wild boars and fallow-deer tested by rapid sero-agglutination and by complement fixation on cardiac clot and lung extract were negative for the presence of antibodies against Brucella spp. 20 fallow deer were positive at PCR for Brucella spp. (n=10 B. melitensis, n=3 B. abortus, 3 for B. melitensis and B. abortus) while 19 resulted positive for Mycobacterium spp. (n=13 M. bovis, n=12 M. tuberculosis, 6 for M. bovis and M. tuberculosis). 5 wild boars were PCR positive for B. melitensis and 26 resulted PCR positive for Mycobacterium spp. (n=18 M. bovis, n=21 M. tuberculosis, 13 for M. bovis and M. tuberculosis) and 1 was PCR positive for Trichinella britovi. Confirmatory diagnosis by culture is ongoing on the organs resulted PCR positive for Brucella spp. and Mycobacterium spp. Further investigations in the area are needed to confirm these findings also in order to evaluate the specific risk for both human and animal health that could rise from the specific zoonotic agents detected.

Poster 30

TUBERCULOSIS IN WILD BOAR IN MARCHE REGION, ITALY: CASES REPORT.

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AIM OF THE STUDY: The role of wild boar in the epidemiology of *Mycobacterium bovis* is not yet well-defined. During the years 2002-2005 in the Marche region of Italy, ten mycobacteria isolates from wild boars affected by tuberculosis were characterised as *M. bovis* bcg-like. In the same area an outbreak of bovine tuberculosis (TB) was spreading in a free range herd. The characteristics of the affected wild boars have been subsequently described.

MATERIALS & METHODS: At post-mortem veterinary inspections, lymph nodes of the head (mandibular and retropharyngeal lymph.) and tonsils from hunted wild boar were removed. Specimens from animals aged 2 years and over with no visible lesions (NVL) and viscera from animals of any age with visible lesions (VL), were examined.

The first step of examination was the histological observation; the specimens with TB lesions were subjected to emulsion-PCR procedures and bacteriology.

RESULTS: Ten wild boars had TB: four cases featured acute generalised disease, three exhibited a pulmonary primary complex and three were asymptomatic.

CONCLUSIONS: Certainly lesions shown by the infected animals confirm the dead-end host role of wild boar for TB. However, acute and generalised lesions make possible the *Mycobacteria* spread in the pasture. In this hypothesis wild boar may be a maintenance host and a new policy approach is necessary for TB.

MARBLE SPLEEN DISEASE (MSD) : AN OUTBREAK IN GAME PHEASANTS (*Phasianus colchicus*) ANATOMOPATHOLOGICAL AND HISTOPATHOLOGICAL FINDINGS

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AIM OF THE STUDY: The study is supposed to show and review the characteristics of the Marble Speen Disease (MSD), one of the foremost virosis of pheasants. Anatomico-pathological and histopathological findings are emphasized here in order to make it easier for the practitioners to detect the MSD at farm level.

MATERIALS & METHODS: In march 2004, six events of mortality in wild pheasants with anatomopathological lesions referable to MSD, have been submitted to the laboratory: Optical and Electronical microscopy and Agar Gel Immunodiffusion Test (AGID) confirmed the diagnosis.

RESULTS: each subject turned out to be positive for MSD. Typical lesions have been observed at different stages of the pathology.

CONCLUSIONS: since the spread of the disease in wildlife population is not known the affected subject probably belonged to a single group of animals launched for repopulation proposals. A correct identification and management of the disease at farm level is fundamental to avoid the virus spread in wild animals and consequently in MSD disease-free farms.

THE WILD PATIENT AS A MONITOR OF ENVIRONMENTAL CONDITIONS

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AIM OF THE STUDY: The aim of the study was to evaluate the presence and incidence of the different diseases in wild animals submitted to the Wildlife Rescue Center of Treviso. Trauma, toxicosis, parasitological and bacterial disease are an expression of the environmental conditions and human impact on wild populations. In this work several diseases and their incidence in wild animals submitted to the attention of the authors are described.

MATERIALS & METHODS: In this work 223 casualties (65 raptors, 30 aquatic birds, 163 other birds, 50 mammals and 15 reptiles) are described with their pathologies and their popular impact. This work reports the total patients of the Wildlife Rescue Center of Treviso in the year of 2006, from January to June .

RESULTS: Depending from the season trauma, infectious diseases, parasitic diseases are more present in the casualties examined.

CONCLUSIONS: The wildlife rehabilitations centers in Italy represent monitoring stations for environmental conditions, biological status of wildlife, diseases present in the environment itself. Furthermore the rehabilitation centers ,in Italy are the most important educational place for the common people ,students, technicians were to gain informations on wildlife biology, pathology and potential zoonotic diseases. And at last, the wildlife rehabilitation centers are the main place where to educate the common people in interacting with wildlife

EVALUATION OF SEROLOGICAL DIAGNOSIS TO DETECT *Brucella* INFECTION IN WILD BOAR

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AIM OF THE STUDY: Evaluation of serological test performance to diagnose swine brucellosis in wild boar. MATERIALS & METHODS: Serological methods described by Alton (1967) and optimised by the Italian National Institute of Health was used. Bacteriological isolation was also performed on animal tissues: spleen, testicles or uterus. The whole material was inoculated onto *Brucella* medium developed by Farrell, enriched with 10% horse serum and selective Supplement and incubated at 37°C in an atmosphere containing 5% CO₂ for at least 10 days. Colonies resembling *Brucella* spp. were then identified to species by classical techniques and typed by biochemical and molecular tests. Statistical analysis: Agreement between RBT and CFT has been evaluated using Kappa di Cohen. Also, sensitivity (Se), specificity (Sp), negative (NPV) and positive predictive value (PPV) have been estimated by WinEpiscope v. 2.0. RESULTS: 352 samples (200 serum coming from swine *Brucella*-free; 152 serum coming from wild boars, positive to bacteriological test) have been tested. Negative samples were confirmed both by RBT and by CFT. Positive samples gave different results: 15 of them positive only to RBT, 13 only to CFT and 87 positive to both tests. [Kappa: 0.805 (IC 95%: 0.737-08.874); Sp RBT: 100%, Se RBT: 66.23% (IC 95%: 58.68 – 73.77); Sp CFT: 100%, Se CFT: 67.11% (IC 95%: 59.64 – 74.57); NPV RBT: 79.68 (IC 95%: 74.70 – 84.66), PPV RBT: 100; NPV CFT: 80% (IC 95%: 75.04 – 84.96), PPV CFT: 100]

CONCLUSIONS: Kappa value indicates a good agreement between RBT and CFT. It remains to underline that serological tests have a very good specificity, but there is a lack of sensitivity, so it is not possible identifying correctly all of the really infected animals. To date, none of conventional serological test s has been also shown to be entirely reliable in routine diagnosis in individual wild boars. Their preferred use is for the identification of infected groups of animals. Evaluation of an ELISA commercial kit is still in process, to increase sensitivity of serological diagnosis.

SEPTIC SHOCK IN A FOUR YEARS OLD PERSIAN FALLOW DEER (*Dama mesopotamica*)

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AIM OF THE STUDY: Septicemia is the acute invasion of the systemic circulation by pathogenic bacteria, which may cause sepsis or septic shock with possible localization in various body systems or organs if the animal survives. Many different infectious agents can result in septicemia. The major clinical finding in septicemia are toxemia, fever, and submucosal and subepidermal hemorrhages. Specific signs may occur as the result of localization of the infection in joints, heart valves, meninges, eyes or other organs

MATERIALS & METHODS, A male, four years Persian fallow deer was referred to large animal internal medicine department with a history of depression and recumbency from 2 days ago. The animal kept on very poor quality roughage. RESULTS: In clinical examination, the deer was comatose. Its rectal temperature, heart rate and respiratory rate were 35.8°C, 90/min. and 64/min, respectively. On inspection, the head, under left eye region was swollen and on palpation was gaseous. Paracentesis of this region yielded inflammatory fetid fluid. Hypopyon was seen in left eye. In hemogram, white blood cell was 2600/ μ lit (Neutrophil 31%, band cell 5%, and lymphocyte 64%). CONCLUSIONS: According to clinical finding and hemogram septic shock was diagnosed and the animal treated with ampicillin, gentamicin and dexamethason. Fluid therapy was done, too. Unfortunately, the animal died one day later.

PRELIMINARY REPORTS ON SANITARY CONDITIONS OF WILD ANIMALS HOLD IN THE RECOVERY CENTRE “CRAS DEL PIEMONTE ORIENTALE”: SOME RESULTS ON THE MOST COMMON PATHOLOGIES

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AIM OF THE STUDY: The recovery centre of wild fauna receives animals coming from areas with various sanitary problems and so that they maybe infected with different pathogens, either viruses or bacteria and they can be infectious both for animals or humans beings. On behalf of this topics we undertook preliminary monitoring on the health condition of the wild animals cared in the regional recovery centre of “Piemonte Orientale”, with a particular interest in zoonosis diseases and security for technical and sanitary operators.

MATERIALS & METHODS: We undertook the diagnostic analysis on the animal specimens that could be found death naturally, released or even euthanized. After necroscopy samples were taken for virology, bacteriology, parasitology and histology. In the case of released animals, blood samples were collected, as well as swabs for microbiology and feces for parasitology **RESULTS** The diseases more frequently observed have been those associated with bacteria infections. In particular were isolated *Salmonella* sp. and *Yersinia* sp. in raptors as carriers. Frequently parasites like Coccidia, trematodes, *Capillaria* sp. and *Serratospiculum* sp. in young and adult wild birds. In the sanitary examination infections by Avian Influenza and *Chlamidia* spp., were taken into consideration. The presence of *Trichinella* sp. was investigated in the muscles of raptors and carnivorous mammals.

CONCLUSIONS: The findind of potentially zoonotic bacteria such as *Salmonella* sp. and *Yersinia* sp. in wild raptors arises the question about human health risk. Specifically, the risk associated with contact with sick animals and/or fecal contamination. This not only for the sanitary operators, but also for visitor of the park. However *Chlamidia* spp., Avian Influenza and *Trichinella* sp. were never detected.

ECTOPARASITES OF RAPTORS IN THE PROVINCE OF LUCCA (TUSCANY-ITALY)

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AIM OF THE STUDY: The knowledge of ectoparasitic fauna of raptors found dead and delivered to a rehabilitation centre for wild animals located in Viareggio (Lucca, Italy) represented the main aim of this study.

MATERIALS & METHODS: They were examined 28 deceased animals coming from the province of Lucca (Tuscany-Italy) and belonging to the following different species of raptors: *Accipiter nisus*, *Buteo buteo*, *Falco tinnunculus*, *Pernis apivorus*, *Pandion haliaetus*, *Athene noctua*, *Otus scops* and *Tyto alba*. The skin and the feathers of each animal were macro and microscopically observed. Ectoparasites were isolated, counted, fixed in 80% ethanol, mounted by using Hoyer medium, evaluated microscopically and identified at the species or genus level.

