**BC-01**

## Study on efficacy of anthelmintic drugs in German alpaca farm

Luise Kultscher[1], Barbara Hinney[1], Ronald Schmäschke[2], Anja Joachim[1], Thomas Wittek[1].

*[1]Veterinary University Vienna, Vienna, Austria; [2]University Leipzig, Leipzig, Germany.*

**Objectives:** Endoparasites are considered a major health problem of South American camelids. Although prophylactic and therapeutic measures such as application of anthelmintics are commonly used, treatment efficacy is typically not assessed. In a previous study a number of alpaca owners expressed significant concerns regarding the efficacy of anthelmintic treatment; further imported animals from countries with higher percentages of anthelmintic resistances may also contribute to decreased efficacy of anthelmintic drugs. The present study aimed to evaluate the efficacy of anthelmintic treatment with different anthelmintic drugs in German alpaca herds.

**Material and Methods:** Overall, 617 samples from 538 clinically healthy alpacas >1 year from 27 farms (n=11-157 animals/herd) were examined. After initial coproscopic examination by flotation and strongylid egg quantification (McMaster technique), animals with at least 150 eggs per gram faeces were included in a faecal egg count reduction test (FECRT) using fenbendazole (FBZ; n=71 samples), moxidectin (MOX; n=71) or monepantel (MON; n=66) which are the most commonly used drugs in Germany.

**Results:** The most frequent parasites detected by flotation were *Eimeria* spp. (75.1%) followed by strongylids (55.0%), *Nematodirus* spp. (19.3%), cestodes (3.1%) and *Trichuris* (2.7%). Pre-treatment larval cultures (n=23 positive pooled farm samples) revealed *Haemonchus* (87.0% of the samples), *Cooperia* (43.5%), *Trichostrongylus* (21.7%), *Ostertagia* (13.0%), *Nematodirus* and *Oesophagostomum* (4.3% each). On average FBZ treatment reduced egg excretion by 45%, MOX by 91% and MON by 96%. On the farm level, 13/18 farms that used FBZ, 6/6 farms that used MOX and 2/5 farms that used MON had individual FECR values <90% (FBZ) or 95% (MOX, MON). *Haemonchus* and *Cooperia* were overrepresented on the farms with reduced treatment efficacy.

**Conclusions:** Gastrointestinal strongylids are common in German alpacas and especially FBZ was not sufficiently effective to reduce strongylid egg excretion. Although the FECRT could not unambiguously determine anthelmintic resistance in the present study, the finding that small ruminant strongylids, especially *Haemonchus*, are common in alpacas indicates that determination of effective anthelmintic doses for alpacas, monitoring of efficacy and adapted (targeted selective) treatment regimens must be implemented as part of sustainable deworming practices.

**Keywords:** Alpacas, endoparasites, antiparasitic drugs, drug efficay.

**BC-02**

## Abortion in Alpaca and seroprevalence to *Leptospira* sp. in a herd in Treviso, Italy

Matteo Cornaggia[1], Luca Palazzolo[2], Letizia Ceglie[3], Laura Bellinati[3], Laura Viel[2], Ernesto Pascotto[4], Luca Zandonà[4], Giovanni Trombetta[5], Luca Bano[2], Alda Natale[3].

*[1]Istituto Zooprofilattico Sperimentale delle Venezie, Padova - Istituto Zooprofilattico Sperimentale della Lombardia ed Emilia-Romagna, Brescia, Italy; [2]Veterinary Diagnostic Laboratory, Istituto Zooprofilattico Sperimentale delle Venezie, Treviso, Italy; [3]Veterinary Diagnostic Laboratory, Istituto Zooprofilattico Sperimentale delle Venezie, Padova, Italy; [4]Animal Health Veterinary Service, Unità Locale Socio-sanitaria 2 "Marca Trevigiana", Treviso, Italy; [5]Private Veterinarian, Paese, Italy.*

**Objective:** Leptospirosis is a zoonosis affecting all mammals sustained by *Leptospira* sp.

*Leptospira* is worldwide distributed due to its persistence in humid environments and, to many asymptomatic carriers, spreading the pathogen for longtime through urines.

