DNA Vaccines Encoding MAP 1 Genes of *Cowdria ruminantium*, the Agent of Heartwater, Protect DBA/2 Mice Against Lethal Challenge

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DNA vaccines encoding the Major Antigenic Protein 1 (MAP1) of *Cowdria ruminantium*, the causative agent of heartwater, were tested using a DBA/2 mouse model. A Crystal Springs (CS) map1 DNA vaccine, VR1012/MAP1.CS, induced protective TH1 type immune responses (characterized by production of IFN-gamma and IL-2 and anti-MAP1 antibodies of predominantly IgG2a isotype) which protected 13 to 23% of DNA vaccinated mice against homologous challenge in various trials performed. Boosting DNA vaccine-primed mice with recombinant MAP1 protein significantly improved the level of protection in various trials to 53-67% on homologous challenge (P < 0.050). The augmented protection by the prime-boost regimen correlated with augmented TH1 type immune responses that were induced by the DNA vaccine. Induction of TH1 type immune responses appears to be critical for protection against *C. ruminantium* infection, because DBA/2 mice immunized with the recombinant MAP1 protein without DNA vaccine priming induced non-protective TH2 type immune responses (characterized by IL-4, IL-5 and IL-10 and anti-MAP1 antibodies of mainly IgG1 isotype). A second DNA vaccine, VR1012/MAP1.Mbz, containing the map1 gene from the Mbizi isolate of *C. ruminantium* also delivered by a prime-boost regime, conferred less protection against heterologous challenge. Hence, in developing DNA vaccines against heartwater that contain the map1 gene, a prime-boost regimen should be adopted and gene sequence heterogeneity of field isolates should also be considered. Additional potentially protective *C. ruminantium* genes are being tested individually and in combinations in an effort to further improve the efficacy of the DNA vaccines.
An inactivated vaccine against heartwater protected sheep and goats against challenge from field *Amblyomma hebraeum* and *A. variegatum* ticks in four southern African countries. This vaccine, consisting of inactivated *Cowdria ruminantium* organisms and the adjuvant Montanide ISA 50, significantly protected boer and angora goats at field sites in Botswana and S. Africa respectively, and merino sheep in Zambia and Zimbabwe against mortality caused by heartwater infections. In comparison, the respective control unvaccinated animals suffered higher mortality rates. The vaccine’s efficacy varied at the various sites. The inactivated vaccine also protected Friesland cattle against field *A. hebraeum* ticks. Although this vaccine is able to significantly protect against heartwater mortalities, its efficacy has to be improved particularly for its use in sheep and goats. The influence of *C. ruminantium* isolate antigenic differences and testing of new adjuvants on the protective efficacy of this vaccine against field challenge are being investigated.
Safety of *Brucella abortus* and RB51 and Strain 19 Vaccines in Coyotes (*Canis latrans*)

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The purpose of this investigation was to evaluate and document the safety of RB51 and Strain 19 (S19) vaccines in coyotes. Coyotes are ubiquitous predators and scavengers, and coyotes are known to become naturally exposed and infected with *B. abortus*. While there may be little concern for any possible deleterious effects of Bruce/la vaccines in coyotes, any negative effects due to the use of *Brucella* vaccines in the Greater Yellowstone Area on wolves (*Canis lupus*) would be disastrous. Both RB51 and S19 vaccines have been widely used in cattle to reduce the risk of abortions and therefore transmission of *B. abortus* to susceptible individuals.

From March 1999 to May 2000, a total of 94 coyotes (35 males and 59 females) were included in the study. Coyotes were randomly assigned to one of three treatment groups (RB51, S19, and non-vaccinated controls). The vaccinated animals were orally exposed to $1 \times 10^9$ colony forming units (cfu's) of either RB51 or S19 while the non-vaccinated controls (NVC) were orally exposed to physiologic saline. Six weeks post-exposure (P.E.) to the vaccines or the saline, or at the termination of pregnancy, all adult coyotes, fetuses, and pups were euthanized and blood and tissues were collected at necropsy.

The mean litter size for the three treatment groups did not differ significantly (3.4 RB51; 3.3 S19; 3.2 NVC). Fourteen (9 females and 5 males) of the 37 coyotes in the S19 group were positive on conventional serology at 25 days post exposure (P.E.). All of the 19 coyotes in the RB51 group were negative on conventional serology, and 18 of 19 (95%) were positive at day 21 P.E. as determined by Western Blots, and 5 (3 females and 2 males) were positive on the day of euthanasia. All of the NVC group were serologically negative throughout the study. S19 was recovered from the spleen and liver from one female coyote at day 21 P.E., and from the tonsils and spleen of another female coyote at day 38 P.E. No isolations of *Brucella* were made from the tissues of the RB51 or the NVC groups.

Since no isolations of *B. abortus* RB51 or S19 were made from the reproductive tissues of either adult males or females and no isolations were made from any of the 84 pups, it would appear that coyotes in the field orally exposed to either of the vaccines at a dose $1 \times 10^9$ cfu will not suffer any negative reproductive effects. Chronic infections with either RB51 or S19 do not appear to be a problem in coyotes.
Construction and Evaluation of a Recombinant Foot-and-Mouth Disease Virus: Implications for Inactivated Vaccine Production

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The South African Territories (SAT) types of foot-and-mouth disease virus (FMDV) show marked genomic and antigenic variation throughout sub-Saharan Africa. This variation is to a large extent geographically linked and requires therefore the use of custom-made vaccines. Adaptation of field isolates as vaccine strains is cumbersome, time consuming and expensive. A possible means of circumventing the adaptation process is to construct recombinant or chimeric FMD viruses, followed by the production of conventional, inactivated vaccine utilizing these viruses. The advantage of such a strategy would be the ability to manipulate the antigenicity of these viruses by substituting the antigenic coding regions (i.e. structural proteins) of a full-length cDNA clone of a suitable strain.

A chimeric cDNA clone between types A and SAT 2 was successfully constructed by inserting the external capsid-coding region of the vaccine strain, ZIM/7/83/2, into the genetic backbone of the A12 cDNA clone. The subsequent evaluation of the resulting recombinant FMD virus indicated the virus to be immunogenically identical to the wild type ZIM/7/83/2. Results regarding the growth properties and stability of the chimeric virus will be presented and its implications for vaccine production discussed.
SURVEILLANCE
Health Surveillance of Rocky Mountain Bighorn Sheep (*Ovis canadensis*) in Idaho: The Aftermath of an Outbreak of Pneumonia

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In 1998 and 1999, 60 bighorn sheep in central Idaho experienced an outbreak of pneumonia, which was attributed to *Pasteurella hemolytica*. In addition, samples from sheep captured at that time indicated exposure to several bovine respiratory viruses, lungworm, coccidia, and brucellosis. Subsequent to the pneumonia outbreak, sheep in several populations experienced declines and poor lamb production and survival. Sheep from the same areas were sampled in 1999, 2000 and 2001 to evaluate health status and the occurrence of *Pasteurella* spp. A high percentage of the sheep sampled in both time periods had *Pasteurella* spp. isolated from nasal and/or pharyngeal swabs or from tonsilar biopsies. The most common isolate of *Pasteurella* spp. in 1998 and 1999 was *P. trehalosi* biotype 2. The same biotype of *Pasteurella* spp. was isolated from 3 of 46 sheep in 2000. Lungworm (*Protostrongylus* spp.) burdens were higher in 1999 than 2000. The persistence or re-occurrence of *P. trehalosi* biotype 2 in sheep 10 years after the original pneumonia outbreak may indicate a chronic pneumonia problem in these herds and creates management problems with supplemental transplants to augment the existing sheep population. Specific health profiles and management problems will be addressed.
Isolations of EHD and BT Viruses from White-tailed Deer in the Southeastern United States, 1990 to 2000

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Hemorrhagic disease (HD), caused by Orbiviruses in the epizootic hemorrhagic disease (EHD) and bluetongue (BLU) serogroups, represents the most important viral disease affecting white-tailed deer throughout their range in North America. In the southeastern United States, serologic studies suggest that of the seven EHD and BLU viruses present (EHDV-1, EHDV-2, BLU-2, BLU-10, BLU-11, BLU-13, BLU-17); EHDV-2 occurs most often. The objective of this study was to examine virus isolation results from white-tailed deer submitted to the Southeastern Cooperative Wildlife Disease Study to determine which viruses were most often associated with white-tailed deer mortality. From 1990 to 2000, 120 EHD and BLU viruses were isolated from white-tailed deer samples submitted from 16 states. Viruses were isolated in all years except 1992 and 1997. Virus isolation in most cases was attempted by inoculation of both baby hamster kidney (BHK) and cattle pulmonary endothelial (CPAE) cell lines. Viruses were isolated from several tissues including whole blood collected in anticoagulants, spleen, lung, lymph nodes, and liver. Of the 120 isolations, 93 were identified EHDV-2. There were 23 isolates of EHDV-1, 2 of BLU-17, and one each of BLU-10 and BLU-13. Results support the premise that EHDV-2 is the predominant virus responsible for HD mortality in white-tailed deer in the southeastern United States. Results also demonstrate a potential bias in utilizing clinical records or virus isolation results alone to determine spatial or temporal distribution of these viruses in white-tailed deer populations.
Epizootiological Investigations on Bovine Viral Diarrhea Virus (BVDV) in Moose (Alces alces) and Roe Deer (Capreolus capreolus) from Sweden

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Since 1985, a disease resembling Bovine Viral Diarrhea (BVDV) has been observed in moose (Alces alces) and roe deer (Capreolus capreolus) in Sweden. Sera from 279 moose and 303 roe deer were examined for the presence of antibodies against BVDV using two blocking ELISA-tests and a microneutralisation test (NT). Of the 303 roe deer sera tested in the first blocking-ELISA, two serum samples were positive, but all samples were negative in the second blocking-ELISA. Of 36 roe deer sera tested in the NT-test, 15 (42%) were positive against the BVDV strain SH9/11. Titers varied between 6 and 32.

Out of 279 moose sera tested in the first blocking-ELISA, 19 (6.8%) samples were positive for antibodies against BVDV. These positive results, as well as the negative finding on 22 randomly selected moose sera, could be confirmed in a second blocking-ELISA. In the NT, 10 out of 27 sera were positive and the 17 negative samples were also negative in the subsequently applied two blocking-ELISA tests. The antibodies in moose sera were detected in the NT test against the BVDV strains NADL, GRUB 313/83, SH9/11 and Osloss, but not against the Border disease strain Moredun. Antibodies in roe deer sera were demonstrated in the NT test against the BVDV strain SH9/11, but not against the other mentioned strains. In moose there was a positive correlation between age and seropositive reaction to BVDV. Seropositive moose were only found in areas where BVDV is regularly observed in cattle, indicating a possible transmission from cattle to moose. There was no correlation between moose or roe deer with disease symptoms resembling BVDV and positive titers to BVDV.
Evil Eyes: Infectious Keratoconjunctivitis in Mule Deer (Odocoileus hemionus)

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Infectious keratoconjunctivitis is relatively common in mule deer (Odocoileus hemionus) in the intermountain west of the United States. Cases of infectious keratoconjunctivitis (also called "pinkeye", "infectious panophthalmitis", and "vascular keratitis") have been reported for more than 60 years in Wyoming. The nature of the clinical signs in deer makes affected animals highly visible to the public. Sporadic cases occur, but of more concern to wildlife managers are local outbreaks involving multiple animals. These outbreaks are most common in the late fall and winter and frequently involve yearling bucks. Affected deer show a spectrum of clinical signs including epiphora, blepharospasm, and corneal opacity which may progress to corneal ulceration, rupture, and blindness. Lesions may be unilateral or bilateral.

Some deer recover from keratoconjunctivitis although those with severe lesions probably die. During the course of investigating cases of infectious keratoconjunctivitis we have identified a variety of potential etiologic agents including Moraxella bovis, M. ovis, Chlamydia psittaci, poxvirus, and more recently an uncharacterized herpesvirus. Overall population impacts appear to be minimal. The etiologies, epidemiology, and consequences of infectious keratoconjunctivitis remain relatively poorly understood.
Disease Interactions of Native Mara (*Dolichotis patagonum*) and Exotic Herbivores in the Patagonia Steppe

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The Patagonian Steppe comprises almost 500,000 km² of Southern Argentina, beginning at 39° S. This fragile arid and semiarid ecosystem was severely disturbed by the introduction of large numbers of livestock, domestic sheep (*Ovis aries*) and wild herbivores, such as the European hare (*Lepus europaeus*) at the turn of the XIX century. Consequently, a large proportion of the steppe ecoregion is affected by desertification, and all Patagonian native herbivores have experienced noticeable population reductions. Worldwide, the introduction of foreign species has been a critical factor in the decline of native species due to new pathogen-host relationships that are established during forced habitat sharing. Among affected Patagonia native herbivores are maras (*Dolichotis patagonum*), large rodents endemic of Argentina, that are monogamous and breed communally. Their historical distribution has been seriously limited and present populations are small and dispersed. To date, there is no reported information on the health status of free-ranging maras, nor about the disease relationships between maras, European hares and domestic sheep.