RESULTS: Ectoparasites found were represented by:

Mallophaga (*Degeeriella fulva*, *D. fusca*, *D. rufa*, *Colpocephalum turbinatum*, *C. apivorus*, *Nosopon lucidum*, *N. clayae*, *Laemobothrion tinnunculi*, *Strigiphilus cursitans*), Flies (*Ornithomya avicularia*), Mites (*Kramerella lunulata*, *K. lyra*, *Glaucalgas attenuatus*, *Hieracolicus nisi*, *Hieracolicus* sp., *Neotrombicula autumnalis*) and Ticks (*Haemaphysalis punctata*).

CONCLUSIONS: In the case of feather mites and mallophaga most of the examined animals presented heavy infestation levels; however, no macroscopic lesions were found both in the skin and in the feathers of these infected animals. The isolation of *Hieracolicus* sp. from *Pandion haliaetus* and *Neotrombicula autumnalis* from *Falco tinnunculus* represent the first record in these two raptor species.

ENDOPARASITES, BACTERIA AND HISTOPATHOLOGICAL LESIONS FOUND IN RAPTORS IN THE REHABILITATION CENTRE FOR WILD ANIMALS “LA CIVETTA” (VIAREGGIO, ITALY)

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AIM OF THE STUDY: The knowledge of endoparasites of birds of prey and owls found dead or sheltered in the rehabilitation centre for wild animals “La Civetta” (Viareggio, Lucca, Italy) represented the main aim of this study.

MATERIALS & METHODS: We examined 40 animals coming mainly from the province of Lucca and belonging to ten different species of raptors: *Accipiter nisus* (n= 3), *Buteo buteo* (n= 5), *Falco tinnunculus* (n= 5), *Pernis apivorus* (n= 2), *Pandion haliaetus* (n= 1), *Athene noctua* (n= 15), *Asio otus* (n= 1), *Otus scops* (n= 2), *Strix aluco* (n= 4) and *Tyto alba* (n= 2). All animals were examined for the occurrence of endoparasites and, in deceased animals, bacteriological analyses and histopathological examinations were also performed in order to assess the localization of parasites and the type and severity of lesions found.

RESULTS: Isolated endoparasites comprise Protozoa (*Sarcocystis/Frenkelia* sp.), Trematodes (*Neodiplostomum pseudoattenuatum*, *N. attenuatum*, *Neodiplostomum* sp.), Cestodes (*Hymenolepis* sp., *Raillietina* sp.), Nematodes (*Porrocaecum* sp., *Capillaria falconis*, *C. strigis*, *Capillaria* sp., *Procyrnea mansioni*, *P. leptoptera*, *Procyrnea* sp., *Physaloptera alata*, *P. apivori*, *Diplotrriaena falconis*, *Spirocerca lupi*, *Synhimantus* sp.) and Acantocephala (*Centrorhynchus aluconis*, *Centrorhynchus* sp., *Prosthorhynchus cylindraceus*). *Salmonella typhimurium*, *Salmonella enterica* sub. *diarizonae*, *Clostridium perfringens*, *Yersinia enterocolitica*, *Pasteurella multocida* and *Escherichia coli* represented bacterial species isolated in this study.

CONCLUSIONS: Most of the examined animals were infected by several parasitic species. Histopathological examinations revealed that, in many cases, both endoparasites and bacteria caused lesions found in infected tissues of deceased animals.

M. bovis INFECTION IN WILD BOAR AND CATTLE: AN OVERVIEW IN NORTH-WESTERN ITALY DURING THE YEARS 2000-2005

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AIM OF THE STUDY: Tb infection in wild animals is not easily controllable and it raises problems of public health, wildlife management and it also may interfere with eradication program. The purpose of this work is to focus on homology and relations among *M. bovis* strains isolated in wild boars during the 2000-2005 Wildlife Surveillance Plan and those ones isolated in cattle in the same areas.

MATERIALS & METHODS: 23 strains of *M. bovis* were isolated in wild boars from 2000 to 2005, by mean of bacteriological methods and then they were identified and typed using molecular methods (Multiplex PCR, Spoligotyping, Variable Number Tandem Repeat). Spoligotype and VNTR profile of these strains were subsequently compared to 79 *M. bovis* strains isolated in cattle from the same areas during the considered period. GIS program was applied to establish correlation to geographical areas of bovine and wild boar homologous strains.

RESULTS and CONCLUSIONS: A low prevalence (2,1%) of *M. bovis* infection in wild boars was observed. Through a spatial analysis, in some cases we have observed homology between bovine and wild boar molecular profile: particularly in some areas of the province of Imperia (Liguria Region). It's well-known that in areas where there is close contact between feral and farm animals, programs aimed to bovine Tb eradication often fail, due to the occurrence of sporadic outbreaks. In this context, it would be suggested for wild boars a role as bio-marker of Tb infection in cattle.

In other cases, the lack of homology between wild boars and bovines strains led to suppose different sources of infection in the two animal species.

ANATOMO-PATHOLOGICAL FINDINGS IN WILD BIRDS

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AIM OF THE STUDY: Due to High Pathogenic Avian Influenza (HPAI) emergency and according to Decision 2006/101/CE, Istituto Zooprofilattico of Piemonte, Liguria and Valle d'Aosta (IZS PLV) Laboratories have to analyze numerous wild birds to establish cause of death. At the same time, it was possible drawing up a report about likely most common causes of death in wild birds.

MATERIALS & METHODS: From February to June 2006, 486 animals were collected by Local Veterinary Services (A.S.L.) and analyzed by IZS PLV. They came from several zones of Piedmont, Liguria and Valle d'Aosta. Carcasses were submitted to necropsy and, conveniently, to bacteriological and virological test to establish etiological agent.

RESULTS: Results have been splitted in different categories, basing on observed lesions: "bacterial agent", "micotic agent", "trauma", "toxicants", "metabolic disease", "tumors" and in case of any etiological diagnosis, they have been located in "different causes", "no visible lesions" and "n.d."

In "n.d." Group there are rotten or plundered carcasses. In "no visible lesions" Group there are animals without macroscopical lesions.

In "different causes" Group there are animals with several type of lesion: emaciation, enteritis, sign of respiratory disease, hepatic and renal lesions.

One case of Fowl cholera, 2 cases of Chronic Respiratory Disease, one case of Salmonellosis caused by *S. Typhimurium*, a case of Avian Tuberculosis, 4 cases of Coligranulomatosis and 4 cases of Aspergillosis have been identified. Anatomico-pathological findings have also revealed the presence of 8 cases of uricosis, 6 cases of tumors and 19 cases of intoxication.

CONCLUSIONS: Any positivity versus viral diseases have not been detected. Except sporadic events, rate of death animals was low. Traumatic event is the most important cause of death in examined wild birds. Wild birds can be reservoir of notifiable disease of domestic ones.

EPIDEMIOLOGICAL STUDY OF BRUCELLA INFECTION IN WILD BOAR IN LA MANDRIA PARK (ITALY)

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AIM OF THE STUDY: Due to the numerous wild boar population in Piedmont, since 1999 a monitoring programme was implemented to check their health status. Particularly, considering the results at our disposal about *Brucella* infection monitoring, it was interesting discovering the situation in a small and bordered area, "La Mandria" Park.

MATERIALS & METHODS: Sampling was carried out from 2001 to 2005. During the first year, sera without corresponding organs samples were collected mainly for serological screening on the wild boar population. From the year 2002 systematic sampling of serum and spleen in every culled wild boar has been carried out. Serology and Bacteriology – We used a technique described by Alton (3). Statistical analysis – EpiInfo v. 6.0 was used to evaluate association among serological/bacteriological positivity, gender and age groups. WinEpiscope v. 2.0 was used to estimate the prevalence of infection.

RESULTS: Serological investigation during the years 2001-2005 has showed difference in prevalence are statistically significant and a constant trend in following years, ($\chi^2_{trend}=20.4$ p=0.00001). Prevalence based on bacteriological test (years 2002-2005) is statistically significant: there is a relevant decrease of pathogen isolation during 2005 but there is no a statistically significant trend. During the year 2002-2003, the bacteriological and serological prevalence of infection are included between 9.24% and 35.44%, 11.05% and 38.24% (2004), 4.78% and 23.50% (2005).

CONCLUSIONS: Results suggest infection is appeared before 2001. The positive observed trend can be linked to reaching of the sexual maturity of the infected subjects born after 2001. The obtained prevalence confirm *Brucella* infection is endemic in this area: trend is constant during the years 2002, 2003 and 2004 and decreases in 2005.

STUDY ON THE CARRIER STATE OF *Pasteurella multocida* IN BUFFALO IN AHVAZ, IRANHaji Hajikolaie, M.R.¹; Ghorbanpoor, M.²; Seifi, M.R.²; Rasouli, A.¹; Jafari, H.³

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Haemorrhagic septicemia (HS) is an acute, septicaemic highly fatal diseases in cattle and buffalo which caused by *Pasteurella multocida*. The presence of carrier animals in HS well established. Such animals are clinically normal but the causative organism can be isolated from the nasopharynx. In order to investigate the prevalence of *Pasteurella multocida* infection this study was carried out on 247 buffaloes slaughtered at Ahvaz abattoir. Immediately after the slaughter, samples were taken from the pharyngeal and nasal regions by swab for culture. Samples were cultured in blood agar and incubated for 24-48 hours at 37° C. Suspected colonies were identified biochemical methods. Ten ml blood samples from the jugular vein for serological survey were taken. Sera samples were examined by IHA test to detect the antibody titer against *Pasteurella multocida*. Out of the 247 buffaloes studied 10(4.05%) were infected and *Pasteurella multocida* were isolated from pharyngeal and nasal regions in 9 and 1 case, respectively. In the serological study 67(37.12%) buffaloes were positive and had titers between 1:16 to 1:256. statistical analysis showed that there were no significant relation between carrier state and age or sex, but serological result showed that there were significant differences between age and sax groups.

FATAL *Babesia divergens* INFECTION IN FREE-RANGING CHAMOIS (*Rupicapra r. rupicapra*) IN SWITZERLANDS. Hoby¹, N. Robert¹, M. Meli², A. Mathis³, P. Deplazes³, H. Lutz², N. Schmid³, and M.-P. Ryser¹¹Centre for Fish and Wildlife Health, Institute of Pathology, Vetsuisse Faculty, University of Berne, Switzerland; stefan.hoby@itpa.unibe.ch²Clinical Laboratory, Vetsuisse Faculty, University of Zurich, Switzerland³Institute of Parasitology, Vetsuisse Faculty, University of Zurich, Switzerland

AIM OF THE STUDY: *Babesia divergens*, a piroplasm transmitted by the tick *Ixodes ricinus*, is the causal agent of a widespread cattle disease in Europe and of a rare zoonosis. With the exception of a fatal outbreak of *B. divergens* infection in a farmed reindeer (*Rangifer t. tarandus*) herd in Scotland, no fatal disease due to this parasite has been reported in other wild ungulates. In this study, we describe recent cases of fatal infection due to a piroplasm compatible with *B. divergens* in free-ranging chamois (*Rupicapra r. rupicapra*).

MATERIALS & METHODS: In spring 2005, an increased mortality of unknown origin occurred in a small chamois population in the Tösstock region (eastern Swiss Alps). Two females (6- and 8-yrs-old) were submitted to the Centre for Fish and Wildlife Health in Berne for detailed pathological investigation.

