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BREEDING PRACTICES OF CASHMERE GOAT HERDERS IN WESTERN MONGOLIA: CURRENT STATE AND POSSIBLE INTERVENTIONS

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The aim of this survey was to describe the current goat breeding practices and to reveal the feasibility for the development of community based breeding strategies in Western Mongolia. Randomly selected 94 herders in Khovd, Uvs and Govi Altai provinces were interviewed using the focus group, individual discussions and structured questionnaire. The goat production system is pastoral in Western Mongolia. There were also enough the motivations of goat herders to improve their cashmere quality and quantity through CBBP in Ulgii and Bayan-Uul sums, thus this study reveals possibility to design CBBP in Ulgii sum, Uvs province and Bayan-Uul sum, Govi Altai province. There were high importance on the livelihood of goat with high flock sizes, but the important factors to create sustainable CBBP would be on the organizational, technical and financial supports from the Research Institute of Animal Husbandry, Government and other agencies for the development of livestock sector in Mongolia.

Key words: goat, cashmere, study, community based, breeding, program

CORRELATIONS BETWEEN GASTROINTESTINAL PARASITISM AND CLINICAL PARAMETERS OF SMALL RUMINANTS IN MONGOLIA

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A major losses in animal husbandry due to gastrointestinal parasitism in throughout the world, particularly in the Mongolia with huge of animal population, third of the human lives as a pastoral animal husbandry and livestock production plays an important role in the national economy.

The goal of the study was to compare gastrointestinal parasitism to clinical parameters, measured probability of disease in small ruminants. This study was conducted on 30 sheep and 30 goats each from three different landscapes (Songino Khaikhan district, Ulaanbaatar; Orkhon, Darkhan-Uul; Gurvan Tes, Omnogobi) of the Mongolia. Feecal and blood samples were collected and evaluated FAMACHA and BCS, individually. Feecal samples, analyzed by parasite egg counts (FEC) and blood samples for haemoglobin and PCV.

The FEC, mixed of helminthes egg and coccidian oocyst were estimated significantly lower in Omnogobi than other landscapes that 100% of the feecal samples, analyzed by no or low parasite burden but a moderate and high of infection rates were shown in 50% (UB) and 46% (Darkhan-Uul) of sheep; in 40% (UB) and 30% (Darkhan-Uul) of goats. There were found a significant differences for FAMACHA estimations in locations (≥ 3 in Gobi, ≥ 4 in grassland and forest) and a direct correlation between FEC and FAMACHA. Goats in Omnogobi had a high values of FAMACHA and haemoglobin with lower BCSs. There were a negative correlations between haemoglobin and FAMACHA and also PCV and FAMACHA. But there was not shown any correlation between FAMACHA and BCS.

Animal species differences were observed between gastrointestinal parasitism with FAMACHA, haemoglobin and BCS values. Targeted location (Tost mountain area) in gobi appears as like as a parasite free in the Mongolia. However, we have found a causel relationships between parasitism and clinical parameters, it would be require future wide range research.

ANTI-INFLAMMATORY EFFECT OF ERGOSTEROL PEROXIDE IN LPS-STIMULATED CELLS

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Aim of the study: By comparing different fractions and components of Chaga mushroom (*Inonotus Obliquus*) on viability and apoptosis of colon cancer cells, ergosterol peroxide showed the most effective growth inhibition by NMR analysis. In this study, we investigated the anti-inflammatory effect of ergosterol peroxide in LPS stimulated cells.

Materials and methods: We used MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assays, Western blot analysis, reverse transcription-polymerase chain reaction (RT-PCR), LPS stimulation to study the molecular mechanism of metastatic activities in RAW 264.7 cells.

Results: Ergosterol peroxide inhibited NFkB activation by LPS and this was associated with the abrogation of IkBa phosphorylation and subsequent decreases in nuclear p65 protein levels. Further, the phosphorylation of p38, pERK1/2 and pSAPK/JNK was suppressed by EP in a concentration dependent manner. EP diminished the cytokine expression of iNOS, TNF α , but did not change IL-6, IL-1 β .

Conclusion: Our data suggest that ergosterol peroxide effectively inhibits NFkB and TAK1 which is a common upstream cytokine for 3 MAPK signaling pathways. Ergosterol peroxide, which is the most effective component of Chaga mushroom (*Inonotus Obliquus*) has anti-inflammatory effects.