To look for possible causes limiting mara population growth, we conducted health evaluations during the austral spring of 2000. Our main objectives were: 1) to determine baseline hematological and biochemical parameters for maras; 2) to analyze the prevalence of infectious and parasitic diseases in mara populations; 3) to establish infectious and parasitic disease prevalence in European hare and sheep populations; and 4) to interpret the intra and inter-specific relationships of these native and exotic hosts with their pathogens. During October 2000, six adult maras (2 females and 4 males) were immobilized and sampled at Valdés Peninsula, in Argentine Patagonia. At the same field site, blood and fecal samples were collected from 15 sheep and 7 European hares respectively. Basic hematology was conducted in the field, while selected infectious disease serology was run at laboratories in Argentina and the US.

The results from this study have provided the first data on the health status of free-ranging maras and are currently being interpreted comparatively with those of sheep and hares. Identifying diseases present in these exotic herbivore populations will allow us to define disease interactions between species, evaluate the risks of disease transmission and design management strategies to lessen their ecological impact on native species and the steppe.
Avian Vacuolar Myelinopathy in Southeastern US: The Search for the Causative Agent

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Since its initial discovery in bald eagles and coots at DeGray Lake, Arkansas in 1994 and 1996 respectively, avian vacuolar myelinopathy (AVM) has been confirmed in eagles or coots on 11 lakes in 5 states (Arkansas, North Carolina, South Carolina, Georgia, and Texas), several waterfowl species, and most recently a great horned owl and a killdeer. The disease causes incoordination, motor dysfunction, and often death, and is characterized by a distinct microscopic lesion in the brain and spinal cord of affected birds. This neurologic lesion is suggestive of a toxic process, but unfortunately, the cause of AVM has not been identified, despite extensive diagnostic testing at several laboratories. To learn more about the epizootiology of AVM, in the winters of 1998, 1999, and 2000, we placed sentinel birds (coots and/or mallards) on Lake Surf near Vass, North Carolina, where the disease has recurred in coots every year since 1997. Sentinel birds were also placed in similar lakes nearby, where the disease has never been diagnosed. With this approach, we verified that the disease is site-specific, i.e. acquired at the location where sick and dead birds are found, and the onset is fairly rapid, e.g. as short as 5 days after placement in the lake in one case. We also attempted to determine the source of the agent for coots and waterfowl by feeding water, vegetation, sediment, and other materials collected from Lake Surf or other lakes during ongoing AVM outbreaks to mallard ducks, coots, or quail, but none of the experimental animals developed the characteristic lesion. Since it is has been speculated that eagles acquire AVM from eating affected birds, tissues from affected coots were fed to kestrels, ducklings, and mice in hopes of reproducing the disease, but so far, these attempts have also failed. Other experiments and analyses are still in progress. Although to date, there is no evidence that other vertebrates are affected, fish and mammals trapped at sites with ongoing AVM outbreaks are currently being evaluated for similar brain lesions. Despite our inability to identify the source or cause of this disease, additional work on AVM is being planned, including studies to characterize biogeochemical features of lakes with AVM outbreaks in comparison to similar lakes without outbreaks.
A Comparison of Endangered Southwestern Willow Flycatcher Blood Parasites: Arizona, USA and Chomes, Costa Rica

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The southwestern Willow Flycatcher (*Empidonax trailli extimus*) is a neotropical migrant songbird, presently listed as an endangered species in the United States. Over the past seven years, wild birds were mist-netted every summer on the breeding (Arizona, USA) and wintering (Chomes, Costa Rica) grounds. At each sampling location, 15-m mist-nets, of 5.6 mg/m (50 denier), 2-ply, 36-mm mesh, were erected within a bird's territory, utilizing playback recordings to capture individuals. Each captured bird was bled by clipping a toenail, with blood collected in a buffered solution for genetic studies. A thin blood smear was then taken, the slide fixed for 30 s in absolute methyl alcohol, and later stained with Geimsa. Birds were banded with unique combinations of metal color bands and released.

A comparison of hematozoans revealed a very low prevalence, and no significant difference between breeding and wintering Willow Flycatcher populations. We postulate that low hematozona prevalences in this species are a direct result of habitat affinities for wetlands, and the coevolutionary aspects of vector/host associations over time with wetland habitats. It thus appears that blood parasites have not been a significant factor in the reduction of this host species, and we must search elsewhere for factors that have contributed to southwestern Willow Flycatcher population declines.
Duck Plague Field and Vaccine Virus Carrier Waterfowl Identified by PCR in England, UK and Maryland, USA

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Duck plague (DP) is a herpesvirus disease of Anseriformes (ducks, geese and swans) that causes annual mortality in the United Kingdom and the United States. Waterfowl surviving field virus exposure become asymptomatic virus carriers and shedders. Previous studies in both countries indicated that DP carrier waterfowl could be identified by polymerase chain reaction (PCR), but the virus strain (field or vaccine) present could not be determined. Since the Holland modified live DP vaccine is used in the US, and to a limited extent in the UK, differentiation between the vaccine and field virus is of epizootiological importance. Known PCR positive samples and recently collected cloacal swabs were assayed with a new PCR that distinguishes between field and vaccine viral DNA to determine which strain of DP virus waterfowl were shedding. Stored DNA and cloacal samples collected from 102 ornamental and free-flying waterfowl in 1997 and 1998, respectively, at The Wildfowl & Wetlands Trust, UK were retested. The virus type was determined for eight samples (8%), including seven from different captive species and one from a free-flying mallard (Anas platyrhynchos). Three of seven captive birds were shedding field virus, three birds were shedding the vaccine virus and one bird had evidence for both field and vaccine virus shedding. The free-flying mallard was shedding the vaccine virus. Stored samples from 85 captive raised and released mallards and free-flying waterfowl collected at several sites in Maryland, USA during 1998 were retested and the virus type for 52 samples (61%) was determined. Seven of eight samples from free-flying mallards were shedding field virus and one was shedding the vaccine strain. Thirty-six of 44 samples (82%) from released mallards were shedding field virus and three samples (7%) were shedding vaccine virus. Five samples (11%) had evidence of both field and vaccine virus. In 2000, 29 of 90 (32%) Canada geese (Branta canadensis) sampled at the Blackwater National Wildlife Refuge, Maryland were found positive for DP virus. Field virus was detected in one Canada goose, vaccine virus in one goose, and three geese had evidence of both field and vaccine virus shedding. For some samples, virus or DNA was either lost during storage or PCR results were too faint to interpret. Study results provide the first evidence that DP vaccination can produce virus carrier waterfowl, that vaccine virus can be transmitted to non-vaccinated waterfowl, and vaccine shedding waterfowl can also become concurrent asymptomatic carriers of DP field virus. The possible role that DP vaccination may play in establishing or expanding the number of field virus carrier waterfowl and the possibility for vaccine virus reversion to virulence will be discussed.
Epidemiological and Clinical Study of an Outbreak of Avian Pox in Red-legged Partridges (*Alectoris rufa*) in Southern Spain

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In spring 2000, 48 adult wild red-legged partridges (*Alectoris rufa*, L.) were captured and radio-tagged in Medina Sidonia (Cádiz, southern Spain). From July to September, 72 chicks were also captured and radio-tagged, and 26 of them (36.1%) showed pox-like lesions. The October bag records showed 59.1% of young and 30.2% of adults with different degrees of pox-compatible lesions. The tagged birds are used to analyse the mortality of both age-classes during the pox-outbreak.

Cutaneous nodules were apparent on the dorsal part of the digits, the hocks and the eyelids. Histologically, hyperplasia of the epithelium with large eosinophilic intracytoplasmatic inclusions consistent with Bollinger bodies were evident. Contamination of the lesions with short rod-shaped or coccoid bacteria associated with ulceration and heterophil infiltration of the dermis and epidermis was frequent in lesions of digits.

On ultrastructural examination large ovoid virions containing dumbbell-shaped cores and outer envelopes were observed in the cytoplasmatic inclusions. Virus isolation was achieved on chicken embryo fibroblast (CEF) cultures and in embrionated eggs. To this point the isolated viruses have been identified as Poxvirus by biochemical properties and ultrastructural examination of cell culture supernatant. Further investigations are under way in order to further characterise the isolates and to determine whether they are specific of red-legged partridges.
Survey of Classical Swine Fever in the Northern French Vosges Wild Boar Population

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An outbreak of classical swine fever (CSF) has occurred in late 1991 in the wild boar (Sus scrofa) of the Vosges Mountains, north-eastern France. Considering the risk of heavy losses that could be generated in pig farming by the transmission of CSF from this wild reservoir, the outbreak has been monitored. At first, the monitoring was easy because viral carriage was associated with massive mortality and obvious lesions. Then, clinical signs and lesions have progressively disappeared. Fewer and fewer virus isolation were performed, and no viropositive animals have been found since late 1997. Consequently, investigations have been implemented in early 2000 aiming at answering three main questions (i) how has the outbreak spread in space and time since 1992?; (ii) is the outbreak still active and where?; iii) which classes of animals are the main virus carriers? The retrospective study covered 8 years of monitoring, from March 1992 to March 2000. Serological and virological test results from 14 000 hunter-killed and found dead wild boars were analysed. At the animal level, gender, age, sample origin (shot, found dead), location (community) and date were registered and studied as potential risk factors of the disease. Then statistical modelling of data has been used to map the evolution of the infection in space and time over the whole period 1992-2000.

The study showed: (i) a recession of the outbreak from 1993 to 2000, and a residual viral circulation within a little area at the German border on the 1999-2000 hunting season; (ii) a more frequent virus isolation in individuals younger than 12 months of age (OR = 2.9, confidence interval at risk 5% [1.63;5.17], p<0.002); (iii) a significantly higher seroprevalence in females than in males (OR = 1.42, confidence interval at risk 5% [1.22;1.65], p<0.001).

Regarding biological risk factors of the disease, the observed effect of age on viral carriage is reliable to literature, but the effect of gender has not been reported yet and its relation to wild boar ecology is to be clarified.

Concerning the methodology of the monitoring, it is suggested that:

(i) The very low viral circulation among wild boars does not enable the monitoring to be based on a virological survey but only on a serological one. Testing the 6-12 months aged individuals provides the more reliable indication of a viral circulation in the population.
(ii) In the future, coordination with Germany could be opportune to improve the monitoring of classical swine fever over the whole Vosges Mountains.
Reproductive Behaviour of Captive White-tailed Deer in Relation to Progesterone Level in Does, Mexico

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Little research has been conducted on reproductive aspects of white-tailed deer (*Odocoileus virginianus*) in México. This research analyzes the reproductive cycles of this species in Zacatecas (focusing Jalpa and Valparaíso) and San Luis Potosí (SLP), México. We analyzed the reproductive behavior of captive white-tailed deer from September 20th, 1998 until March 17th, 1999. We also collected twice monthly fecal samples from the females to monitor the luteum corpus. The progesterone concentrations in feces were determined using the enzyme-immunoassay technique (EIA). The aim of this study was to determine the beginning of the cycle on each herd and the relation among the progesterone levels and the reproductive behavior. The SLP white-tailed deer began its reproductive cycle from middle-November until the end of January. The behavior peak was during December. The progesterone levels in feces were higher during December, January and November (73%, 97% and 70% of the females herd respectively). In Zacatecas 50% of the females began the reproductive cycle by the end of September (Valparaíso herds). Then all females in the herd began the reproductive cycle early in December until the beginning of February, while in Jalpa began about mid-December, all the way down until mid-March; the peak of this behavior in both sites was observed during December. The progesterone levels in feces from the first herd reached their highest in December and January (100% of the herd's females respectively). The lower progesterone levels were found during September (100% of the herd's females). In Jalpa, the progesterone levels reached their highest during December and March (80% and 60% of the herd's females respectively) and went down during January and February in about 100% and 76.19% of the herd's females respectively. Using Spearman's Analyses we found significant correlation between progesterone levels in feces and the increasing females' activity versus aggressivity of the male (P>0.05). We found a significant difference (P>0.05) in the feces progesterone levels during the sampling months (ANOVA). We conclude that in SLP the reproductive cycle of the white-tailed deer herd begins in November prolonging it until January, having a peak in December. In Zacatecas the beginning of the reproductive cycle of the herds was in December and last longer into March. The progesterone levels in feces was evidence from ovulations and pregnancy during the study period.
Function of Scent-marking Behaviour in South African Oribis (*Ourebia ourebi*)