RESULTS: The predominant gross lesions consisted of jaundiced serosal membranes, pale mucous membranes and musculature, swollen spleen with soft and dark red parenchyma, and haematuria. On Giemsa stained blood smears, 1 to rarely 3, basophilic, round to piriform, peripherally located inclusions of approx. 1 µm were present in the erythrocytes. Histopathological examination revealed distinctive features of haemosiderosis in the spleen and acute, centrilobular hepatic necrosis. In both cases, *B. divergens* was identified by PCR and sequencing of part of the 18S rRNA gene. Similar pathological lesions were observed in another 6-yr-old female chamois from the same region as well as a 4-yr-old female chamois from the Bernese Oberland found dead in spring 2006. Intra-erythrocytic inclusions were also present, and PCR investigations are pending.

CONCLUSIONS: To our knowledge, this is the first report of fatal *B. divergens* infection in chamois. In order to elucidate the possible role of reservoir for *B. divergens* played by cattle and free-ranging roe deer (*Capreolus capreolus*), and to assess the susceptibility of chamois to develop the disease, blood samples and ticks are collected from cattle and free-ranging ungulates in the Tösstock region.

ILLEGAL USE OF POISONED BAIT IN CENTRAL SPAIN: EVALUATION OF THE IMPACT ON ENDANGERED BIRDS OF PREY

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The illegal use of poison in Spain is closely linked to small game hunting and lately also to the extensive raising of small livestock. The region of Castilla-La Mancha in central Spain is one of those with most cases recorded, largely because efforts for law enforcement through screening in the field are in place longest and are carried out more intensively. Aimed mostly at foxes and corvids, the bait causes frequently the death of carrion eating birds of prey, such as the endangered Spanish Imperial Eagle (*Aquila adalberti*) or the Black vulture (*Aegypius monachus*). The impact from this practice appears to be important, but is difficult to quantify. In this study we analyse data from forensic analysis of 505 cases of suspected poisonings, carried out between 1996 and 2005. The most important periods for baiting are early spring, prior to the hatching of red legged partridge (*Alectoris rufa*) chicks, and september, prior to the release of captive bred partridges. Both periods coincide with either increased foraging of adults in the breeding period, or the dispersal of unexperienced juveniles in birds of prey. The most frequently used poisons are legally available acetylcholinesterase inhibiting pesticides from the Carbamate and Organophosphate families. In the Imperial eagle significantly more juvenile than adult birds were encountered poisoned. In contrast in the Black vulture and the black kite (*Milvus migrans*) significantly more of the poisoned individuals were adults. Also, in the black kite, among the affected birds were significantly more males than females.

GANGRENOUS CELLULITIS IN THE FEET OF MALE HEDGEHOGS

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Hedgehogs (*Erinaceus europaeus*) commonly inhabit urban areas. In Finland, hedgehogs are active during the warm season from late April to September and spend the winter hibernating. Breeding season starts in early May and lasts about three weeks. During mating ceremonies males fight over females by biting and pushing each other. Also, the female pushes the male with her spines and may even bite the male.

In late May and early June 2005, weak or dead hedgehogs with severely swollen paws started to emerge in the town of Joensuu (63°N 29°E) where a radio telemetric study of urban hedgehog ecology was under way. Nine of these hedgehogs were submitted to the Finnish Food Safety Authority for a post mortem investigation.

All examined hedgehogs were adult male individuals with active genitalia. Body condition varied from normal to poor, but none of the hedgehogs was emaciated. The main pathological finding was severe deep gangrenous cellulitis and myositis in the affected limbs. Typically, the front feet were affected most severely but four individuals had lesions in the back feet as well. Some hedgehogs had infected wounds in the skin of their limbs. Purulent arthritis (4 cases) and necrotic pneumonia (3 cases) were also found. Bacterial cultures of affected tissues revealed rich mixed infections with i.a. *Corynebacterium ulcerans*, β -hemolytic streptococci, *Pasteurella multocida*, *Staphylococcus intermedius* and *Fusobacterium necrophorum*.

The cause of the infections were most probably stab and bite wounds gained in mating efforts and fights since only male individuals were affected and all cases were observed only during a restricted period (from May 25th to June 10th) soon after the breeding season. Also, bacterial cultures of tissues yielded mixed flora consistent with bite and scratch infections. Interestingly, similar severe infections have not been observed during the radio telemetric study in Joensuu in 2004 and 2006. In May 2005, it rained 40% more than the previous year and the latter part of the month was warmer. The moisture and warmth may have promoted the development of bacterial infections.

BLACKBIRDS (*Turdus merula*) ATYPICAL MORTALITY DURING A BIRD RINGING CAMPAIGN

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AIM OF THE STUDY: Several avian species were sampled by capture in the area of Palermo (northwest Sicily) with a view to estimate density and population trends.

MATERIALS & METHODS: For capturing and ringing purposes, a mist-nest station was set in the countryside surrounding the suburbs of Palermo, an area characterized by a mediterranean climate with hot and dry summers and short temperate winters. One trapping session performed during the last week of May led to the capture and release of different wild birds subjects (collared doves, sardinian warblers, spanish sparrows, tree sparrows, blackbirds, greenfinches).

RESULTS: Three blackbird (*Turdus merula*) male subjects died immediately after capture, showing blood loss from the mouth and nose but no signs of muscle contractions whatsoever. Gross necropsy examination revealed that the birds death was related to both aortic or atrial rupture.

DISCUSSION: Dissecting aneurysm is a natural occurring pathology of intensively bred and rapidly growing birds. In turkeys, the disease is related to nutritional overload and mineral deficiencies and affects mainly male subjects with a genetic susceptibility background. A peculiar hormonal pattern and a high nutritional level (high protein and lipid intake) due to increased preying and parental care during the reproduction season could be considered as predisposing factors for the syndrome in the case reported here. These concurrent factors together with a high temperature (34° C) and high humidity level (51%) recorded during the trapping session could have induced a stress overload against which the physiological response of the affected birds was ineffective. Obtained gross pathological evidences suggest that in specific environmental conditions, capture could be regarded as a high stressful situation responsible of major vascular damage in blackbirds. For this reason trapping should only be carried out when climatic condition are favourable and set within the birds physiological tolerance limits.

DETECTION OF *Francisella tularensis* IN THE EUROPEAN HARE BY NESTED PCR

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Tularemia in lagomorphs (brown hare [*Lepus europaeus*] and European wild rabbit [*Oryctolagus cuniculus*]), particularly due to *Francisella tularensis* subsp. *holarctica*, is historically enzootic in Europe. In France, surveillance of tularemia is carried out almost exclusively on lagomorphs found dead or dying within the National Surveillance Network of Game Death Causes (SAGIR).

Bacterium sensitivity to temperature variations, as well as frequent putrefaction of the dead bodies, hamper diagnosis of tularemia in lagomorphs' tissue samples. A PCR assay, with primers targeting the 17-kDa lipoprotein gene has been developed in our laboratory, in which it is used as a complementary test for isolates' identification. In this study, conventional bacteriology and PCR were compared for their ability to detect *F. tularensis* on 337 lagomorphs' tissue samples (spleen or liver) collected from 2003 to 2005. DNA extraction was carried out using a commercial kit. Analytical specificity was confirmed on other 38 bacterial strains frequently isolated from wild animals, particularly from hares.

Our results show that nested-PCR is significantly more sensitive than conventional culture (positive samples: 22.13% vs. 8.41%). Single-PCR detected almost all culture-positive samples but only 84% of the nested-PCR positive samples. However, all culture-positive samples were detected by nested-PCR, while 13.72% of the samples were detected by nested-PCR only, especially on samples putrefied or stored for long periods of time. Sensitivity, fastness, simplicity and reliability of this PCR assay make it a useful tool for tularemia routine diagnosis, more appropriate than conventional bacteriology for an adequate surveillance of tularemia in wildlife.

AVIAN FLU MONITORING IN WILD BIRDS IN THE PIEDMONT, LIGURIA AND AOSTA VALLEY REGIONS

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AIM OF THE STUDY: creation of a pilot monitoring plan on wild bird populations by captures planning and collection of biological samples for isolation of the etiologic agent. The aim of this research is: 1) contribution to the knowledge of the potential risk factors originated from wild birds for the protection of human and other animals health; 2) creation of a permanent surveillance process on wild bird with the purpose to activate an alarm system in case of introduction of high pathogenic inter-species transmission strains.**MATERIALS & METHODS:** Identification of the influenzavirus (LPAI-HPAI) has been executed from suspensions in antibiotic solution of cloacal swabs (or faeces) or pooled samples of organs taken from dead wild birds.**1)Haemoagglutination inhibition (HI) test** for the detection of Avian Influenza antibodies H5 and H7 subtype. HI titres may be regarded as being positive if there is inhibition at a serum dilution of 1/16. **2) Isolation on Specific Pathogen Free (S.P.F.) embryonated fowl eggs** reported in OIE Manual.**3) Biomolecular technique:** direct RNA detection (RT-PCR type A and gel electrophoresis) primers from highly conserved region of the matrix gene M. (with the support of the National Reference Laboratory of I.Z.S. Ve).**RESULTS:** From 22-09-05 to 23-06-06 have been examined 779 wild birds samples (638 Piedmont, 127 Liguria and 14 Aosta Valley). They result all negative for Avian Influenza virus and therefore for subtype H5N1 too. Samples belonging to the Anseriformes order are the most numerous. It's important to remember that the species of this order are considered to be the most susceptible to infection with influenza virus H5N1.**CONCLUSIONS:** The surveillance of the Avian Influenza in the wild bird populations needs efficient standard control measures. HPAI viruses are able to survive also for long periods in the environment especially at low temperatures. Without efficient control of the disease it could spread generating an epidemic. Nowa days diagnostic systems are able to identify new influenza viruses introductions (LPAI and HPAI) with pandemic importance for human.

BACTERIOLOGICAL INVESTIGATION ON TWO SICILIAN COLUBRIS (*Elaphe situla* and *Elaphe quatuorlineata*)

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AIM OF THE STUDY: In present work are discussed results of bacteriological analysis performed on tissue samples taken from two snakes during necroscopic procedures. Classic microbiological methods with enrichment broth and solid selective medium was used for the bacterial determination.

MATERIALS & METHODS: The bacteriological research was effected directly sowing lung, myocardium, liver and kidney on plates of blood agar and incubating them to 37° C per 24h, both in aerobiosis and anaerobiosis. conditions. For enterobacteria's search we analysed faeces, liver and intestine with the following pre-enrichment broth: Peptone Buffered Water (APT) and the enrichment Rappaport Vasiliadis broth (RV) and the Selenite Cysteina broth(SC). The final step was the seeding on the following selective solid agar: XLT4 and BGA . For the search of Brucella spp., we analysed gonads using Brucella broth and subsequently sowing in agar brucella. The search of the Campylobacter was effected from the intestine and from faeces in the first snake and from the liver in the second, using the enrichment Preston broth in microaerobic conditions and subsequently sewing in their selective agar: Karmali and Butzler. For the search of Yersinia spp. we proceeds from intestine and faeces, incubating on ITC broth and subsequently sowing on SSDC selective agar.