MAIN POLLUTION SOURCE OF GER AREA: LOCATION AND DISTANCE OF THE SOURCE

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Due to the nomadic herding families move to city as reason of degradation and market economy. It has large scale migration to city and led to expansion of ger areas. As today, more than 40 % of Darkhan population still lives in peri-urban ger settlement. Residents in ger area lack many of the basic services available to apartment dwellers including heating, sewerage and solid waste services. Most households use simple coal or wood burning stoves for heating and cooking. The lack of infrastructure brings many challenges for society especially in environment such as air, water pollution, soil contamination. Most dangerous pollution source is hygiene toilet in Ger district which is high risk for human health. This paper purposed that to survey location and distance of household's hygiene toilet, their private wells as well as to be sanitation standard of 7.2 in Law on Water. The study area is ger areas which located in flood plain close to the Kharaa river where exposed to floods and high health risks as families often use their own wells for abstraction of shallow ground water. It is not monitored. The method used GIS techniques for location and interview from 320 households for questionnaire. As result of the interviews, there are 87 % of households are living the area at more than 10 years and 67% of households relocate (open new toilet) their toilet at more than 2 times. 39 % of households are planting the vegetable, while 33 % and 20 % of them are farming animal husbandry and others using ground water for irrigation. Distance of household's hygiene toilet and their private wells are at least 50 meter as sanitation standard at 7.2 in Law on Water. There are 6 wells of 191 very close to the toilets by 10 meter and 73 wells are in 20 meter which is high risk for health during the rainy season. Because during the rainy season, the ground water level is only 1 to 3 meter below the surface which was high concern that the infiltrated waste water has contributed to the contamination of the upper ground water level.

As survey of soil sample near the toilet, 310000 bacteria occurred but drinking water extraction sites are only 10-30 meter away from this place and this contamination problem has a high priority for the drinking water supply of households.

MOLECULAR EPIDEMIOLOGICAL SURVEY OF SOME INFECTIOUS DISEASES IN MONGOLIAN LIVESTOCK

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Animal husbandry is inseparable part of agricultural industry and plays a vital role in social and economic evolution of Mongolia. In 2016, about 61.5 million heads of livestock were reported but occurrence of infectious diseases has been increasing in the recent years. However, epidemiological surveillances of infectious diseases are extremely limited in Mongolia. In this study, totally 928 blood samples (300 dairy breed cattle, 117 native cattle, 100 yak, 211 sheep and 200 goats) were collected from 5 sampling areas in the country to conduct molecular epidemiological survey and genetic characterization of several bacterial and viral pathogens in these animals.

The seroprevalence of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) in Mongolian cattle was screened by an ELISA assay on serum samples collected from cattle in various sampling sites, and a low rate of MAP infection was detected in our samples.

Highly prevalent of *Anaplasma ovis* (*A. ovis*) was detected in Mongolian native cattle, sheep and goats, while lower prevalence of the pathogen was found in dairy cattle and yak. Therefore, genetically two distinct *A. ovis* were found and the sequences from cattle and yak were unique.

Bovine leukemia virus (BLV) was detected from dairy breed cattle (Holstein, Alatau, and Simmental) in the Songinokhairkhan district of Ulaanbaatar city and Bornuur sum of Tuv province and was not detected from Mongolian native cattle and yak. Mongolian BLV sequences were clustered into genotypes 1, 4 and 7, and most of them were closely related to Russian isolates, suggesting that BLV was transported from Russia into Mongolia.

Bovine viral diarrhea virus (BVDV) was detected in dairy breed cattle and yaks from Bornuur sum of Tuv province and Bulgan sum of Arkhangai province. Both BVDV genotypes 1 and 2 were found in Mongolian cattle and yaks.

Ovine gammaherpesvirus-2 (OvHV-2) was detected from both reservoir host sheep and susceptible host cattle in Tsenkher soum of Arkhangai province and Lun soum Tuv province. The phylogenetic analysis revealed that the Mongolian sequence of SA-MCF was identical to sequences from high sheep population countries such as Egypt, India, and Turkey.

Further studies are required to determine the prevalence of the infection in other parts of Mongolia and to identify the genetic diversity of the pathogen to develop control strategies for the disease in this country.

PROTEOMIC ANALYSIS OF THE EFFECTS OF *SALMONELLA PULLORUM* INFECTION IN CHICKEN LIVER

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Salmonellosis in poultry is a significant health problem which causes substantial economic loss. One of the common causative agents of chicken salmonellosis is *Salmonella pullorum* (S.P). Infections with S.P can result in acute systemic disease and a high incidence of mortality in young poultry. Vertical transmission of S.P from infected parent flocks, magnified by horizontal transmission in the hatcher, can cause economically devastating losses among chicks. To identify the differentially expressed chicken liver proteins by S.P infection, we have used two-dimensional electrophoresis with mass spectrometry. The goal of this work was to characterize and identify gene expression profiles of chicken liver tissue after infected with S.P.

One Hundred twenty Hy-Line layer chicks of 10 days old were divided into 6 groups of 20 each. G1, G2 and G3 groups were infected with high dose (1×10^9 cfu/ml) of S.P orally and G4, G5, G6 groups were kept as non-infected control. One chick was taken randomly each group after 3, 6, 9 and 12 days, liver was collected. Proteins were separated from all samples. Two-dimensional electrophoresis was done and mass spectrometer identified the protein spots. A total of 480 spots showing an altered expression were identified by Sigma gel program. Among these spots, 13 spots were exclusively analyzed by ESI-MS/MS analyses.