Several studies conducted in South America on new world camelids revealed a widespread seroprevalence to *Leptospira* sp. rising from 6,5 to 89,6% with various serovars positivity and different antibody titers (Rosadio, 2015).

Alpacas seem to not develop any clinical signs of leptospirosis but only some reproductive disorders such as abortion, infertility, and stillbirth (Tibary, 2006).

**Materials and methods:** In July 2021, a 9-month-old alpaca's abortion belonged to an educational farm was delivered to the Diagnostic Service of IZSVe, Treviso, Italy for diagnostic purposes.

Placenta, liver, kidney and lung samples were processed as routine histological investigation.

Major abortion pathogens (Bovine Viral Diarrhea Virus; *Chlamydia* sp., *Coxiella burnetii*, *Neospora caninum*, Schmallenberg virus) were investigated through molecular methods.

Investigations into bacteria were carried out on *Campylobacter* sp., *Salmonella* sp., and *Listeria* sp., and the content of abomasum was cultivated in standard bacteriological media.

*Leptospira* sp. was suspected as a cause of abortion.

A real-time PCR (rPCR) was conducted on DNA extracted from lung, kidney, and spleen following the protocol previously described (Smythe, 2002).

Urines and blood sera of all animals in the herd (3 llamas; 25 alpacas) were collected monthly from the beginning of the outbreak (July, August and September).

Frozen sera collected on December 2020 (before the event of abortion) for other diagnostic purposes were also analyzed to compare the results obtained in July 2021.

Antibody titers were established by means of microagglutination test (MAT; OIE, 2021) while urine samples were analyzed in rPCR.

**Results:** The carcass was partially mummified and a diffuse hemorrhagic infiltration in organs and subcutis was recorded.

Histologically, a mild degree of autolysis was observed. Le-

sions were characterized by hemorrhagic infiltration in organs. A necrotic placentitis occurred.

Molecular and microbiological investigations gave negative results, except for rPCR against *Leptospira* sp. that resulted mild positive in the kidney of the aborted fetus. The weak Ct recorded in rPCR did not permit the sequencing of the amplicon.

The mother of the aborted fetus was tested for *Leptospira* sp. antibodies resulting negative before and after the outbreak.

The serological study conducted to detect specific antibodies against a panel of 9 pathogenic serovars (*Grippotyphosa; Copenagheni; Icterohaemorrhagiae; Pomona; Canicola, Tarassovi, Bratislava, Ballum, Hardjo*) revealed a seroprevalence of 21,4%, 10,7%, 53,6% and, 28,6% to one or more serovars at December, July, August and September, respectively. The antibody titers varied from 1:100 to 1:6400; males showed a higher seroprevalence (*p* 0,0219) and a higher median of 1:200 titer values.

The most frequent serovar detected was *Icterohaemorrhagiae*; followed by *Copenagheni*, *Grippotyphosa* and *Pomona.*

No symptoms were recorded at any times, nor was observed molecular positivity on urine.

**Conclusions:** Our work confirmed a probable pathogenic role of *Leptospira* sp. in new world camelids in Italy, as suggested by other authors in Europe (Rüfli, 2011).

Even if the rPCR on the aborted fetus gave a weak positivity and no bacterial DNA was detected in urine samples, serological investigations allowed us to confirm the *Leptospira* infection within the herd.

In absence of a clear seroconversion, it has been impossible to date the beginning of the outbreak. Due to the high persistent titers in the same subjects, probably the abortion represented its final event.

In a public health vision, to limit the zoonotic risk, a parenteral antimicrobial treatment with doxycycline for at least 2 weeks was encouraged by the Public Veterinary Service in combination with the official detention of the animals until a sink in the antibody titers.