RESULTS: From *Elaphe situla* was isolated *Providencia stuardii* from the intestine and *Morganella morganii* from the myocardium. The search of *Salmonella*, *Campylobacter*, *Brucella* and *Yersinia* gave negative result. From *Elaphe quatuorlineata* has been isolated *Listeria ivanovii* from the brain and *Providencia stuardii* from the intestine. Also in this case the search of *Salmonella*, *Campylobacter*, *Brucella* and *Yersinia* gave negative result.

CONCLUSIONS: We can proves also for wild reptiles, the role of reservoirs of many bacterial species and their potential capacity of spread such bacterial agents, sometimes pathogen, in urban environment, cause their presence, as we saw, in gardens and rural residences.

ENVIRONMENTAL MYCOBACTERIA INFECTION IN BUZZARD (*Buteo buteo*)

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AIM OF THE STUDY: the aim of the present job is to describe the liver lesions found in an anatomopathological examination performed on a sample of Buzzard (*Buteo buteo*), dead for natural causes and hospitalized in the Sicilian Wildlife Fund of Catania.

MATERIALS & METHODS: At the anatomopathological examination, well circumscribed, smooth, nodular masses (0,2 cm in diameter) was found protruding from the hepatic surface of the bird. The cut surface revealed many firm, whitish, subserosal nodules. The adjacent hepatic parenchyma appeared normal. Tissue samples from the lesions were fixed in 10% neutral buffered formalin and embedded in paraffin wax. Sections (4 µm) were stained with haematoxylin and eosin (HE) for histopathological examination.

Other portions of organ were analysed through PCR to typify possible Mycobacterium infection

RESULTS: The histopathological examination has allowed to underline typical tubercular lesions characterized by necrotic area surrounded by lymphocytes and epithelioid cells. The PCR has also found, in the centres of the liver lesions, the presence of genetic material not belonging to tubercular, environmental Mycobacteria (MOTT).

CONCLUSIONS: The results of this work let to reflect on the importance of the environmental MOTT and on the opportunity to deepen the actual knowledges and the meaning that these agents can assume what important pathogens.

PRELIMINARY REPORT ON A SEROLOGICAL SURVEY OF TICK-BORNE ENCEPHALITIS VIRUS (TBEV) IN WILD RUMINANTS OF FRIULI VENEZIA GIULIA (NORTH EASTEN ITALY)

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In the Friuli Venezia Giulia Region (North –Eastern Italy) the first human case of encephalitis caused by tick bite was described in 2003; since then 19 persons were found infected by *Tick-borne encephalitis virus* (TBEV).The spreading of infection has prompted the Public Regional Health Service to program the vaccination of people living and working in areas at risk of infection. At present the geographical areas of infectious risk of the Friuli Venezia Giulia Region are defined on the basis of serological surveys of TBEV in humans but an animal alert system should be set for early mapping and updating. The purpose of the present communication is to describe the preliminary results of a serological monitoring of TBEV infection in wild ruminants (red deer, roe deer and chamois) from three out of the four provinces of our Region. Blood samples were collected from hunted animals soon after shooting. The sample size was defined taking into account the natural estimated population of ruminants and the presence of geographical barriers. A commercial competitive ELISA was used to detect antibodies against TBEV and positive or doubtful sera were confirmed by hemagglutination inhibition (HI) test. Results of 257 sera showed a 6.5% seroprevalence. Three areas with a seroprevalence ranging between 13% and 15% in wild animals were recognized and prevalence was comparable to 11.7% detected in serological surveys of TBEV in humans living in the same areas.

SURVEILLANCE OF TSE IN WILD RUMINANTS IN NORTH-WESTERN ITALY.

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Chronic Wasting Disease (CWD) is a Transmissible Spongiform Encephalopathy (TSE) which has been identified in captive and free-ranging cervids more than 20 years ago in North America, where is currently in epidemic phase. The evidence of the circulation of TSEs in European population of wildlife ungulates does not exist, but the high prevalence of scrapie infection in Italy and the synchronous/alternate use of common grazing areas by domestic and wild ruminants may suggest the possibility of the spread to the latter. Furthermore, due to the strong similarities between CWD and scrapie, i.e. horizontal transmission, clinical signs and lesions, scrapie has been proposed as possible origin of CWD. Starting no later than autumn 2006, each Member State shall carry out a survey to detect the presence of CWD in the cervid population.

AIM OF THIS STUDY is the definition of the maximum prevalence of TSE infection in roe deer (*Capreolus capreolus*), chamois (*Rupicapra rupicapra*), red deer (*Cervus elaphus elaphus*) culled or found dead in North-Western Italy.

MATERIALS & METHODS: brain stem or spleen from animals (older than 1 year) of the above mentioned species are collected and submitted to a USDA approved CWD rapid test (Idexx Herdchek CWD Antigen Kit) and one scrapie rapid test approved according to 260/2006 EC Regulation (Bio-rad TeSeE). Data such as species, sex, age, origin, *causa mortis* are collected in an *ad hoc* database. In case of positivity to one rapid test, the sample is submitted to confirmatory tests (immunohistochemistry and western blotting).

RESULTS: preliminary results on 100 samples don't support the presence of TSE.

CONCLUSIONS: collection of a much wider sample will allow to verify the endemic presence of TSE among free-ranging ruminants in our study area or, alternatively (in the case of negative results), to define the expected maximum prevalence of TSE in the studied population.

MORTALITY EPISODE RELATED TO BUTIROPHENONES USE IN DRIVE-NET CAPTURED UNGULATES

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AIM OF THE STUDY:

These mortality episodes occurred while we were carrying out a study to assess effectiveness of butirophenones haloperidol and azaperone to control capture stress in drive-net captured wild ungulates.

MATERIALS & METHODS:

The capture of the animals was performed by means of drive-nets and a line of beaters who drove the animals towards the nets. Once the animals fell trapped in the net, another group of people hidden beside the net ran to physically control the animals as soon as possible. Animals were immediately blindfolded, unwrapped, their legs restrained and finally introduced in a transport sack net. A blood sample (T0) was obtained and then the tranquilizer treatment was administered. In normal conditions, animals were fitted with heart rate and temperature recording devices and were monitored during 3 hours. Blood samples at 1, 2 and 3 hours were obtained and finally the animals were released at the same place where they had been captured.

RESULTS:

Twelve Pyrenean chamois out of the 39 captured resulted died in a hyperacute way (time \leq 5 min). Eight of them had been treated with azaperone, 3 with haloperidol and 1 received no treatment.

CONCLUSIONS:

After checking-up and discarding several hypothesis such as voluntary or involuntary overdose, prepathological condition of the animals or a capture additive stress effect to chronic environmental, nutritional or pathological stress, we concluded that most of the deaths can have been caused by an adverse reaction to azaperone.

ECTOPARASITES OF WILD AND DOMESTIC CARNIVORE MAMMALS IN IBERIAN LYNX DISTRIBUTION AREAS IN SPAIN

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AIM OF THE STUDY: Ectoparasites can cause important skin disorders in animals, such as sarcoptic mange, and can act as vector of relevant pathogens, such as *Rickettsia* spp., *Ehrlichia* spp., *Borrelia burgdorferi* or *Cytauxzoon felis*. The Iberian lynx (*Lynx pardinus*) is the most endangered felid in the world and such diseases could be a threat for its survival. The aim of this study, included into the "Iberian lynx sanitary survey" (Consejería de Medio Ambiente, Junta de Andalucía), was to survey wild and domestic carnivore mammals for ectoparasites from the areas where the lynx is still present.

MATERIAL AND METHODS: We surveyed 115 wild (44 Iberian lynxes (23 free-ranging, 21 captive), 34 red foxes *Vulpes vulpes*, 24 mongooses *Herpestes ichneumon*, 11 genets *Genetta genetta*, 1 badger *Meles meles*, 1 polecat *Mustela putorius*) and 66 domestic (43 cats *Felis catus* and 23 dogs *Canis familiaris*) carnivore mammals from June 2004 to June 2006 in Sierra Morena (Northern Andalucía) and Doñana (Southern Andalucía), in Spain. Animals were surveyed dead (mostly road-killed or hunted) or alive. Live animals were anaesthetized before sampling with the exception of dogs. Thus, dogs were not systematically surveyed for fleas or lice. Cats were feral or owned but free-ranging. Dogs were hunting or keeper dogs. Lynxes were considered captives when they were in captivity for at least one month. Eleven lynxes were surveyed two (n=9) or three (n=2) times. No statistical differences were found depending on the status (dead or alive) of the sampled animal. Thus, results are presented pooled.

PATHOGENS AND POLLUTANTS IN WILD AND DOMESTIC CARNIVORE MAMMALS IN THE IBERIAN LYNX DISTRIBUTION AREAS IN SPAIN

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AIM OF THE STUDY: Endangered populations are highly sensitive to diseases due to their low genetic diversity. Other more abundant wild or domestic species that share habitat with them can act as reservoir of diseases that could lead to epizooties. This is one of the causes that can lead an endangered species to extinction. The Iberian lynx (*Lynx pardinus*) is the most endangered felid in the world and diseases could be a threat for its survival. The aim of this study, included into the "Iberian lynx sanitary survey" (Consejería de Medio Ambiente, Junta de Andalucía), was to survey wild and domestic carnivore mammals for several infectious, parasitic and toxic agents in the areas where the lynx is still present.

MATERIAL AND METHODS: We surveyed 93 free-ranging (21 Iberian lynxes, 35 red foxes *Vulpes vulpes*, 24 mongooses *Herpestes ichneumon*, 11 genets *Genetta genetta*, 1 badger *Meles meles*, 1 polecat *Mustela putorius*) and 74 domestic (51 cats *Felis catus*, 23 dogs *Canis familiaris*) carnivores from June 2004 to June 2006 in Sierra Morena (Northern Andalucía) and Doñana (Southern Andalucía), in Spain. Animals were surveyed: (1) Dead (mostly road-killed or hunted): they were necropsied to detect lesions and samples were taken from different organs for histopathology, culture, PCR, parasitology, and toxicology; or (2) Alive: they were anaesthetized before sampling (with the exception of dogs) and entire blood, sera and plasma samples; oro-pharyngeal, conjunctival and rectal swabs; oropharyngeal smears for IF; and faeces and urine were taken. Cats were either feral or owned but free-ranging. Dogs were hunting or

INFRARED THERMOGRAPHY FOR EVALUATING HEALT STATUS OF WILD ANIMALS: PRELIMINARY STUDY

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AIM OF THE STUDY: Infrared thermography was used to measure and visualize the surface temperature of wild animals by detecting the thermal radiation that they emit. The aim of the work was a preliminary study on infrared thermography to show some potential future applications of this technique in particular on ungulates for evaluating their health status.

MATERIALS & METHODS: In this study an infrared thermal camera (ITC) (manufacturer: Flir Systems, Model: ThermaCam P25) and related software (Thermacam Reporter 7.0) to analyze images were used. The images were gathered in Val Rhêmes and Valsavarenche of Parco Nazionale Gran Paradiso in Valle d'Aosta (Italy) and they pictured mainly ibexes and Alpine camoises. During the studymore than 300 thermographic images were taken.