Seven proteins including Pyridoxal kinase-1, Pyridoxal kinase-2, Fructose-bisphosphate aldolase C, hypothetical protein, Destrin, Nucleoside diphosphate kinase and Trifunctional purine biosynthetic protein adenosine were induced or significantly up regulated by *S.pullorum* infection.

A significantly decrease or down regulated of 6 proteins including Guanidinoacetate N-methyltransferase, Bromodomain containing 4, C7orf 24 chromosome 7 open reading frame 24, protein DJ-1, pyruvate carboxylase and non-metastatic cells 2, protein caused by *S.pullorum* infection was also identified.

Variations of protein expression were also further investigated at the mRNA level by RT-PCR analysis, which confirmed the proteomic data for 6 out of the representative 7 selected proteins including 3 proteins from up-regulated group and 4 proteins from down-regulated group. These results suggest that the expression of proteome in chicken liver different in salmonella infection which may useful for developing tools for diagnosis, vaccine and treatment of avian pullorum disease.

Keywords: Salmonella, chick, disease, protein, liver

A META-ANALYSIS IN INFLUENCES OF ARSENIC ON FRESHWATER FISH

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Nowadays, researchers in many fields have been moving away from the narrative review to systematic reviews and meta-analyses. Meta-analysis is the statistical procedure for combining data from multiple studies. The meta-analysis results of this study show that fish mortality, growth and arsenic accumulation effects were clear both in acute and chronic exposure to arsenic. Nevertheless, mortality and growth effect tests were conducted with very high concentration of arsenic (as average around 100 mg/L), arsenic accumulation after chronic exposure was detected at much lower concentration. Behavioral, biochemical and physiological effects were evaluated at lower concentrations compared to growth and mortality, but they were not significantly different from their controls and the effects were heterogeneous.

Among biochemical variables some responses were negative and some had positive changes under arsenic exposure. For instance hematological parameters decreased, while lipid peroxidation and some breakdown compounds increased. Oxidoreductase enzyme activities tend to have increased during acute exposures.

Among the physiological measurements, intoxication ability always decreased and immunological effects increased. There were only two behavioural measurements each having two subvariables and none of them were significantly different from controls. In fact, those behavioural measurements were tested with the lowest average concentration compared to the other effects.

EPIDEMIOLOGY OF BRUCELLOSIS IN BACTRIAN CAMELS IN MONGOLIA

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More information on the epidemiology of brucellosis in Mongolian Bactrian camels is needed given their growing economic and livelihood importance for herders and the renewed efforts to eliminate brucellosis from Mongolia through mass ruminant vaccination – that does not include camels. Despite decreasing camel populations the past two decades, brucellosis prevalences in camels increased. During two consecutive years, repeated random multi-stage cluster surveys were done in the Eastern provinces of Dornod and Sukhbaatar and in the Southern & Western provinces of Dornogobi, Umnogobi and Khovd from 2013 to 2015. In each province 6 districts were selected proportional to the size of their camel populations. A total of 1,822 camels, 1,155 cattle, 1,531 sheep, and 1,492 goat sera were collected in 365 herds and tested with the Rose Bengal Test. In addition, 195 vaginal swabs and 250 milk samples for bacteriological culture were taken from livestock with history of abortion. The overall apparent brucellosis seroprevalence in camel herds was 2.3% (95% CI 1.6-3.3). The main risk factor for camel seropositivity was being in an Eastern province herd when compared to Southern & Western provinces (OR 13.2). Camel seroprevalences were stable for the two survey years, despite introduction of ruminant vaccination: 5.7% (95% CI 3.1-10.2%) and 5.8% (95% CI 3.3-10.1%) in Eastern provinces and 0.4% (0.2-1.2%) and 0.5% (0.1-2.0%) in Southern & Western provinces. We have isolated *Brucella abortus* from camel. Camel seropositivity was associated to herding camels with cattle and was closest correlated to cattle herd seropositivity.

Monitoring of vaccination campaigns showed that coverage was insufficient in cattle due to difficulties of veterinarians to restrain the animals. The results of the present study indicate that brucellosis exists up to important seroprevalences in Mongolian camels and was endemic in Eastern provinces. Further monitoring is needed to assess if camel seroprevalences decrease with ongoing ruminant vaccination. This should be coupled with more confirmation about *Brucella* spp. isolates from Mongolian camels (up to date only *B. abortus* was isolated, but camels are also susceptible *B. melitensis*). Good oral and written information on prevention of the disease in livestock and household members are important, particularly for remote camel herders, who had only moderate knowledge on brucellosis epidemiology and preventive measures. Seropositivity of camel herds was closest associated to the infection in cattle. Monitoring of brucellosis in camel herds is need in the near future in Mongolia.

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