Male alpacas showed higher seroprevalence and a higher median of antibody titers with respect to females, included the one who aborted. In cows, it is known that chronically infected subjects can remain seronegative, while very few studies were conducted in bulls.

Although urine collection in alpacas can be challenging, rPCR performed on this matrix is highly recommended to ensure the diagnosis. Authors intend to emphasize the complexity of the diagnosis of leptospirosis and the need to combine multiple diagnostic tools for a proper epidemiological investigation to create management protocols that mitigate the zoonotic risk.

**Keywords:** Alpaca leptospirosis, Alpaca abortion, Leptospira sp.

**BC-03**

## Serum metabolomics assessment of etiological processes predisposing ketosis in water buffalo through the $^{1}$H-NMR spectroscopy

Enrico Fiore[1], Anastasia Lisuzzo[1], Luca Laghi[2], Kevin Harvatine[3], Elisa Mazzotta[4], Maria Chiara Alterisio[5], Matteo Gianesella[1], Chenglin Zhu[6], Barbara Contiero[1], Vanessa Faillace[1], Paolo Ciaramella[5], Massimo Morgante[1], Jacopo Guccione[5].

*[1]University of Padua, Legnaro, Italy; [2]University of Bologna, Cesena, Italy; [3]Pennsylvania State University, State College, United States; [4]Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro, Italy; [5]University of Napoli, Napoli, Italy; [6]Southwest Minzu University, Chengdu, China.*

**Objectives:** The transition period is critically important to health and profitability of dairy buffaloes. The metabolic adaptation to negative energy balance (NEB) induced by the considerable increment of energy and nutrient requirements is still one of the major concerns that may decrease the productivity and predispose to different disorders. An inadequate metabolic adaptation is characterized by elevated concentrations of β-hydroxybutyrate (BHB). Nevertheless, a specifically BHB threshold for dairy buffaloes is not established and dairy cows' reference are often used. The metabolic processes can be investigated using the metabolomics approach, which reflects the animals' health status. The aim of the current study was to use the metabolic approach, specifically with the $^{1}$H-NMR, to assess the metabolomic profile of Mediterranean buffaloes (MBs) to investigate the metabolic changes associated with different levels of energy deficit.

**Materials and methods:** The current cross-sectional investigation received an institutional approval by the Ethical Animal Care and Use Committee of the University of Naples Federico II (n.PG/2017/0099607). Sixty-two Italian MBs were selected within the entire group of fresh buffaloes (< 50 days in milk) from a single high-yielding dairy farm. All the buffaloes received a complete clinical examination before sampling to exclude clinical ketosis or other pathological statuses. The blood samples were collected from jugular vein into tubes containing clot activator to obtain serum for biochemical and metabolomic analysis. According to serum BHB concentration, animals were divided into two groups: Group healthy (Group - H) consisting of 37 MBs with a level of BHB < 0.70 mmol/L and Group at risk of hyperketonemia (Group - RK) made by 25 MBs with a level BHB ≥ 0.70 mmol/L. The statistical differences for biochemical parameters and metabolite's concentration were performed by one-way ANOVA and Wilcoxon test according to data distribution. A post hoc pairwise comparison among metabolite concentrations was performed using Bonferroni correction. A $p\text{-value}<0.05$ was accepted, whereas a $0.05\leq p\text{-value}\leq 0.10$ was considered as trend to significance. A robust principal component analysis (rPCA), a partial least squares-discriminant analysis (PLS-DA) with variable importance in projects (VIP), and the metabolic pathways overrepresentation analysis (ORA) were generated to summarize the structure of the data and to highlight the metabolic pathways influenced by BHB concentration.