RESULTS: *Factors such as the presence of wool, intraspecific social behaviour and fear of humans might limit its objectivity. However, qualities and limits of the technique have been analyzed suggesting possible solutions to the problems related to it. With the close-up images it was possible to measure the temperature of the eye region and at the base of the horn. Same thermal information detected by the instrument were the expression of tissue metabolism and blood circulation of wild animals linked to pathological or physiological variations.*

CONCLUSIONS: Infrared thermography could be used to calculate density of animal population during night surveys or to detect animals hidden in the vegetation. The ability to detect animals in the darkness could be useful to study the behaviour of nocturnal species. The potential uses of this technique include monitoring the state of health to control the spread of transmissible diseases like foot and mouth disease and mange, studying the activity of the rumen, valuating the level of hair insulation and diagnosing pregnancy.

WELFARE EVALUATION OF FALLOW DEER (*Dama dama*) BREEDING HERDS: PRELIMINARY RESULTS

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AIM OF THE STUDY: In recent years in Italy wild ungulate breeding herds became wide spread. Such herds, mostly half- extensive, allow the recovery of hilly and mountainous areas where it is otherwise impossible to practice any agricultural or zootecnical activity. In addition to concerns about health problems associated with species, animals welfare are also of wide importance. Non-specific immunity parameters were implemented in this work to evaluate the welfare status, in terms of zootechnical welfare of the animals.

MATERIALS & METHODS: The research was conducted from January to April on 74 fallow deers (*Dama dama* L.) caught in relation to control programs and on other 74 bred in a half-extensive herd. The animals were one month to three years old. All these animals sera were analyzed to determinate some non specific immunity parameters: haemolytic complement assay, lysozyme serum titration, serum bactericidic activity.

RESULTS: All parameters showed statistically significant differences between the two groups. Especially the wild ones showed values of non specific immunity below the normal standard due to a higher environmental pressure. This different figure might be explained by the fact that blood samples were collected during the winter season and the fallow deers bred in half-extensive system had an easier access to food.

CONCLUSIONS: In order to verify the above pattern, it could be useful to analyze a higher number of samples during different seasons with the aim to determine the normal range values for this species. establishing the range values would allow to monitor the non specific immunity system relating to the different herd typologies. as this production system is reaching a growing economic importance, it is necessary to monitor not only a sanitary status of the animals but also their welfare status.

SARCOPTIC MANGE IN FREE-RANGING WILDLIFE IN SWITZERLAND: CONTRIBUTION TO PATHOLOGY AND EPIDEMIOLOGY

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AIM OF THE STUDY: Sarcoptic mange is a highly contagious skin disease considered to be a potential threat to endangered species and a limiting factor to animal populations in general. The aim of this project is to attempt to identify factors possibly influencing the development of skin lesions and the dynamic of the disease, in order to better understand the pathogenesis and epidemiology of mange in wildlife species.

MATERIALS & METHODS: Mangy and healthy wild carnivores were collected during one year in five specific Swiss areas, selected based upon the different pattern of occurrence of sarcoptic mange. All animals were submitted to pathological examination. An indirect ELISA test was performed on serum samples to confirm sarcoptic mange. In addition, parasitological, bacteriological, and histological examinations were performed on chosen cases.

RESULTS: 305 animals were collected (290 foxes, 11 badgers, 2 stone martens, 1 lynx, 1 wolf). Mites could be extracted from 106 of 151 mangy individuals of different species and from different geographical regions. Apart from skin lesions, cachexia and generally activated lymph nodes, mangy foxes showed a similar pathological picture as healthy ones. In most affected animals, a moderate to severe mange with a combination of crusts and alopecia was observed. *Staphylococcus intermedius* was cultivated from skin samples in 78% of the mangy (n=23), and only in 14% of the non-mangy (n=14) foxes. A secondary bacterial infection in animals with sarcoptic mange is, hence, a major risk factor that will decrease the chances of recovery. All foxes examined parasitologically (49 mangy, 51 non-mangy) were infested with 1 to 6 different species of nematodes and cestodes, whereas the infestation was slightly more severe in mangy than in healthy foxes. **CONCLUSIONS:** Preliminary results demonstrate that different characteristics and grade of skin lesions do not seem to be correlated to season, geographical location (and thus possibly to mite strain), gender and age class. Genetical analysis of the mites is pending.

SARCOPTIC MANGE IN A SPANISH ROE DEER

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AIM OF THE STUDY: To describe a fatal case of sarcoptic mange (*Sarcoptes scabiei*) in a male roe deer (*Capreolus capreolus*) from Asturias (Northern Spain).

MATERIALS & METHODS: An adult male roe deer was found moribund on pasture close to a road. The animal died during examination, and was carried to the Animal Health Laboratory of SERIDA-Jove (Gijón, Spain) for a detailed necropsy. Blood for serum biochemistry, skin scraping samples and skin sections were taken for mite isolation and identification and for histopathological testing.

RESULTS: The animal was extremely weak. Body condition was poor, and the stag showed widespread cutaneous alopecic areas and crusts that were specially severe in the head, neck and back. The isolation of *Sarcoptes scabiei* in the skin scrapings confirmed this mite as the cause of the skin lesions. These were complicated with secondary contaminants. Histological examination of the skin revealed hyperkeratosis with intracorneal tunnels in which mites could be observed, and the underlying dermis presented an inflammatory infiltrate. In addition, miasis was detected in the base of both antlers. The necropsy confirmed the emaciation, and allowed to discard any signs of shots or traumatism. Most lymph nodes were slightly increased, but all the inspected organs presented a normal appearance. Apart from the sarcoptic mange mites, the animal presented a low parasite burden. The biochemical results showed abnormal values for urea, glucose and creatinine in serum.

CONCLUSIONS: After considering all the information obtained in the necropsy and the complementary analytical exams, sarcoptic mange and the renal failure derived from secondary skin infections appear as the cause of the death of the animal. Although in the North of Spain sarcoptic mange has already severely affected populations of other ungulates (chamois), in Europe cervids in general and particularly roe deer have seldom been diagnosed with clinical sarcoptic mange.

SEROPREVALENCE OF *Neospora caninum* IN WILDLIFE FROM SPAIN.

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AIM OF THE STUDY: *Neospora caninum* is recognized as a major cause of abortion in cattle but many aspects of the life cycle of *N. caninum* are unknown and the role of wildlife in the life cycle of *N. caninum* is uncertain. In Europe, few seroprevalence studies of *Neospora* infection in wild ruminants have been performed. We analyzed the presence of antibodies against *N. caninum* in non-carnivorous wildlife to provide information on the epidemiology of *N. caninum* infection from Spain in these species. **MATERIALS & METHODS:** A total of 1034 non-carnivorous wildlife were tested for antibodies against *Neospora caninum* by competitive screening enzyme linked immunosorbent assay (ELISA) and confirmation of samples found positive by ELISA was sought by an indirect immunofluorescence test (IFAT). Only animals that were positive to both techniques were considered positive in the study. Levels of agreement between serological tests were performed using the kappa statistics. The statistical data analysis was performed using the SPSS 12.0 Statistical Program by chi-square test. The differences between variables were analyzed by Bonferroni or Tukey-Kramer Tests. For multiple comparisons Dunn's test was performed and when variances were not homogenous, non-parametric test was performed. The differences were considered statistically significant when $P \leq 0.05$. Seroprevalence was statistically analyzed considering the variables species, geographical area, estate management (open versus fenced), year of sample collection, sex and age of the animals. **RESULTS:** The prevalence of antibodies to *N. caninum* in samples positive to both tests were 11.8 % of 237 red deer, 6.1% of 33 roe deer, 7.7% of 13 barbery sheep and 0.3% of 298 wild boar, with a high kappa value of agreement between both serological tests of 0.929. Antibodies to *N. caninum* were not found in any of 251 wild rabbits, 79 fallow deer, 27 mouflon, 40 chamois and three Spanish ibex. In red deer, significant differences ($p=0.001$) were observed in the prevalence among sampling areas and between management of estates (open versus fenced) with higher prevalence in fenced estates. Seroprevalence of infection was particularly high in some areas (MO estate in South-Central Spain or some estates of Catalonia, North-East Spain), while no contact with the parasite was observed in others. No differences were observed between sexes or age. **CONCLUSIONS:** The results indicate that in certain areas *Neospora* infection is present in wildlife, with especial importance in red deer and this fact could have important implications in both sylvatic cycles as well as influence the prevalence of infection in cattle farms in those areas. This is the first report of presence of *N. caninum* antibodies in wildlife from Spain and the first report of *N. caninum* antibodies in wild boar and in barbery sheep.

HEARTWORM (*Dirofilaria immitis* Spirurida, Onchocercidae) IN WOLF (*Canis lupus*): FIRST REPORT IN ITALY

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AIM OF THE STUDY: description of the first report in Italy of Heartworm in wolf (*Canis lupus*), morphological and genetic identification of *Dirofilaria immitis*

MATERIALS & METHODS: morphological identification through observation under stereoscope and scanning electron microscopy (SEM) and genetic identification with species-specific PCR and DNA sequencing

RESULTS: confirm by genetics of the morphological identification of the parasite *Dirofilaria immitis*

CONCLUSIONS: the possible role of wolf *Canis lupus* in the epidemiology of heartworm in Italy is discussed

DETECTION AND GENOTYPING OF *Mycobacterium tuberculosis complex* IN LYMPH NODES OF WILD BOAR (*Sus scrofa*) POPULATIONS IN LOMBARDY REGION

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AIM OF THE STUDY: The presence of *Mycobacterium tuberculosis complex* (MtbC) in wild boar has been reported in several European countries including Italy. In Lombardy, wild boar population has remarkably increased in the last ten years and bovine tuberculosis (TB) is still present in cattle herds despite application of TB eradication programs. In this context, a TB survey programme has been carried out since 2000 in two wild boar populations located respectively in Bergamo and Como provinces: the study focused on detection and characterization of MtbC mycobacteria present in wild boar collected samples. **MATERIALS & METHODS:** Six hundreds fourteen wild boar lymph nodes were collected and controlled by macroscopic inspection. Culture isolation and PCR analysis specific for detection of MtbC were performed on 149 tissue samples mainly selected for the presence of tuberculosis-like lesions.

RESULTS: PCR results revealed the presence of MtbC DNAs in 80 animals. Further studies performed on 60 out of 80 IS6110 positive samples by PCR-RFLP of *gyrB* and by spoligotyping, revealed genetic profiles compatible with identification of *M. microti* and *M. bovis* respectively in 48 and in 2 tissue samples. Culture isolation was successful only in three cases: two mycobacteria isolates were identified as *M. bovis* and one as *M. microti* by molecular and bacteriological methods.

CONCLUSIONS: Our results show the presence of *M. microti* in a consistent number of wild boar lymph nodes never reported before in this animal species in Italy: difficulty of isolation and application of PCR test for detection of MtbC group, could mislead about correct identification of the species We could isolate only two *M. bovis* strains from wild boar hunted in Como whose genetic profiles are different to those found in recent TB outbreaks occurring in the same area. This study shows that in Bergamo and Como provinces the presence of *M. bovis* in wild boar does not represent a significant problem. Further investigations are necessary to assess the real frequency of TB infection in wildlife population in Lombardy. These data are comparable to results obtained in Piedmont region by colleagues of IZS of Torino.