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Scent marking behaviour of oribi population in tropical regions was determined to be territorial behaviour. However, oribis show a high variation in the mating systems being polygamous in the Serengeti and monogamous in South Africa. Monogamy in South Africa was identified as a result of male’s mate guarding. I investigated the question of flexibility in scent marking behaviour and its function during a one year field observation in a South African population. South African oribis did not show any creation of the dung midden as observed in tropical populations. Females never showed aggressive behaviour, and males were only aggressive against other males when a rival came too close to its mate. Males showed distinguishably over marking behaviour of its mate’s dung with the preorbital gland secretion, both faecal and urine. This behaviour was proved by the result that 95% of the female’s defecation was over marked by its male when present. The male scratches the dung with its hoof to a midden and scent marks the surrounding stems with its preorbital glands. Here it might be likely that scent secretion of both sexes are distinguishable. The results confirm the assumption that oribis alternate between territorial and non-territorial behaviour, and they adjust their scent marking behaviour accordingly.
Impact and Control of Vector-Borne Diseases in the Livestock-Wildlife Interface of Transmara District, Kenya

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Transmara district in Kenya is located to the west of the expansive Maasai Mara Game Reserve and is important dry season grazing for wildlife. The district is inhabited mainly by Maasais whose main dominant economic activity is traditional livestock production. The area abounds with wildlife, which besides being an important range resource, act as reservoirs of livestock diseases and deplete pasture. The area's ecology is optimum for tsetse and ticks, and the area is endemic for several livestock diseases in particular, trypanosomosis and tick-borne diseases, which together with deteriorating pasture conditions constrain livestock production. In the past one and half decade, increased demographic pressure, changes in land tenure and introduction of other farming systems has put pressure on the pastoral way of managing resources. The result has been increased disease pressure and over utilization of range resources leading to reduction of pasture quality. To address the issue of trypanosomosis, community-based tsetse control trials have been carried out, though not successfully and apathy towards the control programmes has been noticed. This project aims to identify reasons for community apathy towards the programmes and identify constraints to adoption of tsetse control technologies. Preliminary findings will be presented and discussed.
BABESIA
Phylogenetic Relationships of Piroplasm Isolates from Humans and Animals Inferred from the 18s Nuclear Small Subunit RNA Gene

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Protozoan parasites within the family Babesiidae are one of the most common intraerythrocytic parasites of mammals. New species of these parasites infecting humans and wildlife have been characterized recently. A phylogenetic analysis of the nucleotide sequences of the 18S nss-rRNA gene was used to evaluate the evolutionary relationships of piroplasm isolates from animal and human cases of babesiosis worldwide. Some relationships of piroplasms previously considered ambiguous were resolved due to the inclusion in this analysis of a large number of piroplasm isolates from around the world and use of the entire 18S gene sequence in the alignment.

Results demonstrated that four major well-supported groups of Babesiidae exist: the “classic” Babesia (sensu stricto), the Theileria species, piroplasms from the western United States (the western group), and small babesial parasites from felines, rodents and humans (the B. microti group). The B. microti group was separate and sister to the monophyletic Babesia sensu stricto, the Theileria, and the western groups. The B. microti group contained B. microti and B. rodhaini, as well as recently characterized babesial isolates from African wild felids. Monophyly of the western group with the Theileria group was not supported in this analysis, unlike previous studies. The western group contained isolates from humans and wildlife from the western United States. Isolates from humans and wildlife from California were indistinguishable from each other, suggesting that large ungulates may serve as reservoirs for human piroplasm infection in California. The Theileria group contained theilerial isolates from large mammals from North American and Africa as well as a theilerial isolate from a North American woodrat (Neotoma fuscipes) and Cytauxzoon felis. The Babesia sensu stricto group contained babesial parasites already known to belong to that group including B. bigemina, B. divergens and B. canis, and, in addition, contained the recently genetically characterized B. gibsoni from canines. Results of this analysis have implications for future taxonomic considerations of the piroplasms.
A Genotypically Unique *Babesia gibsoni*-like Parasite Recovered from a Dog in Oklahoma

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Classification of intraerythrocytic protozoan parasites within the family Babesiidae has been and continues to be controversial. Comparison of the nucleotide sequences of the 18S nss-rRNA gene has been successfully used to evaluate the evolutionary relationships of several parasites within this family of Apicomplexan parasites. Recent identification of “small” *Babesia* parasites from wild and domestic mammalian hosts prompted our comparison of a newly isolated parasite from domestic dogs from Oklahoma with 27 other members of the family Babesiidae, originating from various locations worldwide. We performed a phylogenetic analysis using a genetic distance algorithm on an alignment of the 18S nss-rRNA gene, consisting of 2,141 base pairs. Results indicated that the small canine babesial isolate from Oklahoma is identical to small canine babesial isolates from four other states in the eastern U.S., as well as to a small canine babesial isolate from Okinawa, Japan. In view of genetic identity with previously described isolates from Asia, these isolates were considered to be *B. gibsoni*. These *B. gibsoni* isolates were most closely related to, but distinct from, *B. canis*. It appears that there are three genetically distinct small canine babesial isolates, each belonging in a separate phylogenetic clade. *Babesia gibsoni* appears in the *Babesia sensu stricto* clade. A small canine piroplasm from California is a part of a clade containing recently described isolates from humans and wildlife in the western United States, and a newly described isolate from a dog from Spain is part of the clade containing *B. microti*. 
The Age-related Innate Immune Response in Calves to *Babesia bovis* Involves IL-12 Induction and IL-10 Modulation

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There is a strong innate immunity in calves to infection with *Babesia bovis*. IL-12 and IL-10 have been shown *in vitro* to be important immunoregulatory cytokines influencing the fate of T-cells during *B. bovis* antigen priming. Here we demonstrate *in vivo* that the protective innate response in young naive calves to infection with virulent *B. bovis* involves the early appearance of IL-12 and IFN-γ transcripts, and a nitric oxide burst in the spleen. In contrast, IL-12 and IFN-γ mRNA expression in the spleens of adult cattle that succumbed to the infection, was delayed and depressed and occurred within the context of IL-10 expression. Also in contrast with calves, there was no detectable antibody response before death in adults. A vigorous CD8+ T-cell expansion occurred in the spleen of both calves and adults. These results demonstrate the importance of a type-1 immune response to initial *B. bovis* infection, and suggest that IL-12 may be an important adjuvant with immunization.
Sequestration of Parasitised Erythrocytes in Canine Babesiosis

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Sequestration of parasitised erythrocytes in the microvasculature of the brain is well described in bovine cerebral babesiosis and cerebral malaria. Evidence for sequestration in canine babesiosis (Babesia canis) is inconclusive in the literature: in a few reported cases there is some suggestion of sequestration while in others, evidence is lacking.

In this study, the frequency of parasitised erythrocytes in central thin-film blood smears and in capillaries of brain crush smears were compared in fatal cases of canine babesiosis. Samples were taken at necropsy as soon after death as possible. Central smears were made from either caudal vena caval or heart blood, and brain smears from the endomarginal gyrus, of each case. An index of sequestration (SI) was calculated for each case, based on a proportional difference in the frequency of parasitised erythrocytes between brain and central smears. SI is independent of total parasite load and reflects only the relative frequency of red cell infection. Cases were retrospectively defined as cerebral or non-cerebral on the basis of clinical and/or necropsy findings.

SI ranged from low to high, apparently independently of whether cerebral babesiosis as defined clinically or at necropsy, was present or not. The relationship between sequestration and cerebral babesiosis could not be clearly defined. SI could be high (indicative of sequestration) at both low and high parasitaemias.

Sequestration of parasitised erythrocytes in the microvasculature of cattle infected with Babesia bovis or humans infected with Plasmodium falciparum, is clearly associated with cerebral disease. In Babesia canis infection in dogs in southern Africa, cerebral disease is not as clearly associated with sequestration. It was concluded that sequestration is a dynamic phenomenon in canine babesiosis and the population dynamics of babesial parasites during the course of clinical infection requires further investigation.
Nitric Oxide Metabolites in Naturally Occurring Canine Babesiosis

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Babesiosis, caused by the virulent haemoproteozoa parasite Babesia canis rossi, is an important disease of dogs in South Africa. The role of nitric oxide in canine babesiosis has not previously been investigated. The nitric oxide metabolites, nitrate and nitrite (collectively termed reactive nitrogen intermediates or RNI) were measured in admission sera from dogs in a babesiosis-endemic area. Five groups were prospectively studied: mild uncomplicated babesiosis (n=9), babesiosis with severe anaemia (n=10) and complicated babesiosis (n=11), and two groups of healthy aparasitaemic dogs: endemic controls from the study area (n=10) and experimental dogs kept in tick-free conditions (n=10). Four measures of RNI were analysed: (i) Serum RNI; (ii) Serum RNI/creatinine ratio; (iii) Fractional clearance of RNI (FCRNI); and (iv) Fractional excretion of RNI (FERNI).

Marked elevations of serum RNI occurred in only three dogs, all in the severe uncomplicated group. The highest concentration (196.5µmol/l) was in a dog that died, but concentrations in the four other dogs that died were unremarkable (0, 0.5, 4.3 and 13.1µmol/l). Age, appetite and free serum haemoglobin were significant covariates for RNI measures. There were no significant differences between the babesiosis groups for serum RNI, and adjustment for serum creatinine had only minor effects on the results. All babesiosis groups had significantly higher serum RNI and RNI/creatinine than the tick-free control group, but did not differ from the endemic controls except for the severe uncomplicated group. FCRNI and FERNI were significantly lower in the complicated group than all other groups, except for the tick-free control group, which had similar FERNI. Measures of RNI did not reflect disease severity in this group of dogs, possibly due to the effect of repeated exposure to parasites on nitric oxide production. The results indicate that, in an endemic area, RNI is unlikely to be a useful indicator of severity or outcome in canine babesiosis.
Serum Tumour Necrosis Factor in Naturally Occurring Canine Babesiosis

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Canine babesiosis, caused by the virulent haemoproteozoan parasite *Babesia canis rossi*, has been compared to human malaria, where an excessive cytokine-mediated inflammatory response has been implicated in the complicated forms of the disease. The purpose of this study was to determine whether tumour necrosis factor (TNF) plays a role in the pathophysiology of complicated canine babesiosis. Serum TNF levels were measured in sera obtained at admission from dogs in a babesiosis-endemic area. Five groups were prospectively studied: mild uncomplicated babesiosis (n=10), severe uncomplicated babesiosis (severe anaemia) (n=9) and complicated babesiosis (n=12), and two groups of healthy a-parasitaemic dogs: endemic controls from the study area (n=10) and experimental dogs kept in tick-free conditions (n=10). TNF was assayed using the WEHI-164 bioassay with recombinant canine-TNF used as a positive control.

The results showed a statistically significant difference in TNF concentrations between the different groups of sick dogs, with a general trend of increasing mean log(TNF) with increasing severity of disease. More specifically there was a difference between the severe uncomplicated and complicated babesiosis groups and the tick-free control group (p = 0.045), thus indicating that the dogs with severe and complicated babesiosis had higher serum TNF concentrations than non-infected dogs. The results also indicated that TNF may be associated with severity of disease, with more severely affected dogs having higher TNF values. Of special significance was the finding of very high TNF values in 3 dogs with hypoglycaemia (mean 15.03 ng/ml vs 2.32 ng/ml for other babesiosis dogs without hypoglycaemia). Hypoglycaemia has not been previously recorded in dogs with babesiosis, but is a common clinical feature in pregnant women and children with malaria.

When parasitaemia and TNF were correlated within individual infected groups, there was no statistically significant relationship. However, when the analysis was performed by pooling all cases and treating them as a single group, there was a highly significant positive correlation between parasitaemia and serum TNF concentrations.
Feline Babesiosis in South Africa: An Update

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A number of piroplasms, large and small, have been described from felids. *Babesia felis*, a small piroplasm originally described from wild cats *Felis sylvestris* in the Sudan, was subsequently incriminated as causing clinical disease in domestic cats. Although babesiosis in domestic cats has been reported sporadically from various countries, as a significant feline disease it appears to be a distinctly South African phenomenon. A series of papers was published on the disease 20 years ago; a recent upsurge in interest has resulted in a number of new investigations being published. These findings are reported upon.

Although feline babesiosis is assumed to be a tick-borne infection, the vector has not been identified. Apart from an inland focus, feline babesiosis is reported regularly only from coastal regions. The strong tendency for occurrence during summer in KwaZulu-Natal becomes less clear further south- and westward; it is virtually aseasonal in the Western Cape. This may be related to rainfall patterns.