**Results:** Among biochemical parameters, only AST was significantly increased in Group - RK. A total of fifty-seven metabolites were identified in serum samples: 27 amino acids and derivates, 9 organic acids, 5 alcohols, 4 carbohydrates, 3 amine and derivates, 2 fatty acids, 2 ketone bodies, 1 sulfone, 1 vitamin, 1 imidazole, 1 nucleoside, and 1 guanidine. Six of the identified metabolites showed a statistically significance, specifically: glycerol, taurine, and creatinine showed a significant reduction in Group - RK, whereas acetone, acetate and 3-hydroxybutyrate showed a significant increase. In addition, six metabolites showed a trend toward significance: methanol, proline, and glycine were reduced in Group - RK, whereas formate, citrate, glutamate were increased. The rPCA analysis failed to cluster groups, while the PLS-DA showed two cluster principally related to acetate, 3-hydroxubutyrate, acetone, and glycerol (VIP > 1.5). The ORA analysis identified five metabolic pathways possibly responsible for changes in metabolome profile: glyoxylate and dicarboxylate metabolism; pyruvate metabolism; glycolysis / gluconeogenesis; glycerolipid metabolism and taurine and hypotaurine metabolism.

**Conclusions:** Metabolomic analysis through $^{1}$H-NMR is a useful tool to achieve knowledge about metabolic profiling related to serum BHB modifications in dairy buffaloes. The metabolic state of our animals at risk of hyperketonemia suggests an initial mobilization of body resources, subclinical inflammation and potential oxidative stress status, changes in ruminal fermentations, influence on urea cycle and thyroid hormone synthesis. This study demonstrates that the metabolomic approach identified potential relationships with the development of subclinical ketosis even if the BHB concentration did not exceed the threshold value.

**Keywords:** Metabolomics; Negative energy balance; Mediterranean buffaloes; H-NMR; Ketosis.

**BC-04**

## First detection of "*Candidatus* Mycoplasma haemolamae" in alpaca (*Vicugna pacos*) in Italy

Giulia Sala, Gabriele Ratti, Vincenzo Ferrulli, Donatella Scavone, Angelica Stranieri, Alessia Giordano, Antonio Boccardo, Davide Pravettoni, Stefania Lauzi.

*University of Milan, Department of Veterinary Medicine and Animal Sciences, Lodi, Italy.*

**Objective:** *Candidatus* Mycoplasma haemolamae is a wall-less hemotropic prokaryote that infects camelids. To the author's knowledge, there have been no published reports of *Candidatus* M. haemolamae infection in alpacas in Italy. This study describes a clinical case of *Candidatus* M. haemolamae infection in an alpaca cria from northern Italy and the prevalence in its herd.

**Materials and methods:** A 2 month-old alpaca cria was referred to the Clinic for Ruminants of the Veterinary Teaching Hospital of the University of Milan for weakness and lethargy. At birth, the alpaca cria was immediately rejected by their dam and fed with artificial bovine colostrum (Locatim®, Boehringer Ingelheim, Germany) and pasteurized whole cow's milk. At admission, the cria presented pale mucosae, tachycardia, and moderate dehydration. The hemogasanalysis underlined severe hypoglycaemia (1.1 mmol/L) and anaemia (haematocrit 17%, haemoglobin 5.6 g/dl). The complete blood count (CBC) confirmed mild, regenerative anaemia. The blood smear revealed numerous small basophilic coccoid structures attached to the surface of erythrocytes compatible with *Candidatus* M. haemolamae infection. In addition, parasitology examination of the faeces revealed severe coccidian infestation. To confirm the presence of *Candidatus* M. haemolamae, a portion of the 16S rRNA gene was amplified using a species-specific real-time PCR on blood samples collected at day of admission and at day of discharge. Threshold cycle (Ct) number was used as the measure of bacterial load (the lower the Ct level the greater the amount of target nucleic acid is present in the sample). Subsequently, the other animals of the entire herd from which the primary case was detected were tested by real-time PCR and by blood smear examination to investigate the presence of *Candidatus* M. haemolamae (n=20).