SARCOPTIC MANGE IN RED FOXES IN SWITZERLAND

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AIM OF THE STUDY: Sarcoptic mange is a contagious disease due to an infestation with *Sarcoptes scabiei* and it has been reported in a wide range of domestic and wildlife species. In Europe it has been reported in wild ungulates, wild boars and carnivores. Even when mange epizootic does not affect long-term population dynamics, it can have serious consequence in small population of endangered species. The aim of this study has been the investigation of the dynamic of sarcoptic mange in a population of red foxes in Switzerland. **MATERIALS & METHODS:** Between 2004 and 2006 306 red foxes (*Vulpes vulpes*) were collected from the canton of BE, FR, GE, GR, TI, VS and were examined patologically for the sarcoptic mange. The red foxes examined were found dead or shot. Mites were extracted from 106 of the 151 sarcoptes positive animals and indirect ELISA test were performed on serum samples to confirm sarcoptic mange. The samples collected has been geo-referenced on a map. **RESULTS:** The canton with a higher prevalence were Berne and Vallese and the seasons with higher prevalence were autumn (62%) and winter (52%). Any significative difference were observed between sex. **CONCLUSIONS:** These evidence indicates that there is a temporal variation in the prevalence between seasons and years and a spatial difference in the prevalence between cantons. The observed bias could be due to the sampling collection of the foxes.

COMPARATIVE ANALYSIS OF THE PRION PROTEIN (PrP) GENE IN MARITIME MAMMALS

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AIM OF THE STUDY: In this work the *PrP* gene sequence and the deduced protein of maritime mammals have been determined and characterized in order to: 1) improve the knowledge of *PrP* gene variability in cetaceans; 2) get further insight in the structural and functional aspects of PrP as well as species susceptibility to prions; 3) investigate prion phylogeny in maritime mammal species. **MATERIALS & METHODS:** The PrP gene of eight maritime mammal species was amplified by PCR using degenerate primers. Purified amplicons were directly sequenced by Big Dye terminator cycle-sequencing. PCR products from selected samples were cloned in a UA-cloning vector to identify polymorphisms per allele. The *PrP* gene sequences of maritime mammals were aligned with the consensus sequence of other known mammals. Structure modelling of PrP was performed using homology-modelling program. Genetic distances were computed using MEGA and were used to construct a neighbour-joining tree. **RESULTS:** The nucleic acid sequence coding for the mature protein of maritime mammals was determined. The DNA from the species belonging to family Delphinidae gave identical nucleic acid sequences, with the exception of *Grampus griseus* that was heterozygous for a non coding mutation. The wild-type number of repeats is five in all analyzed maritime mammal. A *Stenella coeruleoalba* specimen included in our study was heterozygous for alleles with five and six repeats. *Balaenoptera physalus* sequence carried two silent mutations. Detailed analysis of primary structure of cetacean PrP, considering point mutations and the main structural domains, has been performed. 3D modelling revealed conservation of tertiary structure of mammal prion proteins. Phylogenetic analysis showed that *PrP* gene tree respects the species taxonomy. **CONCLUSIONS:** This work adds the so far unreported *PrP* sequence of maritime mammals to the collection of known prion genes. Maritime mammals cluster with ruminants and hippo, supporting their association in the order Cetartiodactyla. Analysis of cetacean sequences and phylogenetic similarity to ruminant PrP do not allow to exclude the occurrence of prion diseases in these species.

A FIVE YEARS SEROPREVALENCE DYNAMICS OF RESPIRATORY SYNCYTIAL VIRUS IN CHAMOIS POPULATION (*Rupicapra r. rupicapra*) IN THE ITALIAN CENTRAL ALPS.

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AIM OF THE STUDY: A seroepidemiological survey was carried out in the Orobie Alps (Province of Bergamo, Italy) to detect any variation of antibodies response to Respiratory Syncytial Virus (RSV) throughout five years. The study was performed after a severe die-off that affected chamois (*Rupicapra r. rupicapra*) metapopulation, with evidence of respiratory disease, in autumn-winter 2000-2001.

MATERIALS & METHODS: The study area (51,703 ha) is characterised by five faunistic districts, with an estimated chamois of about 4000 animals. Blood samples were collected by hunters from 1,086 chamois during the 2001-2005 hunting seasons. A blocking ELISA was used to test for antibodies to RSV.

RESULTS: The RSV seroprevalence showed a decrease in the second year, and than values were slightly lower. During the five years prevalence was respectively 46.8% (C.I. 95% 39-54), 36.6% (C.I. 95% 29-44), 35.5% (C.I. 95% 29-41), 30.4% (C.I. 95% 25-36), 33.3% (C.I. 95% 27-39). In relation to age classes, higher prevalence was found in sub-adults and adults than in kids and yearlings. Different seroprevalence values were also observed among the five faunistic districts. Following the severe die-off, sporadic cases of mortality due to acute respiratory disease have been reported.

CONCLUSIONS: The highest seroprevalence observed in 2001 was likely due to respiratory disease outbreak that occurred in the study area few months before the serological survey.

The seroprevalence observed in young animals during all five years suggested that infection is still present in chamois population. The presence in some districts of sheep flocks could represent a risk of interspecific transmission, considering that a RSV seroprevalence of 82% was detected in sheep in 2001.

PRELIMINARY EVALUATION ON THE USE OF A RAPID TEST (FAST Test® AIV Ag) FOR THE DETECTION OF AVIAN INFLUENZA VIRUS IN DUCK FAECES

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Due to the current importance of avian influenza, the according regulations and the need for rapid detection of influenza A viruses in poultry flocks a great number of rapid “penside” tests have recently been developed. The aim of this study was to carry out preliminary testing on the sensitivity of a commercial solid phase immunochromatographic test (Fast test® AIV Ag) for the detection of influenza virus A in duck faeces. The analysis was carried out with inactivated whole avian influenza virus in two replicates. Sensitivity of the test was compared to both, hemagglutination test and Real time Rt-PCR. In a first step, serial two-fold dilutions of the antigen were tested directly. Based on the results, three dilutions (2^0 , 2^4 , 2^6) were selected and mixed with fresh faeces from controlled, influenza A free domestic ducks. The mixture was exposed to ambient temperature, both with and without exposure to UV light and to 4° C in absence of UV light for 24, 48 and 120 hours.

While influenza A virus was detected in all samples using Real time Rt-PCR, the immunochromatographic test ceased to detect Influenzavirus in the samples that had been exposed to ambient temperature for 120 hours. Nevertheless the test proved more sensible than hemagglutination. Further testing with samples from experimentally infected animals that shed live virus, and with field samples positive in RtPCR would be of interest. However the use of this test in ducks is recommended only for fresh faeces or cloacal swabs.

TRICHINELLOSIS EPIDEMIOLOGICAL SURVEY IN SARDINIA: PECULIAR ASPECTS OF A SEASONAL SAMPLING AMONG WILD BOARS.

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As a result of Trichinellosis human cases (due to *T. britovi*) first time reported in Sardinia in 2005, in order to protect consumers health regional authorities ordered to test whole of wild boars shot. So during 2005-06 hunting season it's been examined 6,188 wild boars and all exams were negative. This overall negativity partly contrasts with the detection of *Trichinella britovi* in free ranging pigs (0,62% prevalence) in Orgosolo village (NU) where lives a family which had trichinellosis infection in april 2005. It will need, therefore, to establish how much the carried out sampling sistem has been adequate.

For this reason this work analyses numerical representativity of adopted sampling in each of eight territorial districts, which also correspond to the Sanitary Units in Sardinia region.

Improving numerical representativity in every single district and the amount of muscle from every animal to be checked may help to optimize the whole sensitivity of the sistem in detection of parasite, and at the same time represents the aim to pursue during the next hunting season.

SANITARY MONITORING AIMED AT THE PROTECTION OF THE WOLF ON THE TUSCANY SIDE OF THE NATIONAL PARK OF APPENNINO TOSCO-EMILIANO

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AIM OF THE STUDY: It evaluated the presence of wolves in the study area and it monitored, by faeces analysis, the presence of some pathogens which can be transmitted to wolves from others Canids and can compromise the wellbeing of wolves. It checked the presence of *E. granulosus* which can be spread at long distances by wolves.

MATERIALS & METHODS: The scats were collected for two years covering selected trails and snowtracking. Tests were performed for: species identification by the development of a specific PCR, virologic analysis to check the presence of *Parvovirus*, microscopic analysis to check the intestinal parasites and ELISA test to check the presence of *E.granulosus*. An informative system was set up using software open source Grass and R.

RESULTS: The genetic analysis showed a good concordance between field and laboratory identification of species (91,3%). All the samples were negative for *Parvovirus* (n= 89, IC 95% :0,0-4,5) and *E.granulosus* (n= 142, IC 95%: 0,0-2,6). The copromicroscopic exams showed the presence of the main parasites of canids, with no significant differences in the prevalence of parasites among wolves, foxes and dogs (respectively 39,8%; 50%; 43,6%). In the second year the prevalence of parasites in wolves increased to 86,2%.

CONCLUSIONS: The study confirmed the ongoing presence of the wolf in the area. We consider that while the copromicroscopic analysis can only provide information on the frequency of excretion of the eggs from parasites, yet it can be considered the first step for a sanitary control of the wolf population with a non invasive means.

Salmonella ISOLATES FROM CARCASSES AND FAECES OF WILD CARNIVORES IN AOSTA VALLEY REGION (WESTERN ITALIAN ALPS)

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AIM OF THE STUDY: Salmonellosis has been studied extensively in passerines, gulls and raptors, whilst less is known about mammals, particularly carnivores, even though various serotypes have been isolated in wild (foxes, racoons, badgers) and captive (baboons, rhinoceros) animals. As a consequence, the role played by carnivores in the transmission of the pathogen to men is still poorly known.

MATERIALS & METHODS: Between 2001 and 2005, 258 foxes (*Vulpes vulpes*) and 51 badgers (*Meles meles*), brought to our laboratory for necroscopic exams, have been examined for *Salmonella* serotypes following an inner standardized protocol. Starting from 2003, the sample has been improved by faeces (respectively 204 and 54) collected in the main habitats of the western Italian Alps (Aosta Valley region). All samples were transferred on a digitalized map (1:10.000) by GIS (Arcview 3.1). *Salmonella* prevalence according to three altitudinal belts (500-999, 1000-1499, 1500-2000 m a.s.l.) was compared by the χ^2 test.