Typical disease-causing *Babesia felis*, as well as piroplasm isolates from lions *Panthera leo* and a caracal *Felis caracal*, have recently been sequenced. The lion isolate was distinct from true *B. felis* and has been described as a new species; the two caracal isolates were very similar to *B. felis*. The four felid isolates are related to *Babesia rodhaini* and *Babesia microti* from rodents.

A conservative approach suggests that the *B. microti* clade, including the felid isolates, is ancestral to the other piroplasms.

The clinical manifestation of babesiosis in cats differs from that in other domestic animals in that it is not associated with pyrexia. Unlike babesiosis in dogs, feline babesiosis tends to be a chronic, low-grade disease. The most frequently reported complaints by owners are anorexia and lethargy. The main clinical findings are anaemia, depression and occasionally icterus. Concurrent infections (e.g. *Haemobartonella felis*, FeLV, FIV) are potential complications and may contribute to the clinical picture. Laboratory findings commonly include regenerative anaemia, elevation of alanine transaminase (but not alkaline phosphatase) and total bilirubin concentrations and a variety of electrolyte disturbances. Secondary immune-mediated haemolytic anaemia can be seen occasionally.

Various drugs and drug combinations have been screened for activity against *B. felis*. Drugs effective against other *Babesia* species give variable and questionable results. The drug of choice is primaquine phosphate, which effects clinical cure but does not sterilise the infection. Repeated or chronic therapy may be required. Doxycycline may add potential benefits in treatment of this disease.
STVM STUDENT PAPERS
The Dynamics of Maternal Antibodies to Hemorrhagic Disease Viruses (Reoviridae: orbivirus) in White-tailed Deer at an Enzootic Site

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Virus isolations and antibodies to viruses in both the epizootic hemorrhagic disease virus (EHDV) and bluetongue virus (BTV) serogroups have been reported from white-tailed deer (Odocoileus virginianus) in Texas (USA), but there are few reports of hemorrhagic disease (HD) in these populations. It has been hypothesized, but never proven, that this represents a case of enzootic stability where deer are protected from clinical HD by maternal antibodies, innate resistance, or both. In June and July of 2000, twelve native Texas white-tailed deer fawns were moved by two weeks of age from an outdoor white-tailed deer research facility at the Kerr Wildlife Management Area (Donnie E. Harmel White-tailed Deer Research Facility, Texas, USA) to an indoor facility at the University of Georgia. On July 17, 2000, serum neutralizing antibodies to one or more of five HD viruses (EHDV-1, EHDV-2, BTV-10, BTV-11, & BTV-17) were detected in 100% of the fawns. Serum neutralizing maternal antibodies to HD viruses were measured weekly through November 13, 2000, to track maternal antibody decline. On October 10, 2000 40 fawns that had remained outdoors in Texas were bled and had serum neutralizing antibody titers that suggested recent HD virus exposure. Additionally, EHDV-1 or 2 was isolated from 18% (7/40) of these fawns. Despite this, clinical hemorrhagic disease was not seen in these fawns. The (1) disappearance of maternal antibodies by October when HD epizootics and mortality are known to occur in other locations, (2) detection of antibodies and virus confirming active circulation of EHDV-1 and 2, and (3) the lack of clinical HD in these fawns support the concept that the maternal antibody component of the enzootic stability hypothesis is operative, but does not prevent infection during the animals first year or exclude the possibility of innate immunity.
The Expression of RoTat 1.2 Variable Antigen Type in Trypanosoma evansi and T. equiperdum


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The Variable Antigen Type (VAT) RoTat 1.2 has been cloned from a T. evansi strain, isolated in 1982 from a water buffalo in Indonesia. All T. evansi isolates hitherto tested express this VAT. Its variable surface glycoprotein (VSG) is currently used as antigen in several antibody detection tests for T. evansi infection in buffalo, bovine, camel and Equidae. The VSG gene coding RoTat 1.2 was cloned, sequenced and expressed in insect cells by the ILRI group recently.

Within a study on differential diagnosis of T. equiperdum and T. evansi in horses, we investigated serological evidence for the expression of RoTat 1.2 in eleven T. evansi and six T. equiperdum populations originating from Asia, Africa and America.

Cryostabilate populations were expanded in mice. Mice blood at first peak parasitaemia was injected into New Zealand white rabbits which all developed a detectable parasitaemia and remained infected throughout the experiment. Pre-infection sera and sera of day 7, 14, 25, 35 post-infection were analyzed for the presence of RoTat 1.2 specific antibodies in immune trypanolysis, ELISA/T. evansi and CATT/T. evansi.

Within the duration of the experiment (up to 35 days post infection), all rabbits infected with T. evansi became positive in the three serological tests. Five out of six rabbits infected with T. equiperdum, also became positive in the three tests. Only one T. equiperdum strain (the OVI strain isolated in South Africa) did not induce anti-RoTat 1.2 antibody production and thus might not contain or express the RoTat 1.2 VAT gene.

Our preliminary conclusion is that T. equiperdum can express VSGs containing epitopes serologically similar to those in the T. evansi RoTat 1.2 VAT with the consequence that antibody detection tests based on its VSG cannot reliably distinguish between both taxa. However, molecular analysis currently carried out, might provide evidence that the putative T. equiperdum strains which express RoTat 1.2 are actually T. evansi.
IFN$_y$ as an Indicator of Immunization in Goats Vaccinated with a Killed *Cowdria ruminantium* Vaccine

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Cowdria-induced production of IFN$_y$ was measured by ELISA in supernatants of PBMC and whole blood cultures on a weekly basis during the course of vaccination with killed organisms emulsified in ISA50. As expected, 4 days PBMC cultures gave higher IFN$_y$ titers in comparison to 24-h whole blood assays. However, the use of PBMC is limited due to high backgrounds (response in the absence of Cowdria antigens) especially after booster injections. On the other hand, the 24-h whole blood method shows very little background and is more rapid and easy to perform. Upon challenge, all (3/3) vaccinated animals with the lowest IFN$_y$ response died of peracute cowdriosis. On the other hand, only one out of three animals showing high IFN$_y$ responses to vaccination died but with a delay of 4 days in comparison to naive controls. Thus, there seems to be a threshold level of IFN$_y$ below which the probability for vaccinated animals to survive a lethal challenge is very low.

During challenge, a much lower but still physiologically meaningful production of IFN$_y$ was detected using the 24-h whole blood assay on day five after infection in animals controlling the infection. In contrast IFN$_y$ production was absent or negligible in naive and vaccinated animals that died within 8 to 10 days after infection.

Our data confirm and extend other studies where 81 % (13/16) cattle and 100 % sheep (n=3) immunized by the same method and which produced IFN$_y$ in response to Cowdria antigens survived subsequent challenge (C. Kelly and K. Sumption, CTVM, UK, personal communication). Although these results need to be validated on a larger number of animals they strongly suggest that IFN$_y$ is a useful indicator of protective immunity in animals immunized with killed Cowdria.
Challenges of Regulating the Importation of Reptiles into the United States

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The United States is one of the world's major importers and exporters of live reptiles, accounting for over 80 percent of the total world trade. The volume of legal importations alone is enormous. For example, since 1995, it is estimated that close to 12 million reptiles have been imported into the United States. The magnitude of these imports increases the risk of inadvertently introducing harmful arthropods, especially ticks, that could become a serious problem for the livestock industry in the United States. It has been recognized that for a number of years ticks and other ectoparasites have been found on animals and animal products imported into the United States. In 1995, a study conducted at the Miami International Airport (MIA) by U.S. Department of Agriculture (USDA) personnel revealed that close to 30 percent of reptile imports were infested with ticks. Since it is known that 107 species of ticks have been reported as infesting reptiles, the results of the MIA study were not that surprising. However, in 1997, a potential vector of heartwater, *Amblyomma marmoreum*, was found infesting leopard tortoises, *Geochelone pardalis*, on a premises in south central Florida. This and subsequent findings of *A. marmoreum* in addition to a detailed examination of USDA tick identification reports from 1995 to 1999, led to the USDA promulgating regulations that prohibited the importation and interstate movement of three species of African tortoises, *G. pardalis*, *G. sulcata*, and *Kinixys belliana*.

Veterinary Services (VS), part of the USDA's Animal and Plant Health Inspection Service (APHIS), is charged with enforcing laws and developing and enforcing regulations designed to protect United States animal agriculture. In addition, APHIS, VS has developed a comprehensive system to minimize the risk of introducing pests or diseases of livestock into the United States. However, most of the regulations and the system developed for the safe introduction of animals deal primarily with livestock or ruminant wildlife. Thus, the USDA was faced with a number of challenges when faced with regulating the importation and/or interstate movement of reptiles, including jurisdictional issues, rapid development of effective prevention and mitigation measures, treatment methodologies, and dealing with a non-traditional industry.
Sustainability of Dairy Heifer Calf Production in Smallholder Dairy Farms in the High Potential Areas of Kenya

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The sources of the major constraints and factors associated with growth and mean daily weight gains were examined in a prospective observational study involving 5 cohorts of female calves. The study was conducted in one of the high potential and highland areas of the central province of Kenya. A total of 225 calves on 188 smallholder dairy farms were observed over a period of one-and-a-half-years. The calves were distributed in five agro-ecological zone (AEZ)-grazing strata namely; Upper Midlands (UM) 1 zero-grazing, UM 1 open-grazing, UM 2, UM 4 zero-grazing and UM 4 open-grazing. The calves were visited within the first two weeks of life and thereafter at biweekly intervals up to the age of approximately 6 months. Calves were recruited within the first year of study that was conducted between March 1995 and August 1996. During each visit, the calves were weighed and data on calf management practices on the farm during the visit such as feeding, disease control and housing were recorded. Other events such as morbidity and mortality between or during the visits were also recorded.

The overall mean daily weight gains were: 0.25 kgs and 0.26 kgs in UM 1 zero-grazing and UM 1 open-grazing respectively, 0.29 kgs in UM 2, and 0.26 kgs and 0.24 kgs in UM 4 zero-grazing and UM 4 open-grazing respectively. The initial mean daily weight gains declined by over 50% after the third month expect in UM 4-grazing strata where overall means were the lowest. Given the above poor mean daily weight gains (0.26kg), the heifer calves be served at 30 months (300kg) and first calving be at 44 months.

Calf means daily weight gains were mainly associated with AEZ-grazing strata and calf level factors that included feeding of milk, concentrate feeds and minerals, breed of calf, calf sickness (crude and specific), and interaction between calf age and AEZ-grazing strata. Poor calf feeding presented a continuous and negative effect on calf growth and was the main cause of poor growth whereas calf sickness exerted a temporal effect on poor calf growth at the height of illness with calves compensating for the lost growth. The study showed that optimum and sustainable growth of dairy heifer calves requires that much attention be paid to feeding.
Major Outer Membrane Proteins of *Cowdria ruminantium* Encoded by a Multigene Family

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Heartwater is a disease of domestic and wild ruminants caused by *Cowdria ruminantium*. This organism is taxonomically and phylogenetically closely related to the human and animal pathogens, *Ehrlichia chaffeensis* and *E. canis*. Immune responses of infected animals and humans have been reported to be directed against variable outer membrane proteins of *Cowdria* and both *Ehrlichia* species that are encoded by polymorphic multigene families. In *Cowdria*, two immunodominant major proteins has been identified from sequence data, namely major antigenic protein 1 (MAP1) and ORF2 (open reading frame 2) as well as the partial sequence of ORF3. The aim of the present study was to identify additional members of the outer membrane family in the *Cowdria* genome. A large insert (10-15kb) *Cowdria* lambda GEMII library was screened with a *map1* probe. A clone that hybridized with the *map1* probe was selected from the lambda GEMII library and amplified using long template PCR. The resulting PCR product of 12kb was partially digested with *Alu1* and *Sau3A* and cloned into pUC18. Sequencing analyses demonstrated that five open reading frames, including *map1* are located in tandem in the genome. The upstream members, *orf2* and *orf3* are more closely related to *p28-11* and *p28-2* genes of *E. chaffeensis* and *E. canis*, respectively than to *map1* of *C. ruminantium*. A fourth open reading frame (*orf4*) was found downstream of *map1*. The ORF4 sequence was related to the *p28-20* gene of *E. chaffeensis*. A large open reading frame of 2.4 kb at the 3’ end of the 12kb clone is homologous to SecA, which is part of a multisubunit membrane-bound enzyme responsible for translocation of proteins. The sequence data in this study supports other findings that outer membrane proteins are located in tandem and are encoded by a polymorphic multigene family. Further investigation regarding the variation within each gene (*map1, orf2, orf3* and *orf4*) amongst different *C. ruminantium* strains will be reported.
Increasing Risks of Introduction of Heartwater onto the American Mainland Associated with Animal Movements

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Recent findings have demonstrated that three separate types of animal movements pose serious risks for the introduction of heartwater (\textit{Cowdria ruminantium} infection) onto the American mainland. Firstly, the largely unregulated international trade in live reptiles has allowed three vectors of heartwater (the ticks \textit{Amblyomma marmoreum}, \textit{A. sparsum}, and \textit{A. variegatum}) to be introduced into Florida on reptiles imported from Africa, with at least one species (\textit{A. marmoreum}) establishing breeding colonies in the state. Examination of some of these imported exotic ticks by PCR assay demonstrated that some \textit{A. sparsum} ticks collected from one shipment of leopard tortoises (\textit{Geochelone pardalis}) imported from Zambia were infected with \textit{C. ruminantium}. Secondly, recent studies have shown that eight species of wild African ungulates can become subclinical carriers of \textit{C. ruminantium} infection. Some of these species, as well as other wild game species known to be susceptible to heartwater, continue to be imported into the United States after screening only with serological tests of poor sensitivity and specificity. Thirdly, despite the continuing spread of the tick \textit{A. variegatum} in the eastern Caribbean, cattle are still being exported from at least one \textit{A. variegatum}-infested island in the Caribbean to both the United States and South America where indigenous vectors of heartwater (the ticks \textit{A. maculatum} and \textit{A. cajennense}) are present on cattle. Measures to minimize these risks of introduction of heartwater are being developed at the University of Florida and will be discussed.
Effect of Sheep and Goats Grazing on Vegetation Dynamic in Low-ground Pasture

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Sahelian rangeland are dominated by annual plants with short growing cycle. Intensive exploitation of this ecosystem by animals is known to have negative impact on the vegetation in long term and floristic composition may be modified. Only few studies have been done to determine grazing effect of different animal species.