**Results:** In the blood sample collected at admission, real-time PCR revealed a high level of *Candidatus* M. haemolamae DNA (Ct 11.7). The cria was stabilized by administration of a 10% glucose solution, iron dextran (5 mg/kg, subcutaneously once), B vitamins (10 mg/kg, subcutaneously once), E vitamins, and selenium (0.05 mg/kg, subcutaneously once). Furthermore, the animal was treated with long acting oxytetracycline (20 mg/kg, subcutaneously, q72h for 3 treatments) for the *Candidatus* M. haemolamae infection. By the third day of hospitalization, the animal's clinical condition had improved. Eight days after hospitalization, the haematocrit (30.1%) and haemoglobin (11.7 g/dl) were also within the reference ranges, and the alpaca was discharged. The blood smear, performed on the day of discharge, did not show the presence of *Candidatus* M. haemolamae whereas real-time PCR was still positive, showing lower DNA levels (Ct 24.7) compared to the first blood sample. Anticoccidial therapy was set at discharge with sulfadimethoxine (110 mg/kg, orally, q 24 h for 10 days).

A 65% (13/20) *Candidatus* M. haemolamae real-time PCR positivity was reported in the other animals of the herd, with Ct values ranging from 16.4 to 32. A poor agreement between PCR result and smear examination was observed. The dam of the cria showed positive molecular results. An overall 66.7% (14/21) prevalence was observed in the herd, including the alpaca cria. No animal other than the cria had clinical manifestations correlated to the infection.

**Conclusion:** This study reports the first identification of *Candidatus* M. haemolamae in Italy. As shown in other studies, clinical infection was observed in a young animal, and further parasitic infestations (such as coccidiosis) were associated with *Candidatus* M. hemolamae infection. Treatment with oxytetracycline during *Candidatus* M. hemolamae infection was valid only for symptom remission, but the alpaca cria continued to be PCR positive after treatment, in accordance with previous observations on treatment in positive alpaca. Despite the very high prevalence of *Candidatus* M. haemolamae, most infected alpacas did not show clinical abnormalities. The absence of maternal colostrum intake suggests that the cria was not infected by colostrum. Further investigations are needed to assess the transmission dynamics of *Candidatus* M. haemolamae in Italian alpaca herds.

**Keywords:** Alpaca, Candidatus Mycoplasma haemolamae, Anaemia.

**BC-05**

## Improving the embryo developmental competence and success of in vitro produced calves during hot season in Buffalo

Omaima Kandil[1], Ragab Dohreig[2], Ahmed Abdoon[3], Esraa Esmail[3], Hosam Tawfik[3], Ahmed Shaban[3], Emilie Corbin[4], Pascal Mermillod[4].

*[1]National Research centre, Cairo, Egypt; [2]Haram Institute of Reproduction, Giza, Egypt; [3]National Research Centre, Cairo, Egypt; [4]INRA institute, Tours, France.*