RESULTS: Salmonellae were isolated from 16 foxes and 5 badgers and from 3 fox faeces and 5 badger faeces. Prevalences in badgers and in their faeces were similar (0.11 vs. 0.09 $\chi^2=0.1$, p=0.75), whilst fox faeces seem an unreliable monitoring method, being their prevalence lower than that of foxes (0.015 vs. 0.084 $\chi^2=8.6$, p=0.003). Fox prevalence was higher between 500 and 1000 m ($\chi^2=21.4$, p<0.001), corresponding to the urbanized main valley of the region. Twelve serotypes of *S. enterica* subsp. I were identified, 2 isolates belonged to subsp. IIIb, 1 to subsp. II, 4 to subsp. IV, 3 to *Salmonella* sp. On the whole, 8/24 (33%) isolates belonged to serotypes commonly found in men (Typhimurium, Heidelberg, Infantis) and/or in water (Veneziana). Serotypes Livingstone and Napoli were also found in patients admitted to regional hospitals. **CONCLUSIONS:** The distribution of isolates together with the frequency of occurrence of serotypes that are pathogenic for humans suggest that anthropogenic environmental contamination could represent, directly or indirectly through the food chain, a source of infection for wild carnivores.

ARTERIOSCLEROSIS AND MYOCARDIAL FIBROSIS IN FREE-RANGING LYNX (*Lynx lynx*) FROM SWITZERLAND

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AIM OF THE STUDY: In 2003, an adult male lynx from the Swiss Alpine population died of a circulatory collapse due to severe myocardial fibrosis (MF) and arteriosclerosis (AS) of the coronary arteries. Since then, we observed similar histological lesions in apparently healthy lynx of different age classes. Thus, we started a retrospective study to characterize the histopathological lesions in affected individuals, to compare the weight of the heart and other internal organs in affected and non-affected lynx, and to look for risk factors such as age, sex, and population.

MATERIALS & METHODS: From January 2000 to June 2006, 46 lynx were submitted for necropsy. Organ were weighted (n=22), and samples were collected for histology (n=42).

RESULTS: Preliminary results indicate that about 30% of the investigated lynx present histological heart lesions characterized by MF and/or AS. The prevalence seems to be higher in the Jura than in the Alpine population. Adults are most commonly affected, but lesions are also observed in the subadult and juvenile age classes. Males appear to be more often affected than females. Except for the lethal case mentioned above, neither macroscopical lesions in the heart, nor associated lesions in other organs or clinical symptoms were noticed in the affected lynx. Comparative results on organ weight have to be interpreted with caution due to the small data number and to bias due to age, body weight and nutritional status.

CONCLUSIONS: Cardiac lesions characterized by AS and MF were observed in a significant number of free- ranging Swiss lynx. Lesions were mostly found in older animals, but few younger individuals were also affected. MF is a characteristic feature of cardiomyopathy in both cats and dogs. In contrast, associated AS is rare in cats but common in dogs. To investigate whether these lesions are a common finding in lynx and/or if it is particularly prevalent in re-introduced Swiss lynx, we plan to analyse samples from other Eurasian lynx populations.

TUBERCULOSIS IN WILD BOAR IN PORTUGAL

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AIM OF THE STUDY: To investigate and characterize the presence of tuberculosis in wild boar populations in south-central Portugal.

MATERIAL AND METHODS: Samples of submandibular, retropharyngeal, tracheo-bronchic and mesenteric lymphnodes and lung were collected from hunted wild boars in 2005/06 season. Techniques used to investigate the presence of mycobacteria are macroscopic inspection, Ziehl-Neelsen staining of smears and histopathologic slides, PCR and culture in Coletsos and Middlebrook 7H11 medium. Age and sex data were recorded when possible and all animals were georeferenced to the local of capture.

RESULTS: We collected samples from 139 Wild boars from 7 different areas (85 females, 30 males and 24 of unknown sex). Twelve animals were <1 year old, 34 between 1 and 2 years, and 45 older than 2 years. Tuberculosis-like macroscopic lesions were found in 17 animals from 4 areas, and in 10 animals we detected acid-fast mycobacteria in stained lymphnode smears. Confirmation of diagnosis by culture, PCR and histopathology are ongoing. Macroscopic lesions were mostly located in submandibular (71 %), tracheo-bronchic (57 %), retropharyngeal (29 %) and mesenteric (29 %) lymphnodes. Two animals presented lung lesions.

CONCLUSIONS: This is the first epidemiological study of tuberculosis in wild boar in Portugal. Preliminary results suggest the disease is present in the south-central part of the country. Apparent prevalence seems to vary between zones, but does not greatly differ from those reported in other regions of Europe. Location and characteristics of the lesions are also in agreement with published descriptions.

MYXOMATOSIS AND RABBIT HEMORRHAGIC DISEASE IN A LOW-DENSITY POPULATION OF WILD RABBIT *Oryctolagus cuniculus* IN NORTHWESTERN PORTUGAL

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AIM OF THE STUDY: To describe the epidemiology of Myxomatosis and Rabbit Hemorrhagic Disease (RHD) in a low density population of wild rabbit in northwestern Portugal, based on virology and serology data obtained from hunted, apparently healthy animals.

MATERIAL AND METHODS: We collected liver, palpebrae, blood and lung samples from hunted wild rabbits in 2003/04 and 2004/05 hunting seasons. Study area included 350.000 hectares in northwestern Portugal, where wild rabbit density is known to be low. Presence of Myxomatosis virus DNA was investigated in palpebrae by means of PCR and RHD virus in liver samples by means of ELISA (both techniques in Instituto de Ciências Biomédicas Abel Salazar, Porto, Portugal). Antibodies against both viruses were screened in serum samples by commercial ELISA (both in Instituto de Investigación en Recursos Cinegéticos, Ciudad Real, Spain).

RESULTS: Myxomatosis viral DNA was detected in 2/33 (6 %) palpebrae samples while no RHD virus was detected in 66 liver samples from apparently healthy animals. Serological survey detected 32/45 (71 %) Myxomatosis antibody-positive animals but only 2/72 (3 %) RHD antibody-positive.

CONCLUSIONS: This data suggests different epidemiological behavior of Myxomatosis and RHD in northwestern Portugal. While the first is widespread and possibly endemic, with most animals having antibodies in both years, the latter seems to be more localized and possibly epidemic. Most published field data points to both Myxomatosis and RHD being endemic in wild rabbit populations in Europe. But theoretical data suggest RHD could become epidemic in low density populations, and it seems this could be happening in northwestern Portugal.

PHYSIOLOGICAL OCULAR PARAMETERS IN NORMAL SARDINIAN WILD MOUFLONS: STT, IOP, BACTERIAL AND FUNGAL FLORA, LACRIMAL PROTEINS.

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INTRODUCTION:

Reports on ocular normal parameters in mouflons are scarce. STT, IOP, bacterial and fungal flora and lacrimal proteins were established in 36 normal Sardinian wild mouflons, respectively by steril Schirmer tear test strip, , and. Animals were physically restrained.

AIM OF THE STUDY:

The purpose of this study was to estimate the mean and range of IOP and STT, identify normal bacterial and fungal flora and lacrimal proteins composition in eyes of clinically normal mouflons in relation to age, sex, eye (left vs. right), in order to establish a reference value (currently unavailable) for a correct ophthalmologic analysis of Sardinian wild mouflons.

MATERIALS & METHODS:

The animals were placed in sternal decubitus, no drugs were used to restrain. STT values were recorded using commercial STT tests. Following evaluation of tear production, IOP was recorded by applanation tonometer. After these tests conjunctival swab for detection of fungal and bacterial flora detected on conjunctival fornix were sowed in medium. Lacrimal fluid collected by Eppendorf pipette were submitted at electrophoresis on agarose gel and determined.

RESULTS & CONCLUSIONS: The mean and range of STT in normal mouflons was 15.05 (\pm 1.79) mm/min, range 11-22 mm/min. The mean and range of IOP in normal mouflons was 17.93 (\pm 5.24) mmHg, range 10-28 mmHg. Bacterial population most representative were *B. cereus*, *E. coli*, *B. licheniformis*, *B. subtilis*. Fungal colonies isolated have been classified: *A. fumigatus*, *Microsporum spp*, *Penicillium spp*, and others. Proteins identified on tears of both eyes were particularly albumin and immunoglobulins and other bands probably correlated with proteins with different molecular weight. No significant differences were observed between sexes, ages or place of origin.

PREVALENCE OF *Toxoplasma gondii* ANTIBODIES IN WILD CARNIVORES FROM SPAIN.

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AIM OF THE STUDY: *Toxoplasma gondii* is a zoonotic obligate intracellular parasite that infects a broad spectrum of vertebrate hosts including humans and has a worldwide distribution. *T. gondii* infection has frequently been described in wild carnivores, due to their feeding habits, with prevalences ranging from <0.1% to 90%. The purpose of this study was to investigate the occurrence of antibodies against *T. gondii* in wild and free-ranging domestic carnivores from Spain.

MATERIALS & METHODS: Serum samples from 109 red foxes (*Vulpes vulpes*), 35 badgers (*Meles meles*), 33 wolves (*Canis lupus*), 33 dogs (*Canis familiaris*), 26 cats (*Felis catus*), 23 egyptian mongoose (*Herpestes ichneumon*), 22 genets (*Gennetta gennetta*), 19 stone martens (*Martes foina*), 11 iberian lynxes (*Lynx pardinus*), 7 wildcats (*Felis sylvestris*), 6 otters (*Lutra lutra*), 6 polecats (*Mustela putorius*), and 3 martens (*Martes martes*) were collected between 1990 and 2006 from eight regions of Spain and tested for antibodies against *T. gondii* by the modified agglutination test (MAT).

PRELIMINARY RESULTS: Antibodies to *T. gondii* (MAT 1/25 or higher) were detected in 44 (80%) of 55 animals analyzed. Positive samples included lynx, wolf, fox, wildcat, mongoose and genet sera.

CONCLUSIONS: Serological results indicated a widespread exposure to *T. gondii* among wild carnivores in Spain. Thus some carnivore species can be considered as good indicators of environmental contamination with the parasite. To our knowledge, this is the first report of *T. gondii* in mustelids, wolves and lynxes in this country.

PERSECUTION OF PREDATORS IN FLANDERS, JANUARY 2003 TO MARCH 2006.

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Malicious poisoning was confirmed in 66 (42%) and death from shooting injuries in 19 (12%) of 157 submissions of predators, both birds and mammals, presented for examination between early January, 2003 and the end of March, 2006. Each submission of one or more found-dead animals corresponded to one incident. Out of 242 subjects, 98 (40%) were poisoned and 20 (8 %) were shot. The number of submissions in which poisoning was confirmed gives a better indication for the amount of offences than the number of killed animals.

The percentage of confirmed poisoning incidents was 45 % for the period 2003-2005, 43 % for the first three months of 2003-2005 joined and 40 % for the first three months of 2006. When correcting for the high amount of winter mortality (30%) in the first three months of 2006, a poisoning percentage of 56 % of the deliveries was obtained, coinciding with the gradual increase in poisoning percentages that were calculated from year to year between 2003 and 2005 (i.e. 30 %, 46 % and 56 %).

The most frequently detected poison in poisoned animals and in baits found in the field was carbofuran. Other organocarbamates, organophosphates, and strychnine were less frequently recorded. Rodenticides including coumarines and indandion derivates were recorded sporadically.