This study has been done to estimate the impact of sheep and goats grazing in low-ground pasture during four consecutive years (1996-97, 1997-98, 1998-99). Two groups of 22 growing sheep and 22 growing goats have been introduced in four plots of 1 ha each from which two have been used in cool dry season and the others two in hot dry season. The number of animals per group has been estimated at 2 times the currying capacity of this type of pasture. The method of quadrat points has been used for observations on floristic composition after the end of the rainy season.

It results changes in floristic composition in all plots; and the number of species has increased from 20 to 27, from 1996 to 1999 in plots used by goats against 23 to 26 in sheep’s plots. In addition, the effect of sheep has been revealed by an important number of species with variables specifics frequencies. For goats, it have been observed a great number of new species appeared (12 for goat and 10 for sheep) and species in progression. The pasture value of all plots has also improved with an advantage for sheep effect (44% to 49% with a maximum of 56.8% in 1997, against 46% to 49% for goats).

Vegetation dynamic shown by specifics frequencies distribution revealed a decrease in disequilibria aspects of plants communities grazed; the distribution curve of frequencies showing 5 modes in 1996 in sheep plot, was bimodal in 1999.

The effect of exploitation during cool dry season and hot dry season has increased the pasture value to 10% in cool dry season and 4% in hot dry season, but the last has favour the expansion of many species and apparition of new species.

It is conclude that impact of sheep’s grazing is similar to exploitation during cool dry season and the effect of goats give results close to the effect of hot dry season exploitation.
MARINE
Development of Tools to Monitor Health of Coral Reefs

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The status of coral reefs globally has received increasing attention. This is particularly so in areas where reefs have been adversely impacted by climatic fluctuations and human activity. There appears to be increasing incidence of unusual mortality event of hard corals, particularly in the Carribean where several species of corals have succumbed to unknown syndromes. In the Pacific, coral reefs have not suffered as much, nevertheless, severe bleaching events have occurred in some areas such as Palau. Given that the Pacific contains the majority of the coral reef biodiversity in US administered territories, there is a clear need to develop capabilities to systematically investigate causes of mortality and morbidity in these organisms so that we can be positioned to respond to potential problems. As such, we are attempting to adapt biomedical tools used to investigate disease in vertebrates to assess health of coral reef organisms. This poses particular challenges that, if overcome, may allow veterinary medicine to play a more significant role in elucidating cause of disease in coral reefs and in assessing marine ecosystem health.
Emerging Morbillivirus Infections of Marine Mammals: Diagnostic Approaches

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Two challenges face diagnosticians attempting to detect viral infections in marine mammal specimens. First, standard immunological reagents such as anti-species conjugates are unavailable for most marine mammal species, rendering definitive serological diagnosis difficult. Second, marine mammal species can be infected by multiple closely related but distinct morbilliviruses, making definitive virus identification unattainable by classical diagnostic methods. This study presents data on two diagnostic approaches that can alleviate these diagnostic difficulties.

Viruses in the Morbillivirus genus now known to infect marine mammals include: canine distemper (CDV) in seals and polar bears; phocine distemper virus (PDV) in seals and sea lions; dolphin morbillivirus (DMV) and porpoise morbillivirus (PMV). The morbilliviruses are closely related antigenically and genetically. The DMV and PMV are so indistinguishable that they are now collectively called cetacean morbillivirus (CMV). Panels of monoclonal antibodies (MAbs) generated against the marine morbilliviruses were screened for their ability to compete with serum for binding to antigen. Two MAbs specific for CDV and CDV/PDV were selected for use in competitive ELISA (c-ELISA) for antibody detection. Compared to the serum neutralization test (SNT) as the gold standard, the overall relative sensitivity and specificity of the c-ELISA were 94.9% and 97.7%, respectively. The c-ELISA is thus a suitable replacement of the SNT. In comparison to standard indirect ELISA, the c-ELISA is faster, cheaper, and obviates the need for specific marine mammal conjugates, thus allowing sera from various species to be tested using a single anti-mouse antibody conjugate.

For virus detection in animal tissues, the gold standard remains virus culture. However, because of long turn around time, expense, and non-availability of adequate cell culture facilities in many laboratories, nucleic acid detection methods are attractive. We have developed and applied a rapid two-step method for diagnosis of all three marine mammal morbilliviruses (CDV, CMV and PDV) by combining reverse transcriptase PCR (RT-PCR) and restriction fragment length polymorphism (RFLP) analysis. First, a morbillivirus consensus RT-PCR was used to amplify RNA from suspect tissues, resulting in a 78 bp fragment. Second, three restriction endonucleases (RE) were used to digest the RT-PCR product prior to gel analysis. Following RT-PCR, all positive samples for any morbillivirus yielded the 78 bp fragment. However, because each RE can cut only the fragment from a specific virus, the length of fragments on the gel following RE treatment clearly differentiates among CDV, PDV and CMV. This approach obviates the need for three separate RT-PCRs, thus saving time and money.
Seroprevalence of *Toxoplasma gondii* in Canadian Phocids - An Example of Pathogen Pollution?

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*Toxoplasma gondii*, a coccidian parasite, has been reported in marine mammals for almost 50 years. Initially it was reported from marine mammals either born in captivity, captured from the wild or undergoing rehabilitation and it was believed that somehow they were exposed to oocysts of *T. gondii* in food or water contaminated by infected cat faeces. Lately, there are increasing reports of *T. gondii* in histologic sections of tissue from dead stranded marine mammals, or in live stranded marine mammals with clinical toxoplasmosis. Marine mammals reported infected with *T. gondii* include otariids, phocids, West Indian manatee, sea otter, dolphins and beluga. To date reports of *T. gondii* in marine mammals are primarily from North America but there are a few reports from Europe. A serological study of over 600 marine mammals (harp, ringed and hooded seals and minke whale) from the North-east Atlantic Ocean did not detect any seropositive cases.

The present serological study examined over 300 phocids from the east coast of Canada including harp, hooded, grey and harbour seals. Sera from seals were obtained from hunted seals or live-captured seals. Using a direct modified agglutination test 327 sera were diluted 1:25, 1:50, 1:500 and tested for antibodies to *T. gondii*. Titers greater than 1:25 were considered evidence of exposure. Grey seals (11/122 or 9%), harbour seal (3/34 or 9%), and hooded seals (1/59 or 2%) were seropositive with titers of 1:25 and 1:50. Harp seals were seronegative.

How marine mammals are exposed to or acquire infections of *T. gondii* is presently unknown. It has been suggested that human sewage containing oocysts from cats or natural runoff of oocysts in the terrestrial environment enters marine waters, contaminating marine organisms. The presence of *T. gondii* in marine mammals may be an example of pathogen pollution whereby human activities contaminate or facilitate the contamination of the marine environment with viruses, bacteria or parasites not endemic to this environment. Non-felid hosts such as seals and whales appear to act as intermediate hosts, and it could be that the life cycle of *T. gondii* in the marine environment differs from that in the terrestrial environment. Further research on the pathogenesis of *T. gondii* in marine mammals and its transmission in the marine environment is needed to understand fully the significance of this parasite in marine mammals.
Update on the Southern Sea Otter (Enhydra lutris nereis): Are They Trying to Tell Us Something about Marine Ecosystem Health?

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The southern sea otter (Enhydra lutris nereis) is listed as “Threatened” under the Endangered Species Act (ESA) and is a “keystone species”, one which strongly influences the abundance and diversity of the other species within its kelp forest ecosystem, primarily by preying upon sea urchins which eat the kelp stipe and holdfast and which can reduce a kelp forest to an urchin barren. Sea otters are very susceptible to marine pollutants such as petroleum, which may be directly toxic and/or alter their fur’s insulating properties. Sea otters are also an excellent bioindicator species. They eat approximately 25% of their body weight per day in shellfish and other invertebrates and can concentrate and integrate chemical contaminants. In addition they appear to be susceptible to a number of diseases and parasites that may have anthropogenic origins, and shellfish may serve as an intermediary for some of these infections. Many of the shellfish otters eat are also harvested for human food. In their role as a bioindicator, sea otter health has implications for human health, economic sustainability of shellfisheries, as well as overall marine ecosystem health. The recent southern sea otter decline has been viewed with some alarm by conservationists and indeed, recovery seems a long way off. High mortality rather than depressed recruitment appears to underlie the decline. A good deal of debate has centered on the role of infectious diseases and parasites, exposure to contaminants, nutrition and prey availability, net and pot fishery interactions, and other sources of mortality. We will provide an update on investigations into major classes of mortality, various types of pollutants and some specific organisms causing southern sea otter mortality, and discuss their implications for marine ecosystem health and sustainability.
IMMOBILIZATION
Chemical Immobilization of Free Ranging South American Fur Seals (*Arctocephalus australis*)

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Safe chemical immobilization of free ranging pinnipeds is often challenging. Primary concerns include the proximity of the aquatic environment, relative high incidence of anesthetic related complications and the potential for harm from other individuals in the group. This abstract describes the successful use of chemical immobilization of South American fur seals (*Arctocephalus australis*) in a rookery setting. (Punta San Juan, Nasca Department, Peru).

Immobilizations were done in conjunction with population health surveys and ecological studies that are part of a long-term conservation effort in this area. While these studies included infants and adults of both sexes, only the adult male fur seals required chemical restraint for examination. The project was conducted during November when large numbers of South American fur seals gather to give birth and breed for the next year. Dominant males for each harem group were identified for immobilization using the following criteria: safe access to the animal once anesthetized and confirming that the animal would not abandon its territory if disturbed. Animals were darted in the lateral pelvic region using 3-ml plastic darts with 1.5 x 38 mm collared needles.

Forty-five male fur seals were immobilized using Telazol (equal parts tiletamine hydrochloride and zolazepam). Animals that maintained enough mobility to prohibit safe sample collection were further supplemented with intramuscular injections of either ketamine hydrochloride and/or midazolam. Flumazenil, which is a benzodiazepine antagonist, was used to reverse zolazepam in the fur seals. In 19 immobilizations, atropine was combined with Telazol to prevent excessive vagal bradycardia. Dosage ranges for Telazol were from 1.0 – 1.8 mg/kg, IM. The mean dosage was 1.43 mg/kg, with a dosage of 1.6mg/kg providing the best anesthetic level for sample collection. Maximum effect was usually obtained in 10 – 12 minutes.

Respiratory depression is a common anesthetic problem in pinniped anesthesia. We found that partial benzodiazepine reversal with with low dose flumazenil (0.05 – 1.0mg) was effective in aiding cases with respiratory depression. Complete reversal of benzodiazepines can be accomplished with 1mg of flumazenil per 20 mg of zolazepam. This greatly decreased the anesthetic recovery time and allowed the animal to resume its position in their previously occupied territory. The tiletamine portion of Telazol takes approximately 30 minutes to become partially metabolized. Reversal prior to this time with flumazenil can cause poor anesthetic recoveries. One animal was reversed at 15 minutes from darting and had a very stormy recovery with severe ataxia. This animal attempted to resume his position on his previous territory and was severely traumatized by other males in the area.