Heat stress is a major problem for animal breeding in tropical and equatorial area as well as in the Mediterranean countries. This translates into several pathologies and high rates of reproductive failure through early embryonic loss in buffalo. The present work was conducted to investigate:1) Effect of cold and hot season in the oocyte quality and in vitro embryo development competence of buffalo cultured in buffalo oviduct epithelial cell (BOEC).2) Effect of heat stress (41°C) & IGF during in vitro oocyte maturation in oocyte maturation rate and embryo developmental competence.3)Transfer of in vitro produced embryo during hot season to Egyptian buffalo. Egyptian buffalo's ovaries were collected during hot (June-August) and cold (December-February) season from abattoir. Oocytes were classified to Excellent (Ex), Good (G), Fair (F), Denuded (D). EX and G oocytes were matured in in-vitro maturation medium (IVM) (TCM-199+ 10% FCS + 10 µg/ml FSH+ 10 ng/ml EGF+ 50 µg/ml gentamicin (gn) for 22 h in 38.5C and 5% $CO_2$. The matured oocytes (1st pb) fertilized using Frozen – thawed buffalo semen, for 18 hours incubation. Zygotes cultured in SOFM + 10% FCS, 5 µg/ml insulin and 50 µg /ml gentamicin, with or without BOEC and incubated for 8 days. 2) Ex & G oocytes IVM in TCM-199 + 10% FCS+ 10 µg/ml FSH + 10 ng/ml IGF + 50 µg/ml, for 41°C /1hr- then 38.5°C vs. 38.5°C incubation for 22 hours. Then matured oocytes were fertilized and cultured as described before. Blastocyst were Fixed for cell counting to validate the quality of blastocyst. 3) Non-surgical embryo transfer during hot season in National Research Centre farm, Fresh Two in-vitro produced embryos (IVM,TCM+IGF, cultured in BOEC) were transferred to each buffaloes came in natural oestrus (buffalo number=5).Pregnancy diagnosis after 40 days from transfer. Results, Oocytes were collected from (349) buffalo ovaries giving an average of 2.4 oocytes/ovary (range 1.8 – 3.0 oocytes/ovary).There were highly significant (P<0.01) differences in the recovery rate of total oocytes between the two seasons, cold and hot season (3.02% ± 005 and 1.76% ± 0.05 respectively). Analysis of quality of buffalo oocytes revealed that, there were highly significant (P<0.01) differences in the mean % ± SE of excellent and good quality oocytes between the two seasons cold (38.63% ± 0.5, 51.35±0.50 resp.) and hot (11.29% ± 0.64, 21.37±0.74 resp.). While, fair and denuded oocytes increased with higher significant differences (P< 0.01) in summer (58.45% ± 0.86) when compared with the cold (9.86% ± 0.23). Maturation rate (85- 84 %), cleavage rate (75-71 %), blastocyst rate (33- 2%) were significantly higher (P<0.1, P<0.5) in cold temperature when compared with hot temperature season, in range 71-70%, 63-60 % and 22-17 respectively. In vitro culture of embryo using BOEC vs. without BOEC significantly increase the blastocyst rate either in cold (33 vs. 27 %) or hot temperature (22 vs. 17 %). The cell number of the blastocyst was significantly higher (P<0.1) in the cold temperature (mean= 106-90) when compared with hot temperature (80-60) and in vitro culturing in BOEC significantly increase (P<0.1) the blastocyst cell number either in cold or hot season. Effect of heat stress 41°C during in vitro oocyte maturation on in vitro embryo developmental competence in buffalo. Higher temperature 41°C for one hour during in vitro oocyte maturation in buffalo significantly (P<0.01) decreased the mean ± SD and rate of maturation (32±3.79, 51), cleavage (16.5±2.65, 26) and blastocyst (13.5±2.65, 22), when compared with in vitro oocyte maturation in 38.5°C (77.50±7.46, 87%, 42.67±2.52, 72% and 37.00±5.03, 41% respectively). Non- Surgical transfer of in vitro produced fresh buffalo embryos to five buffalos (day 6 of natural oestrus), pregnancy and calving of two calves (2/5, 40% Emy & Medo) with 42 kg body wright.

**In conclusion:** Heat stress either during hot season (summer) or through experimental rise temperature during in vitro maturation of buffalo oocytes significantly decrease the in vitro oocyte competence and blastocyst rate. Supplementation of IGF in in vitro maturation medium and co-culture of in vitro fertilized oocytes using BOEC decreased effect of heat stress and improved in vitro embryo production of buffalo. Success of calving of two calves (EMY& Medo) through transfer of IVP buffalo embryos matured in TCM+IGF during hot season (summer).

**Keywords:** Buffalo, season, BOEC, embryo, ET.

**BC-06**

## Herd, buffalo, and quarter specific prevalence and risk factors of subclinical mastitis in water buffaloes of Bangladesh

Shuvo Singha[1], Gerrit Koop[2], Momena Khatun[3], Fabrizio Ceciliani[1], Sofia Boqvist[4], Marjolein Derks[5], Md. Ahasanul Hoque[6], Mohammed Kawser Hossain[7], Md. Mizanur Rahman[6], Ylva Persson[8].