Ignoring the target species for malicious poisoning and not taking into account the poisoned animals that were not recovered, buzzards (*Buteo buteo*) were the most frequent victims of fatal poisoning incidents. Out of 162 buzzards, 91 (57 %) were deliberately killed from which 79 (49 %) were poisoned and 12 (7 %) were shot. The buzzard is a regular carrion eater and it is amongst the most common raptor species in Flanders. The current data do not allow to estimate possible effects of persecution on the population of buzzards in Flanders.

RESULTS OF 2 YEAR SAMPLING FOR AVIAN INFLUENZA IN FREE RANGING GEESE IN BELGIUM

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Official monitoring for avian influenza in wild birds in Belgium started from september 2005 on. Out of 1667 cloacal swabs from *Anseriformes*, *Charadriiformes*, *Gruiformes* and *Passeriformes*, only one low pathogen (LP) avian influenza H3N6 strain was isolated from a mallard (*Anas platyrhynchos*). Independently of the official surveillance program, free ranging geese were sampled since the early summer of 2005, on the occasion of several interventions aiming to reduce locally the excess populations of Canada geese (*Branta canadensis*) and crossbred geese, and one banding activity. During two consecutive years geese were caught at 3 different locations in Flanders at the end of June in their moulting period. Cloacal swabs (n = 564) were collected and analysed by RT-PCR. Serum samples (n = 465) were collected from the V.basilica and subjected to an IgG ELISA test for the detection of antibodies against avian influenza M2e antigen. M2e is an influenza A virus induced cell membrane protein that is abundant on virus infected cells. Additionally an hemagglutination inhibition (HI) test was carried out on the serum samples. All of the cloacal samples were negative for influenza viruses. From the 2005 serum samples, 10/302 showed moderate to high titers of anti M2e IgG, ranging from 100 to 8100. HI was negative for all of the sera. The complete results including those not yet available at the writing of this abstract will be presented in the poster. Though no HP avian influenza virus could be demonstrated until now by RT-PCR from wild living birds in Belgium, the detection of anti M2e antibodies in sera from geese proves the circulation of hitherto unidentified influenza viruses. Further sampling should be extended to the migration periods in order to get a more complete picture of the circulation of avian influenza viruses in Belgium.

Leptospira interrogans ANTIBODIES IN WILD BOAR FROM SLOVENIA

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AIM OF THE STUDY: The population density of wild boars in Slovenia has increased drastically during the last decade despite the hunting-related reduction of wild boar population. In the last decade evidence has accumulated that in some situations wild boar can act as a reservoir for diseases which may pose a significant risk to the health of other free-living mammals and humans. There is currently no recorded data regarding prevalence and distribution of the *Leptospira interrogans* among wild boar in Slovenia. In view of this, our objective was to expand the information on the prevalence of *Leptospira interrogans* in wild boar in Slovenia. **MATERIALS & METHODS:** Blood samples were collected from 439 shot wild boar (*Sus scrofa*) throughout Slovenia during the hunting season 2004/2005. Directly after the shooting of a wild boar, blood was collected from the animal into sterile tubes and transferred to the laboratory. Serum was obtained by centrifugation and frozen at -20°C until examination. Serum samples were tested for antibodies using the microscopic agglutination test (MAT). As antigens for testing the sera of different serovars (sv.) were used: sv. *grippotyphosa*, sv. *sejroe*, sv. *pomona*, sv. *terassovi*, sv. *icterohaemorrhagiae*, sv. *canicola*, sv. *austrelis*, sv. *bataviae*, sv. *saxcoebing* and sv. *hardjo*. Samples giving titers of ≥ 100 against one or more sv. were considered positive for leptospiral antibody. **RESULTS:** Examination of 438 blood sera from the wild boar has revealed antibodies against at list one serovar of *L. interrogans* in 186 sera (42%). Of the 186 positive samples 86 samples (46%) had positive titre against a single serovar, while 100 (54%) samples had positive titres against 2 or more serovars. Most frequently established sv. was *L. interrogans* sv. *terassovi*. **CONCLUSIONS:** The investigation confirmed the presence of different serovars of *L. interrogans* in wild boar trouaught Slovenia. It can be conducted that wild boar are natural reservoirs for leptospires and represent a significant potential source of leptospirosis for other wild and domestic animals as well as for humans.

PRELIMINARY SURVEY ON PARASITIC AND INFECTIOUS DISEASES IN A RED FOX (*Vulpes vulpes*) POPULATION LIVING IN THE CENTRAL ITALY.

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The objective of this study was to evaluate the general health status of a red fox population living in Central Italy and to investigate whether this population was exposed to selected pathogens.

One hundred ninety four red foxes, shot during the regular hunting season in the Province of Pisa (43° N, 10-11° E) Central Italy, were submitted to diseases investigation to the Department of Animal Pathology, University of Pisa from January 2003 to December 2005. During necropsy, all animals were submitted to a biometric analysis. Eye lenses were removed for age determination and 2 distinct weight peaks, around 200mg and 250mg, corresponding to yearlings (80/194; 41.2%) and adults (114/194; 58.8%), respectively were found.

The most common pathologies were gastrointestinal and broncopulmonary parasitosis. Adults of *Dirofilaria immitis* were also found by heart examination, with a prevalence of 7.2% (14/194). Ectoparasites were collected and identified and a sarcoptic mange prevalence of 5.1% (10/194) was also recorded. The presence of dermatophytes on the coat of animals was moreover investigated through cultural examination, performed by the MacKenzie's brush technique. The two main pathogenic species identified were *Trichophyton terrestre* (13/194; 6.7%) and *Trichophyton erinacei* (6/194; 3%). The presence of Leishmaniosis was investigated by a specific PCR on 50 spleen samples, collected during necropsy, with a prevalence of 16% (8/50). When possible, blood samples were collected to investigate the presence of antibodies against *Toxoplasma* (29.1%; 7/24), *Leptospira interrogans* (25%; 6/24), *Ehrlichia. canis* (8.3%; 2/24), and *Rickettsia rickettsii* (16.6%; 4/24). No positivity to *Rickettsia conorii*, pathogen responsible of mediterranean tick fever, was found

THE SPECIMEN AND DATA COLLECTION FOR THE SARCOPTIC MANGE'S SURVEY IN CHAMOIS (*Rupicapra rupicapra*) FROM THE DOLOMITI FRIULANE PARK, EASTERN ALPS, ITALY: PROTOCOL, DATA SHEETS AND CARCASS DISPOSAL

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The quality of information obtained from a wildlife health survey depends on several factors including numerosity of the subject examined, condition of the specimen, use of clear and detailed sampling protocols, care maintained in packaging, storing and shipping the samples. In fact information has scientific value only when carefully documented. For these reasons the Dolomiti Friulane Park developed a full protocol for the management of the specimen and data collection related to the survey of sarcoptic mange in chamois (*Rupicapra rupicapra*) inside the 36.950 hectares of the Park. Every year the numerosity of the sample was estimated using an epidemiological approach based on biological data like population size/structure and according to the known prevalence of the mange. Clinically healthy chamois belonging to different age and sex classes were sampled in different areas of the Park. The personnel filled a standard sampling form for each chamois and after a morphobiometrical evaluation of the carcass, lung (about 5-10 cm) and serum (about 5 ml) were collected and stored at -30°C. Furthermore blood from living chamois and ibexes obtained during translocation and radio-tracking activities was collected and stored as above. Laboratory tests were conducted by the Department of Animal Production, Epidemiology and Ecology, Faculty of Veterinary Medicine, University of Torino, Italy on lung or serum using a specific ELISA test. Positive samples were confirmed by a western blot. The protocol contains also detailed instructions for the carcass disposal of dead chamois even if no clinically ill subject has still been found inside the Park. The protocol approach is to leave the carcass where it is when found in remote areas and where there is no concern about public health or to shift the intact carcass to a more appropriate site avoiding at the same time mange dissemination.

THE SURVEY OF SARCOPTIC MANGE IN CHAMOIS (*Rupicapra rupicapra*) FROM THE DOLOMITI FRIULANE PARK, EASTERN ALPS, ITALY

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The Dolomiti Friulane Park is located in the Eastern Alpine Area, in the Friuli Venezia Giulia Region. It extends over a surface of 36.950 hectares and it has a high level of biodiversity. The particular orography of long and narrow valleys and Dolomitic peaks, with few main roads keep lower the anthropic pressure. The Park hosts a colony of about 3.000 chamois (*Rupicapra rupicapra*) whose number is increasing every year. According to the great expansion of the sarcoptic mange among the chamois populations of the Eastern Alps since 1995, a survey plan of mange in this ungulate species was developed three years ago. The aim was monitoring this parasitic diseases in the chamois Park's population. The numerosity of the sample to be collected was estimated using an epidemiological approach based on biological data like population size/class structure and according to the known prevalence of the mange. Lung and serum from 118 clinically health chamois were collected starting on winter 2002 (20 chamois during 2002-2003; 40 chamois during 2003-2004 and 58 chamois during 2005-2006). Laboratory tests were performed using a specific ELISA kit and positive samples were confirmed with a western blot. In the first year of survey there was no positive sample while during the second and third year we found 4 (2 + 2 respectively) chamois positive to serology. However until now there was no finding of chamois with clinical symptoms of sarcoptic mange inside the Park. This phenomena could suggests that seroconversion not necessarily develop to a clinical sarcoptic mange at least in a short time and that the immune resistance on a genetic base to sarcoptic mange probably has a great importance for the appearance of epizootic mange in a chamois population.

EFFECTS OF EXPERIMENTAL REDUCTION IN ECTOPARASITE NUMBERS ON COAT CONDITION IN A WILD POPULATION OF AUSTRALIAN MOUNTAIN BRUSHTAIL POSSUMS (*Trichosurus cunninghami*)

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AIM OF THE STUDY: To investigate the causes of the disease “rumpwear”, which is perhaps the most common disease of Australian brushtail possums (*Trichosurus sp.*) and which manifests itself by varying degrees of damage to the coat and skin of the rump region. In the past, it has been suggested that “rumpwear” is caused by a hypersensitivity reaction to ectoparasites, but little work has been conducted to confirm this.

MATERIALS & METHODS: In the study presented here, a wild population of mountain brushtail possums (*Trichosurus cunninghami*) with a high prevalence of “rumpwear” were monitored for an association between ectoparasite burdens and coat condition over two years. As part of this study, and in order to further test whether a relationship between “rumpwear” and the presence of ectoparasites exists, a field experiment was conducted to eliminate ectoparasites from a group of possums. Selamectin (6mg/kg) was applied topically every 3-4 weeks for 5 months to a group of free-ranging possums with varying degrees of rumpwear, and ectoparasite numbers and rumpwear severity in this group were compared to a control group. **RESULTS:** After 5 months of treatment, ectoparasite burdens were significantly reduced in the treatment group. There appeared to be some improvement in the individual rumpwear severity of animals in the treatment group, but overall rumpwear severity was not significantly different to the control group.

CONCLUSIONS: Based on the data collected so far, there is no strong evidence of a significant correlation between “rumpwear” and the presence of ectoparasites.

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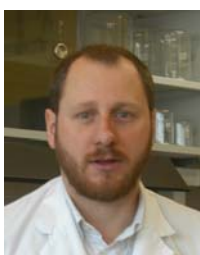


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