Telazol proved to be a safe and effective anesthetic agent for field immobilization of fur seals. Flumazenil was useful in reversing the zolazepam, increasing anesthetic recovery times and allowing the males to re-establish their harem and territory in a timely fashion. Since flumazenil is only an antagonist for benzodiazepines, it should not be utilized until the effects of tiletamine have ceased.

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Risk Assessment of Etorphine Immobilization in Moose: A Review of 1,347 Captures

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An initial dose of 7.5-9.0 mg etorphine per animal was used in 1,347 immobilizations of 1,149 free-ranging moose (Alces alces) in Norway, 1984-2000. The animals were captured as part of ongoing ecological studies or for management purposes. All captures were done in winter (November-April). The animals were darted from a helicopter using standard remote drug delivery systems. Diprenorphine at 12 mg per 9 mg etorphine was used for reversal.

Immobilized animals were grouped according to age: 391 calves (animals < 1 year) and 956 adults (animals > 1 year). Seven animals (0.5%) died or were euthanized during the capture process, five calves (1.3%) and two adult cows (0.2%). Four of the calves died due to respiratory arrest shortly after darting. Necropsies showed poor body condition in all these animals. The fifth calf developed bilateral hind leg paresis and was euthanized. Necropsy showed traumatic spinal lesions, caused by dart impact in the lumbar region, osteoporosis, cachexia and verminous pneumonia. One of the cows was hit high in the neck and died within two minutes of darting. This cow was pregnant and in good body condition. Necropsy showed possible intravascular drug injection and shock development. The other cow drowned during the induction phase when it tried to cross a deep river.

Follow-up radio telemetry was done for at least 1,119 of the animals (97.4%). No mortalities caused by the capture (residual drug effects, stress, myopathy or predation) were seen.

We conclude that etorphine (9 mg/ml) is a very safe and effective drug for immobilization of free-ranging moose from helicopter in winter. A review of the literature showed that mortality rates routinely range from 2 to 18% during capture and translocation of free-ranging moose in North America. By using immobilizing drugs with proven safety and by refining the capture methods, we believe that such mortalities can be significantly reduced. In Sweden, a mortality rate of 1.7% was reported in 663 immobilizations of free-ranging moose using a combination of etorphine and xylazine. In our opinion, etorphine should be considered the drug of choice for moose immobilization.
Using A3080, Medetomidine and Ketamine for Anesthesia of Problem Free-ranging Africa Hoofstock

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The art and science of anesthesia/immobilization of free ranging hoofstock has developed rapidly in the last decade due to the availability of newer drugs and improved anesthesia protocols. However, there remain a number of species with a history of anesthesia problems, including unacceptable morbidity and/or mortality. This paper will address how two newer anesthetic agents, A3080 and medetomidine, sometimes combined with ketamine, were evaluated in selected problem hoofstock.

A3080 (Thiafentanyl oxalate) is a synthesized potent fentanyl derivative with rapid pronounced opiate agonist activity. It has a very short induction time and duration of action and is completely reversed by naltrexone. Medetomidine is a potent selective and highly specific agonist at both the pre and postsynaptic alpha2 -adrenoreceptor. It binding affinity is 10 X that of xylazine with potent sedative and analgesic and anxiolytic properties and produces anesthesia at high dosages. The effects of medetomidine are reversed with atipamezole.

This project developed anesthesia protocols with appropriate physiological monitoring for the following species:

1) Giraffe using medetomidine and ketamine,
2) Impala using medetomidine and ketamine or A3080 and ketamine,
3) Roan Antelope, Gemsbok and Nyala using A3080, medetomidine and ketamine,

The depth and quality of anesthesia appear to be better than with previously used combinations and may provide greater safety for both the animals and their human handlers. Immobilization was very rapid and reversible. Although the cost of these new drug combinations may be greater than traditional drugs used for these species, reduced induction times, reduced helicopter rotor time, increased daily capture rates, and/or reduced mortality may offset the greater drug costs.
SESSION 6

TUBERCULOSIS GENERAL SESSION
Bovine Tuberculosis in Michigan Wildlife and Livestock

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Since 1994, the state of Michigan has recognized a problem with bovine tuberculosis (TB), caused by *Mycobacterium bovis*, in wild white-tailed deer from an twelve county area in northeastern Lower Michigan. A total of 65,000 free-ranging deer have been tested and 340 have been found to be positive for M. bovis. The disease has been found in other wildlife species, including 1 wapiti, 14 coyotes, 2 raccoons, 2 opossums, 4 bobcats, 4 black bears, and 2 red foxes, and, in 1998, in domestic cattle, where to date 13 beef cattle and 2 dairy cattle herds have been diagnosed with bovine tuberculosis. Recognizing the potential economic and public health consequences of bovine tuberculosis to the state, the governor has issued orders to eradicate *M. bovis* from the state's deer population. Unfortunately, the situation is unique in that there have never been reports of self-sustaining bovine TB in a wild, free-ranging cervid population in North America. There are no existing control programs for TB in wild deer, and there is much about TB in deer that is currently unknown. Scientists, biologists, epidemiologists, and veterinarians that have studied this situation have concluded that the most logical theory is that high deer densities and the focal concentration caused by baiting (the practice of hunting deer over feed) and feeding are the factors most likely responsible for the establishment of self-sustaining TB in free-ranging Michigan deer. By congregating deer into close contact with each other repeatedly, baiting and feeding provide ideal conditions for the transmission of TB via both inhalation of infectious aerosols and ingestion of TB contaminated feed. The two main strategies for eradicating TB from free-ranging Michigan deer are to minimize concentrations of deer by eliminating baiting and feeding, and to reduce deer numbers through hunting to the biological carrying capacity. Baiting and feeding have been banned since 1998 in counties where the disease has been found. In addition, the deer herd has been reduced by 50% in the endemic area with the use of unlimited antlerless permits. The measures of apparent TB prevalence have decreased by half since 1997, providing hopeful preliminary evidence that eradication strategies are succeeding.
The Spectrum of Pathology from *M. bovis* Infection in European Badgers (*Meles meles*) and its Implications for Disease Control

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European badgers (*Meles meles*) are a reservoir of bovine tuberculosis in parts of the United Kingdom and Ireland. Epidemiological and experimental evidence suggests that badgers are a source of *M. bovis* infection in cattle. That cattle tuberculosis has proved impossible to eradicate from areas of endemic badger infection supports this view.

Tuberculosis in the badger is essentially a pulmonary disease, and the lungs and respiratory lymph nodes are the most frequent sites of lesion development. Pulmonary lesions range from scarce foci barely discernible macroscopically (1-2mm diam.), through larger single or multiple granulomas, to extensive tuberculous consolidation. Renal lesions are also frequent, particularly in disseminated tuberculosis. Probably as much as 20% of badger tuberculosis is contracted via bite wounds inflicted by tuberculous badgers, often resulting in acute fatal miliary tuberculosis. Advanced end-stage disease results in involvement of respiratory, gastrointestinal and urinary tracts, bite wound tuberculous lesions often develop into chronic fistulas or open wounds. All these sites of infection are potential routes for the shedding of *M. bovis*. Lesion involvement at mucosal sites, with potential for shedding, occurs at even earlier stages of disease.

Gross tuberculous lesions are present in only a small proportion of the infected individuals whilst the majority carry clinically inapparent infections termed "No visible lesion (NVL) tuberculosis". Survey of tuberculosis in some badger populations in the UK revealed an incidence of NVL tuberculosis in 80% of animals. These are only identified by culture of *M. bovis* from their lymph nodes.

Histopathology shows that badgers develop typical epithelioid cell granulomas that are highly cellular and proliferative. There is minimal necrosis, calcification and fibrosis, with variable amounts of lymphoid cells, few neutrophils and no giant cells. Tuberculous lesions are often revealed in the tonsils by histopathological examination. Small, solid epithelioid cell granulomas observed histopathologically in lymph nodes and spleen are rarely detectable grossly. Microscopic lesions are also found in NVL badgers, typically as small, healed necrocalcified foci in the lungs; some of them still harbouring acid fast bacilli.

The wide spectrum of badger tuberculosis pathology is reflected in a variable clinical presentation of the disease and an even wider range of immunological reactivity. A live ELISA-based test for the detection of antibodies to a serodominant *M. bovis* antigen only detected 40% of infected badgers, these being the ones with more severe disease.

It is hoped that a better understanding of the spectrum of badger tuberculosis pathology will help in the evaluation of risk factors for the transmission of tuberculosis, help establish immunological correlates of disease status, and inform the development of a vaccine for badger tuberculosis.
Scientific Tools as a Practical Aid in the Management of Tuberculosis in African Wildlife

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Tuberculosis caused by *Mycobacterium bovis* is on the increase, especially in those areas where there is interfacing between wild and domestic animals, furthermore the alarming presence of tuberculosis in the Kruger National Park (KNP) and a number of other nature reserves in South Africa is cause for great concern. Therefore an effective monitoring practice is of paramount importance. DNA Fingerprinting is proving to be a powerful and practical epidemiological tool in the study of tuberculosis in African wildlife. Data was obtained from different species of domestic and wild animals throughout South Africa and other countries in the region. Using DNA Fingerprinting for analysis we were able to identify the source of infection in the KNP and determine possible modes of transmission. Furthermore we were able to differentiate, as well as show relationships between strains from various locations and species of animals. Results showed the dominant strain in the KNP to have come exclusively from a single herd of cattle adjacent to the park. This strain has so far been identified in all infected species within the KNP indicating unique properties with regard to transmissibility and virulence. The establishment of a proposed Transfrontier Conservation Area in the not so distant future commands the availability of these epidemiological data, which will enable us to identify foreign strains and be of assistance in the design of adequate control measures.
The Hook Lake Wood Bison Recovery Project: Preliminary Results of an Attempt to Eradicate Bovine Tuberculosis and Brucellosis from Free-ranging Bison in Northern Canada

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Bovine tuberculosis (Mycobacterium bovis) and brucellosis (Brucella abortus) were introduced to Wood Buffalo National Park with the translocation of over 6000 plains bison (Bison bison) from Wainwright, Alberta in the 1920s. Both diseases remain enzootic to free-ranging bison herds in the Greater Wood Buffalo National Park Ecoregion. The Hook Lake Wood Bison Recovery Project (HLWBRP) is a conservation project run cooperatively between the Deninu Kue’ First Nation, Fort Resolution Aboriginal Wildlife Harvesters’ Committee, and the Government of the Northwest Territories, Canada. The main objective is to establish a healthy captive herd of wood bison from a wild population infected with bovine tuberculosis and brucellosis, and use the captive herd to re-establish a disease-free wild population. The HLWBRP’s novel approach to disease eradication involves the capture, isolation, and prophylactic treatment of neonatal calves from a known disease-exposed population of wild wood bison. Captured calves were paired and hand-raised in isolation at a captive breeding facility, treated for brucellosis and tuberculosis using antibiotics, and subjected to an intensive testing protocol that includes bi-annual whole herd tests and post-calving brucellosis testing. The project has been successful thus far. This captive herd represents more genetic diversity than two previous attempts to conserve wood bison from WBNP, and there have been no confirmed clinical cases or serological evidence of tuberculosis or brucellosis in the captive herd, suggesting that disease-free status is an achievable goal. We provide a synopsis of the northern bison disease issue and report on the progress of this pilot project. We also discuss the benefits and necessities of working within a co-management framework to achieve meaningful progress on a contentious wildlife management issue.

WDA Contributed Paper: Relevant to Session III (Sustainability): Papers on ecologically, economically & socially sustainable animal husbandry & wildlife mgmt. systems & practices worldwide.
Wildlife and Agricultural Policy as it Relates to Eradication of Bovine Tuberculosis and Brucellosis in Free-ranging Bison of Northern Canada

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In northern Canada, free-ranging bison (Bison bison) herds in the greater Wood Buffalo National Park region are infected with bovine tuberculosis (Mycobacterium bovis) and brucellosis (Brucella abortus). Nonetheless, those wild diseased bison herds represent a source of genetic diversity that is vital to both conservation and long-term commercial value of the northern wood bison (B. b. athabascae). Current efforts of the Hook Lake Wood Bison Recovery Project (HLWBRP) to salvage genetic diversity from a diseased wild herd and establish a disease-free founder herd, represent important steps to securing additional disease-free stock for conservation purposes. The primary long-term option for dispersal of surplus bison is reintroduction back into the wild, but contingencies may include translocation to other jurisdictions as part of the National Wood Bison Recovery Plan. Clearly, these options will be affected by wildlife and livestock policy within Canada and abroad. Although disease is often an important limiting factor in population dynamics of wild ungulates, it is largely the threat (both real and perceived) that sylvatic disease reservoirs pose to the health status of commercial livestock or game farm industry, which has led government agencies to establish policy and legislation for disease management (i.e., eradication), trade, and movement of ungulates. These policies are largely borrowed from the existing regulatory framework for domestic livestock and do not address cases in which wild free-ranging ungulate populations are infected with federally or internationally 'reportable' diseases. In this paper we summarize previous attempts of eradicating a reportable disease(s) in free-ranging wild ungulates, with an emphasis on bovine tuberculosis and brucellosis. We also review international and national policy on reportable diseases that occur in domestic livestock and free-ranging ungulates as it pertains to defining, establishing, and maintaining disease-free status. Finally, we argue that the decision-making framework to define disease-free status is a critical step to the HLWBRP and to conservation of other diseased ungulate populations because it outlines the criteria by which health status and project success will be measured. This framework needs to be science-based and acceptable to conservationists, agriculturists and animal health regulators alike.