*[1]Department of Veterinary and Animal Sciences, Università degli Studi di Milano, Via dell'Univesrità 6, Lodi, 26900, Italy, Lodi, Italy; [2]Department of Population Health Sciences, Faculty of Veterinary Medicine, Utrecht University, Yalelaan 7, 3584 CL, Utrecht, The Netherlands, Utrecht, Netherlands; [3]Veterinary Physiology, University of Bern, Bremgartenstrasse 109a, 3012 Bern, Switzerland, Bern, Switzerland; [4]Department of Biomedical Sciences and Veterinary Public Health, Division of Bacteriology and Food Safety, The Swedish University of Agricultural Sciences, BVF, Bakteriologi och livsmedelssäkerhet, 750 07 Uppsala, Sweden, Uppsala, Sweden; [5]Farm Technology Group, Wageningen University and Research, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands, Wageningen, Netherlands; [6]Department of Medicine and Surgery, Chattogram Veterinary and Animal Sciences University, Chattogram 4225, Bangladesh, Chattogram, Bangladesh; [7]Department of Surgery*

*and Theriogenology, Faculty of Veterinary, Animal and Biomedical Sciences, Sylhet Agricultural University, Sylhet-3100, Bangladesh, Sylhet, Bangladesh; [8]National Veterinary Institute, 751 89 Uppsala, Sweden, Uppsala, Sweden.*

**Objectives:** Subclinical mastitis (SCM) in water buffaloes is a prevalent production disease responsible for reduced milk yield with compromised milk quality. The risk factors for SCM in water buffaloes are largely unknown since little information is available in this species. The study objectives, therefore, were to i) estimate the prevalence of SCM in water buffalo at quarter and buffalo-level; ii) identify the quarter the risk factors associated with SCM at quarter and buffalo-level, and iii) determine risk factors for high bulk milk somatic cell count (BMSCC) at the herd-level.

**Material and Methods:** This cross-sectional study was carried out between February 2020 and April 2021 and included individual lactating water buffaloes or buffalo herds belonging to17 buffalo concentrated sub-districts in Bangladesh (11 coastal and semi-coastal districts regions). The buffalo herds represented five different production systems: bathan (n = 51), semi-bathan (n = 106), households (n = 33), semi-intensive (n = 54), and intensive (n = 4). The native name "bathan" is used to define solely grazing-dependent free-ranging system in remote islands while "semi-bathan" implies to the partial stay at household when feed source is very limited in islands. Herd-level and buffalo-level data were collected using a structured questionnaire. Milk samples were collected on a herd basis (average 1-5 buffaloes/herd) from the bathan, semi-bathan, household, and semi-intensive production system and all individual buffaloes of the intensive production system. A total of 3,491 functional quarters of 880 lactating buffaloes of 248 herds were included in the study. A buffalo was considered positive for SCM if any functional quarter was tested positive in California mastitis test (CMT) score ≥2 (1 to 5 scale) and no signs of clinical mastitis (CM). The composite milk mixture (n = 242) collected in the morning was used for herd-level BMSCC using a portable DeLaval cell counter. Quarter and buffalo-level risk factors for SCM were identified using two sets of univariable and multivariable logistic generalized linear mixed-effects models, with random buffalo and herd effects. Population averaged beta estimates or cluster-specific estimates were used to calculate odds ratios (OR) for different risk factors depending on whether these effects happen at quarter or buffalo level. The linear regression model was used to link the herd-level data for the identification of the risk factors of BMSCC. The significant (P≤0.05) variables from multivariable regression models were considered as the risk factors of SCM at quarter or buffalo level and BMSCC at the herd-level.