WDA Contributed Paper: Relevant to Session VIII (What makes sense?) Papers should look into the future & address policy, veterinary health & management issues for captive &/or free-ranging wildlife, livestock, &/or poultry.
The Zoonotic Importance of *Mycobacterium tuberculosis*: A Potential Threat to Free-ranging Wildlife Populations?

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Expansion of ecotourism based industries, changes in land use practices, and escalating competition for resources has increased contact between free ranging wildlife and humans. The threat of disease transmission from wild animals to humans is well understood and considerable focus has been placed on the development of appropriate zoonotic public health programs. In contrast, this paper describes the first report of an outbreak of *Mycobacterium tuberculosis*, a human pathogen, among free ranging wildlife species: banded mongoose (*Mungos mungo*) in Botswana and meerkat (*Suricata suricata*) in South Africa. Spatial, and temporal features of the outbreaks, possible sources of infection and implications to ecotourism and wildlife health are discussed.
Mycobacterial Isolations in Captive Elephants in the United States

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The interest in mycobacteriosis in elephants has been increasing over the past several years in the United States (US). Between 1994 and 2000, Mycobacterium tuberculosis was isolated from 21 captive elephants from 5 different parts of the United States. Mycobacterium bovis has been isolated from one captive elephant from another part of the US in 2000.

In November of 1997, new guidelines were implemented by the USDA Animal Care staff in response to an outbreak of tuberculosis at an Illinois facility where 1 elephant died in 1994 and 2 elephants died in 1996. A fourth living elephant was culture positive in October of 1996. Twenty-two animal handlers were screened for tuberculosis and eleven had positive reactions to intradermal injection with purified protein derivative. One animal handler was smear-negative, culture-positive with active tuberculosis. DNA fingerprint comparison by IS6110 and TBN12 typing showed that the isolates from the four elephants and the handler were the same strain of M. tuberculosis. This event resulted in increased testing of all captive elephants owned by licensed exhibitors in the United States.

Over 4000 trunk washes or swabs were submitted to the National Veterinary Services Laboratories, Ames IA, from 1997 to present. The most common mycobacterial species other than M. tuberculosis isolated from trunk washes or swabs were M. avium, M. terrae, M. gordonae, M. scrofulaceum, M. ulcerans, M. fortuitum, M. gastri, M. chitae, M. phlei, M. xenopi, M. szulgai, Runyon Group IV and M. bovis.

DNA fingerprinting has identified 6 different strains of M. tuberculosis from elephants located in 5 different areas of the country. Nucleic acid amplification tests (Gen Probe®-Amplified™ Mycobacterium Tuberculosis Direct (MTD) Test) have identified 10 positive elephants where M. tuberculosis was isolated, 15 positive elephants where mycobacteria were not isolated and 1 positive elephant where M. bovis was isolated.

The current USDA Animal Care regulations (January 2000) require annual culture of all captive elephants by licensed exhibitors in an effort to prevent future zoonotic outbreaks like the one which occurred in Illinois in 1996. These guidelines can be found at www.phis.usda.gov/ac/ElephTBGuidelines2000. Treatment and management guidelines are listed in these guidelines. Currently, there are 3 elephants undergoing treatment that are resistant to Isoniazid (0.1 and 0.2 mcg/ml) and Streptomycin (2 mcg/ml). Each of the elephants had been on treatment previously. Treatment guidelines are still under evaluation especially the dosage of drugs and the length of time which they are given.
Bovine Tuberculosis in Michigan Wildlife

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In 1994, a hunter in southwestern Alpena County, Michigan, shot a white-tail deer with bovine tuberculosis (TB). Since the fall of 1995 through September, 2000, wildlife surveys have been conducted in the surrounding area and over 39,734 white-tail deer, 641 elk, and 743 carnivore have been examined for bovine TB in the laboratory. From 1996 through 1999, a total of 49,356 deer carcasses have been examined for TB lesions at deer check stations. During these surveys, 285 deer, 8 coyotes, 2 raccoons, 1 black bear, 1 red fox, 2 opossums and 2 bobcats have been confirmed to be infected with \textit{Mycobacterium bovis} by the National Veterinary Services Laboratories (NVSL), Ames IA and/or the Michigan Department of Community Health (MDCH), Lansing MI. All of the infected deer, coyotes, raccoons, black bear, opossums and bobcats have come from 11 northeastern Lower Peninsula counties in Michigan (Alpena, Montmorency, Alcona, Oscoda, Otesgo, Presque Isle, Osceola, Mecosta, Antrim, Crawford, and Iosco). As of September, 2000, bovine TB has been confirmed in 23 cows from 10 premises in 4 of these counties. Thus far there have been 2 dairy herds and 8 beef herds diagnosed with bovine TB. Positive animals have been found in Alpena County (2), Alcona County (12), Presque Isle County (8) and in Montmorency County (1). No human cases of \textit{M. bovis} have been traced to the TB-infected deer. Restriction fragment length polymorphism analysis was performed by the MDCH and National Animal Disease Center (NADC). They have concluded that the index deer and subsequent deer, carnivore, and bovine isolates have identical IS6110 and TBN12 patterns, indicating that the same strain of \textit{M. bovis} is involved in the outbreak in cattle and wildlife. The most likely source of the infection in the carnivore and omnivore population was through the consumption of tuberculous white-tailed deer. The white-tailed deer in Michigan is recognized as a reservoir host of bovine TB. Once the disease is eliminated from the deer, the disease should die out in the carnivorous and omnivorous species. As long as bovine TB exists in the wild, free-ranging deer population, there will be some risk to local wildlife species that feed on bovine TB infected deer carcasses or gut piles, therefore continued surveillance will be necessary.
SESSION 7

COMBINED GENERAL SCIENTIFIC SESSION
Balancing International Animal Movement Restrictions with Animal Health Status and Veterinary Infrastructure

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A country’s animal health import requirements should be in accord with the health status of its animal population and not excessive to its needs. In its Animal Health Code, Aquatic Animal Health Code, and Manual of Standards for Diagnostic Tests and Vaccines, the OIE provides guidance for health certification and the testing of specimens for the majority of the diseases generally considered to be important in the trade of animals and animal products. The import requirements established by a country may be more exigent if the national veterinary services has determined that the country’s animal health status is significantly at risk, such as may be the case for economically important transmissible animal diseases under active eradication. This determination should be based on an appropriate description of risk (risk analysis). The OIE publications make available basic methodology for risk analysis and the evaluation of veterinary services.

Countries have occasionally established zoosanitary requirements that are more restrictive than are apparently necessary, basing these on the premise that it is better to protect their animal health status and not invite unwanted animal diseases. Disadvantages to requiring excessive measures include the animals may be unnecessarily naïve to disease agents that are present in the destination country, the country’s veterinary services will likely be challenged to present appropriate justification for the restrictions, and an excessive number of animals and countries may be disqualified from international commerce. Excessive measures may also invite a less honest health certification process.

Exporting countries are obliged to meet the import requirements of the destination country and in any case should guarantee a basic standard for export animal health certification. Some examples of appropriate movement control requirements will be given as well as instances of less defensible requirements and some apparent reasons for these.
Host preference of ticks is still the subject of debate, but most tick species can be broadly classified as host-specialists or generalists. However, even generalist ticks do not usually infest host species according to their availability in a given environment, and it has been suggested that habitat use by hosts is a major determinant of tick burdens. The knowledge of such infestation patterns is important for the control of the vectors of some major stock diseases in Africa, particularly in the context of mixed game/cattle ranching.

In a ranch of Zimbabwe (9,400 ha), we monitored the number of adult ticks found on cattle and wild ungulates. Tick species encountered included mainly *Rhipicephalus appendiculatus*, *R. zambeziensis*, *R. evertsi* and *Hyalomma marginatum rufipes*, which are considered as generalist species, and *Boophilus decoloratus*, usually found on large ungulates. Tick burdens were measured weekly during one year on 12 heifers of an experimental herd (no acaricide used during the survey), and on several wild ungulates (including impala *Aepyceros melampus*, wildebeest *Connochaetes taurinus*, greater kudu *Tragelaphus strepsiceros*, eland *Taurotragus oryx* and zebra *Equus burchellii*) occasionally shot for meat during 3 hunting seasons. Although the results were variable according to the tick species and the seasons considered, adult ticks were usually not evenly distributed between wild hosts, which corresponds to observations made by several authors in similar conditions. For instance, eland and zebra harboured 10 times more adults of *R.evertsi* than impala and kudu, with wildebeest having an intermediate level of infestation. Habitat use by ungulates had been previously monitored by road transect at the scale of the ranch, but the species most infested by ticks do not have remarkable habitat preference. What is more, an indirect survey of ungulates abundance (255 sites sampled for tracks and signs during one seasonal cycle) revealed that 60% of the sites sampled had been recently visited by two or more species of ungulates. In an attempt to relate habitat use during one day with the number of adult ticks collected by a host, we followed the heifers of the experimental herd during a full day of grazing. Between February 1997 and 1998, 130 recording sessions (for a total of 940 hours) were performed, during which the behaviour and the GPS position of the target animal was recorded at regular interval. No correlation was found between the number of ticks collected and the distance travelled in each vegetation type (calculated using a GIS) or the time spent in each vegetation type. The possible role of other behavioural and physiological parameters is discussed and the results are compared with those found for other tick-host associations studied.
Domestic Sheep but not Alpine Chamois is a Reservoir of *Mycoplasma conjunctivae* in Switzerland

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Infectious keratoconjunctivitis (IKC) is a contagious disease of ruminants, localised in the eyes and characterised by inflammation of the conjunctiva and cornea. *Mycoplasma conjunctivae* is the major, if not the only, cause of IKC in domestic sheep and in wild Caprinae species such as Alpine chamois (*Rupicapra rupicapra rupicapra*) and Alpine ibex (*Capra ibex ibex*) in Switzerland. In wild animals, IKC outbreaks can lead to mortality rates close to 30%.

Using an indirect ELISA we assessed level of infection in the Swiss domestic sheep herds as well as in Alpine chamois populations. Our results show that *M. conjunctivae*-infection is endemic and self-maintained in the domestic sheep population in Switzerland. In contrast, seroprevalence in Alpine chamois populations was very low even in areas with recent IKC outbreaks. This indicates limited transmission of *M. conjunctivae* between different chamois subpopulations usually separated by rivers. We conclude that mountain pasture-reared sheep are a disease reservoir in which the wild animals themselves are only an epidemiological cul-de-sac. Further investigations are necessary to assess risk factors for infection maintenance and to develop tools for the control of *M. conjunctivae* infections in domestic sheep.
Aujeszky Disease in a Wild Boar Population from Central Spain

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During the 1999/2000 and 2000/2001 hunting seasons, a serological survey for Aujeszky disease virus (ADV) antibodies was carried out in wild boar populations from central Spain. These preliminary studies revealed a high diffusion of the virus, with one third of the boars showing seropositivity in an ELISA test.

In one fenced 1,000 ha hunting area it was possible to estimate the spring population (n=150 boar) and the population structure. Any dead animal was reported by the game rangers and (if fresh enough) necropsied. In that context, we describe the epidemiology of the infection in a monitored population suffering several outbreaks of fatal ADV.

Clinical, anatomo-pathological and immunological findings due to fatal ADV are described. Clinical findings were ataxia and fever. Lesional findings consisted of congestion and haemorrhages, especially affecting the brain and lymphoid tissues. Indirect immuno-fluorescence revealed the virus presence. Clinical cases of ADV were diagnosed mainly in 6 to 7 month old individuals. Also, stress factors such as concomitant mycobacterial infections and chronic diseases were found in individuals suffering fatal ADV.

The results are discussed in the context of previous studies on Aujeszky´s disease in Europe and the current changes in wild boar management.
Public Health Considerations of Human Consumption of Wild Game

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Wild game or bush meat was the original meat protein source for the human species and continues to contribute significant amounts of protein to human populations in poorer countries or poorer areas of more developed countries. Though it may be unnecessary for survival, hunting continues to be a popular hobby activity in many societies. In addition, the export of wild game from developing countries provides income for local individuals while satisfying desires for unique cuisines in other locales.

Though long practiced, consumption of game is not without public health implications. Handling and/or consumption of wild game may result in illness or disease caused by parasites, viruses, bacterial or novel agents such as prions.

Current work in infectious and zoonotic diseases have increased our understanding of the array of diseases which can affect humans through meat consumption. In addition, disease agents may frequently pass between wild and domestic species. Not all zoonotic diseases are of tropical origin, but many emerging or previously unknown diseases are from these less well studied areas.

The world-wide emphasis on food safety has focussed primarily on the safety of domestically produced food. However, it is prudent to develop more sophisticated understanding of the safety of all foods, and particularly those not under domestic production. This presentation reviews the safety of food of animal origin as it pertains to wild game.
Serosurvey for Selected Infectious Disease Agents in Free-ranging Gray Brocket Deer (Mazama gouazoubira) and Domestic Cattle and Goats in the Gran Chaco, Bolivia

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The Gran Chaco is a region that covers approximately 1 million sq. km of land in Bolivia, Argentina, Paraguay, and Brazil. It is the largest surviving tropical dry forest in the Americas, a biome more threatened than tropical moist forests. The Kaa-lya del Gran Chaco National Park, a 3.44 million hectare protected area within the Bolivian Chaco, was established in 1995 to help preserve this region. The diversity of large (> 1 kg) mammals in this park rivals that of Latin America's most biologically diverse rainforest protected areas. Although hunting is illegal within the core area Kaa-lya Park, the protected area includes Integrated Management Areas where wildlife can be harvested in a "sustainable" way by local people, as well as a buffer zone comprising the Izoceno indigenous territory of 1.9 million hectares where community wildlife management plans are being developed and implemented. Mammals hunted in both the management area and the buffer zone include armadillo sp., collared peccary (Tayassu tajacu), white-lipped peccary (T. pecari) South American tapir (Tapirus terrestris) and gray brocket deer (Mazama gouazoubira).

Many Izoceno Indian villages surround the core area Kaa-lya Park. A number of domestic animals including cattle, goat, chicken, dogs, and pigs live near and within these villages. Additionally, a number of commercial cattle ranches are in close proximity to the park borders. Health care for domestic animals in the villages and on most cattle ranches is minimal and vaccination is rarely performed on any of these species. Therefore, the transmission of infectious diseases between the domestic and wild animals may be a concern for the long-term conservation of wildlife within the region.

The objective of our study was to determine the seroprevalence of selected infectious agents in gray brocket deer and to compare these findings with the prevalence of these agents in domestic cattle and goats in the region. In 1999 and 2000, blood and feces were collected and necropsies were performed on 17 brocket deer. In 2000, blood was collected from 20 cattle and blood was collected and complete necropsies were performed on 18 domestic goats. This is the first study on the health status of free-ranging gray brocket deer. It is also the first known comparative study of wildlife and domestic ungulate species in the Gran Chaco, Bolivia. The serologic results from this study will be presented with emphasis on the possible wildlife/domestic livestock disease interface implications.
Equine Infectious Anemia in Free Roaming Horses in the Uintah Basin Region of Utah, USA

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Equine Infectious Anemia (EIA) was discovered in 1997 affecting free ranging horses in the Uintah Basin region of Utah, U.S.A. A Native American tribe made an effort to remove free ranging horses from the range in preference to native wildlife. The index animal was detected when the tribe pressured one of their members to remove his privately owned horses that were in excess of his grazing permit. The State Veterinarian was not able to require testing of the horses while on the reservation because of tribal claims of sovereign nation status, but did act to require testing of all horses leaving the reservation. This testing revealed an infection rate of approximately 16% (n = 47).

As a result, the tribe requested the help of the State Veterinarian in testing the remaining free ranging horses owned by them. Two separate herds, dispersed at opposite ends of a 40km stream corridor, were gathered and tested. Only two (2) infected animals were found in the herd (n = 260) at the upper end of the drainage. The other herd (n = 42), located in close proximity to the index herd, showed a 57% (n = 24) infection rate, revealing the presence of an endemic area.

Cooperation in gathering and testing of other free ranging horses under jurisdiction of the U.S. Department of the Interior, Bureau of Land Management (BLM) was sought. Four separate herds were gathered and tested. A 50% (n = 53) infection rate was found in the herd (n = 107) in proximity to the endemic area. The other 3 herds (n = 321) located outside the stream corridor revealed only a single positive animal. The affected BLM herd was confined and re-tested after 45 days and one additional positive animal was found. After a 16 month interval, spanning two vector seasons, the affected herd was subsequently gathered and re-tested in 1999 and 15% (n = 33) of the herd (n = 216) were found positive. Additionally, in a survey requested by the private sector in April 2000, only 1 of 558 horses was found to be infected. Epidemiology was conducted and the case was not felt to be directly related to the problem in free ranging animals.

The eradication effort was unique in scope and participation. Over 1350 free roaming horses were removed from the range following testing and adoption, or through slaughter for meat. Approximately 125 were returned to the range. Native Americans, federal authorities, and private individuals claimed jurisdiction over various portions of the herds, which were allowed to freely commingling. The BLM horses are subject to the Wild Horse and Burro Act. Multiple animal protection organizations offered frequent legal challenges to administrative decisions concerning their handling and disposition. The Utah State Veterinarian was faced with bringing these distinct and extremely varied stakeholders together in an effort to control and eradicate this disease.
Buffalo in Botswana: Political Football, Disease Threat or a Rural Asset?

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Botswana has an enviable reputation on the African continent for political stability and has vast wilderness areas that support significant biodiversity. Diamonds earn major foreign currency but both tourism and agriculture, make a significant contribution.

It is the conflict between livestock, people and wildlife in Botswana that paints the only negative picture of an otherwise progressive desert and delta country. In terms of agriculture and livestock, Botswana has a programme for disease prevention that includes disease surveillance and monitoring, movement controls, quarantine and vaccination. Movement control is achieved through the use of veterinary cordon fences. The Government and Department of Agriculture have been severely criticised by conservationists for its fencing policy which was first implemented in the 1950's to separate wildlife, in particular the African buffalo (*Syncerus caffer*), from livestock. The primary reason for the erection of the fences was the perceived threat from wildlife of Foot-and-Mouth disease (FMD) transmission to livestock. When the fences were planned and then erected no consideration was made for wildlife, their migration routes, feeding and watering habits. In more recent years, Botswana has erected more fences in response to a severe outbreak of Contagious Bovine Pleuropneumonia (CBPP).

Buffalo are perceived as a major disease threat to cattle in Botswana in terms of FMD. They are restricted to disease control zones north of 20°S, namely the Vaccinated Zone and Cattle Free Zone. Major populations are located within the buffalo fence that separates the Okavango Delta and other wildlife areas from areas to the south. In 1998, an isolated population of buffalo (n=75) was located in the vaccinated zone within the Makgadikgadi Pans National Park. This population appeared to have been isolated for at least 15-30 years from the major buffalo populations to the north. The Wildlife Unit of the Department of Animal Health and Production (DAHP), in collaboration with the Botswana Wildlife Department and South African National Parks Kimberley based Game Capture Unit, captured and sampled 35 buffalo in July 1998. Due to political pressure, the unwillingness of DAHP to recognise neither the potential for disease free animals nor wait for test results, these animals were moved back into the Okavango Delta. Subsequently, FMD serology indicated an unusual disease profile suggesting the potential of developing a FMD free herd. Further political pressure, intransigence and a lack of appreciation of the potential value of these buffalo to the country and the local rural community, resulted in the remaining 40 animals being captured and removed to the Delta.

This case study emphasises the difficulties in gaining acceptance by the authorities of the value of a wildlife resource when livestock predominates, both politically and culturally. In a country where the gap between the rich and poor is widening rapidly, it is a tragedy that the rural communities around the Makgadikgadi Pans National Park were not able to benefit from a potentially valuable natural resource that posed no disease threat.
SESSION 8

WHAT MAKES SENSE?
Relating National Veterinary Services to the Country’s Livestock Industry: Case Studies from Four Countries - Great Britain, Botswana, Peru and Vietnam

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At the end of the Second World War, the British Government of the time decided that it was essential for Britain to become self-sufficient in food. In consequence there was a large investment in services to agriculture and in particular many new veterinary investigation centres were opened to help farmers produce more animal products. The upsurge in world trade led the Government of Mrs Thatcher to decide that livestock was just another commodity and so there has been a massive scaling down of money available to assist the livestock farmer.

For Botswana the livestock industry is vital to the well-being of the people: successive Governments have continued to invest in veterinary services. As a consequence Botswana has one of the best and most efficient Veterinary Services in Africa.

By contrast, the livestock industry in Perú has an insignificant effect on the gross national product. The fibre exports from camelids are just a small international market, while the dairy industry is unable to provide sufficient milk for the nation. Partly as a result of this the Peruvian Government invests very little in the livestock industry or the veterinary services that support it.

Vietnam is in a transitional stage: there is a large but as yet unorganised livestock industry with a mass of smallholder farmers. The Government has made a large investment in people in the Department of Animal but without a concomitant investment in equipment and training. If the industry is to develop it will require much more investment from the government.

These countries will be discussed in more detail and an attempt will be made to show how by relating the services to the livestock industry, governments can improve services and at the same time cut the costs.
Health Monitoring and Conservation of Wildlife in Sweden and Northern Europe

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Monitoring of wildlife diseases started in Scandinavia as sporadic post mortem examinations in the early 20th-century. In 1945 a monitoring program for wildlife health, sponsored by the Swedish Hunters Association, the Swedish Environmental Protection Agency and the Swedish government, was initiated in Sweden. The program is today an integrated part of the environmental monitoring programs in Sweden. On an annual basis 1000 – 3000 animals are investigated and the total material today comprises more than 80 000 recorded investigations. Similar programs are today in place in Denmark, Finland and Norway. However, no comparable program exists in other Northern European countries.

The program has lead to discoveries of new diseases in many mammals and birds and to the demonstration of several environmental pollutants, such as mercury and cadmium, in wildlife. The success of the program is due to several factors such as: A rich wildlife with economically important game species such as moose (Alces alces), roe deer (Capreolus capreolus), game birds like capercaillie (Tetrao urogallus) and willow grouse (Lagopus lagopus); a good cooperation with hunter and conservation organizations, a stable financial support from government funds, a cool climate allowing material of good quality and a very successful relationship with media with frequent reports supporting the monitoring program.

The program has set a good basis for our knowledge about the kind of diseases and pollutants that are found in wildlife in Scandinavia and the relative importance of these different factors. Current work also includes more directed investigations on different specific pathogens and pollutants, as well as investigations in single animal species.
Wildlife and Pastoral Society – Shifting Paradigms in Disease Control

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The dramatic changes in the human and animal population in Africa over the last century demand the re-examination of priorities and policies set during Colonial times. The introduction of developed medical and other human technologies into the continent has contributed to a burgeoning of population and a rapid unsustainable increase in the utilisation of resources. This in turn has led to the destruction of flora and fauna on an unprecedented scale with little real improvement in the human condition. One factor in this has been the increase in livestock in line with human demographic growth, as it is a traditional livelihood of the African peoples. This situation has led to a destructive cycle of degradation in many areas and fertile ground for disease, especially with traditional pastoral systems with a close physical association between people, livestock and wild animals. Viral and other pathogens benefit hugely from the dynamic state created by animal migration but to some extent the livestock and certainly wildlife show considerable tolerance to this but the consequence has been collapse of the export trade.

In many countries the sanitary status is worse than ever before, with a virtual collapse of the state veterinary services. Even in this state they continue to follow traditional policies of absolute disease control within National borders, without consideration of cross border ecosystem dynamics and environmental health or the resources to implement even the most basic systems. One reason for the decline is that Government investment in the livestock sector has decreased dramatically over recent years. This is partly due to the increasing demands of human health programmes, education, security services, urban infrastructure but also due to failure of the veterinary policies to bear fruit as well as to increasing corruption and poor governance. The livestock lobby, the backbone of which is the pastoral community, has been increasingly marginalised socially and politically.

In order for Africa to fully benefit and share in world trade, the sanitary condition must improve. To do this and not destroy the natural resource and traditional pastoral systems, will require a careful land use policy with zonation of land along ecologically sound criteria. Export livestock will have to be maintained in areas, probably free of ruminant wildlife, with strict veterinary controls. If this can be balanced with sufficient areas retained for traditional pastoralist communities and wildlife, with perhaps the main income from recreational tourism and local consumption, the benefits will be considerable. The answer may be community based low cost decentralised systems for pastoral communities, with less stringent sanitary mandates, a private/parastatal sector servicing specialised sections e.g. wildlife, dairy and export livestock and a central veterinary policy, surveillance and monitoring service with small well resourced professional teams.