**Results:** The prevalence of SCM was 27% (95% C.I. 25-28) at quarter-level and 50% (95% C.I. 47-54) at buffalo-level. Out of 17 analyzed variables two (e.g., rearing system and quarter position) were associated with quarter-level SCM, and three (e.g., teat symmetry, previous history of CM, and the number of milkers) were associated with buffalo-level SCM. For quarter level SCM, intensive buffalo rearing system (OR, 6.6, 95% C.I. 2.2-19.6; P < 0.001) had a greater risk than bathan system; and left quarters had a greater risk than right quarters (OR, 0.8, 95% C.I. 0.6-0.9; P = 0.006). There was a greater risk of asymmetric teat position (OR, 1.8, 95% C.I. 1.3-2.4; P <0.001) than symmetric teats; previous occurrence of CM in last 12 months (OR, 3.1, 95% C.I. 1.2-8.0; P = 0.02) than no occurrence; hand milking performed by single milker (OR, 1.5, 95% C.I. 1.2-2.1; P = 0.005) than multiple milkers for buffalo-level SCM. In the herds, the BMSCC were lower in swamp-type buffalo than river-type buffalo; when caretakers were more experienced; and milking performed in full hand with occasional stripping or knuckling than full hand only (all, P < 0.05). Intensive rearing systems (P = 0.08) had a higher BMSCC (435,000 cells/mL) than any other rearing systems.

**Conclusions:** The water buffaloes in Bangladesh have a high prevalence of SCM where risks are associated with the rearing system, teat symmetry, teat position, and milking performed by a single milkman. The fact that several manageable risk factors were identified suggests that effective buffalo udder health control strategies can be designed.

**Keywords:** Water buffalo, SCC, CMT, risk factor.

**BC-07**

## Comparative Efficacy of Herbal, Oral and Injectable Anthelmintics against Toxocara vitulorum infestation in Nili-Ravi buffalo calves

Muhammad Avais, Mohammad Qasim.

*Department of Veterinary Medicine, University of Veterinary and Animal Sciences, Lahore, Sheikh Abdul Qadir Jillani (Outfall) road Lahore, Pakistan.*

**Objectives:** Parasitic infections are major constraint of large ruminant production and causes colossal economic loss to dairy industry. Among these *Toxocara vitulorum is* most important infecting calves in tropical and subtropical climates. It is responsible for retarded growth, low productivity and increased susceptibility of animals to other infections. Present study was accomplished to evaluate the comparative efficacy of herbal, oral and injectable anthelmintics against *Toxocara vitulorum* infestation in Nili-Ravi buffalo calves.

**Material & Methods:** For this 24 buffalo calves positive for *T. vitulorum* were randomly divided into 4 groups of 6 viz. A, B, C and D. Calves in group A were treated with Albendazole at 10 mg/ kg PO while the calves in group B were given Levamisole at 8 mg/kg PO. The animals in group C were treated with Doramectin at 0.2 mg/ kg SC whereas calves in group D were given *Chenopodium album* (herb) 2g/kg PO. All the treatments were given once. Eggs per gram (EPG) of calves in each group was determined at days 0 (pre-treatment) and then at day 4, 7, 14, and 21 (post-treatment). Efficacy of particular treatment was calculated on the basis of fecal egg count reduction test (FECRT).

**Results:** At day 4 (post-treatment), fecal egg reduction in groups A, B C and D was 59.67%, 48.79%, 39.82% and 1.82%, respectively. At day 7, fecal egg reduction in groups A, B C and D was 98.43%, 82.50%, 73.0% and 3.5%, respectively while at day 14 fecal egg reduction was 100.00 %, 98.25%, 95.95% and 6.7% in groups A, B, C and D, respectively. While

100.00% fecal egg reduction was recorded in group A, B and C on day 21 (post-treatment).

**Conclusion:** It was concluded that oral wormers ( albendazole, levamisole) and injectable wormers (doramectin) are equally effective in treating *T. vitulorum* infestation in buffalo calves while Chenopodium herb is not effective to treat *T. vitulorum* in buffalo calves.

**Keywords:** Albendazole, doramectin, herb, buffalo, calves.