Monitoring dairy cattle health and husbandry including by use of drones. D. J. Wilson*, L. E. Cheetham, and K. A. Rood, Utah State University, Logan, UT.

Unmanned aerial vehicles (UAV, drones) have been used to observe beef cattle; flying below 33 m (100 ft) caused animal flight. Objectives were to learn to fly UAVs and evaluate UAV disease (Dz) monitoring and dairy cattle response. Current Dz detection and recording methods for cows and calves were studied. Experts in piloting and operating UAV assisted in model selection and hands on flight training; 2 UAVs were purchased, and flying, still and video photography, and data handling skills were gained. A questionnaire about Dz recording was developed for key farm personnel, and live color and thermal images and videos were captured by UAV on 4 dairy farms with large housing areas. Animal acclimation was achieved by first flying at 33 m, and then reducing flight altitude in 8 m increments; final tolerated height was approximately 4.3 m (14 ft). Animals in high-traffic areas adapted to UAV sooner than those in low-traffic areas, but all required <15 min. Animal ID was clear. Thermal imaging recorded cows’ skin temperature within 0.1°C, but black vs. white hide color, sun and shade affected the observed temperature by approximately 17°C. Cows with metritis or in estrus were detected by thermal imaging, but clinical mastitis was not readily detected by UAV. All farms used >1 method to record Dz. Cow records: notebook to computer 50% of farms, computer only 25%, not readily detected by UAV. All farms used >1 method to record Dz.

Real-time automatic system for calving detection in dairy cows. A. Arazi* and D. Rak, Afimilk, Afikim, Israel.

Calving is a crucial event in a productive cows’ life cycle and has significant influence on herd profitability and cow’s welfare. Calving detection is a key factor to ensure successful calving with minimal harm to the calf and the cow. It is used to decide if intervention is needed, when to move a cow to a maternity pen and to obtain a proper colostrum administration soon afterward. An automatic monitoring system to detect the onset of parturition could contribute to reduce calves morbidity and mortality and ensure better performance in the consequent lactation. The objective of this study was to test a real-time, automatic cow monitoring system for detecting calving in dairy cows based on rest and activity behaviors. The study was conducted on 4 Israeli dairy herds, between August 10 and October 22, 2015. Herds ranging from 356 to 1,012 Israeli Holstein milking cows. Cows were fitted with 2 tags (AfTag II, Afimilk, Israel) on front and rear legs, when moved to the close-up pen. Calving times were recorded by the herds’ teams. Calving alerts generated by the system (Af/Act II, Afimilk, Israel) were compared with the actual calving time. In total 231 and 187 successful calving detection alerts were recorded for cows fitted with tags on rear and front leg, respectively (not all the cows were fitted with tags on the front leg). Detection timing before calving were similar for front and rear legs. The distribution was about 35.5%, 28%, 26.5%, 8% and 2% for the last 1 h, 1–2 h, 2–4 h, 4–8 h and more than 8 h before calving, respectively. In all 4 herds, 50% and more of the alerts were provided in the 2 h preceding calving for both legs (range 50%–79%) and more than 80% of the alerts were in the last 4 h before calving (range 81.9–94.8%). The average time from detection to calving was about 2 h for both front and rear legs (range 01:18–02:38 h). These results suggest that a real-time automatic monitoring system based on cows’ rest and activity behavior can be a useful tool for detecting calving events in dairy cows. The use of such a system can help improve calving management and human interventions.

How to sanitize dairy herds from the contagious genotype B of Staphylococcus aureus? A new molecular biology approach. C. Sartori*1, 2 and H. U. Graber2, 1ETH, Zurich, Switzerland, 2Agroscope, Bern, Switzerland.

The aim of the present longitudinal field study was to compare the efficiency of 2 analytical approaches for the sanitation of Staphylococcus aureus genotype B (GTB)-positive dairy herds. S. aureus is one of the most widespread mastitis pathogens worldwide. Typically, it causes subclinical, chronic mastitis leading to reduced quality and production of milk, and to substantial economic loss in the dairy industry. In Switzerland, different genotypes of S. aureus have been identified, whereby the genotype B demonstrated to be the only contagious subtype, causing herd problems. Furthermore, this pathogen can cause food poisoning because of enterotoxin production. As the efficacy of antibiotic therapy and vaccination against S. aureus is not satisfactory, the most promising strategy for controlling this udder pathogen is the implementation of specific sanitation programs. In the present study, a new qPCR assay (very sensitive and specific for S. aureus GTB) was evaluated in the field for the sanitation of GTB-positive herds and compared with classical bacteriology. Both analytical methods were demonstrated to be effective, although the qPCR approach showed some key advantages, which enable the sanitation of entire herds in short time. The use of clean, instead of aseptically collected, milk samples facilitates sample collection in terms of time and cost, enabling the sampling of even big herds during a normal milking time. Because of the high sensitivity of qPCR, the rate of false-negative results is minimal, so that each GTB-positive cow can be correctly identified at any time point during lactation. The conclusive identification of GTB-positive cows can be accomplished within 2 d after sampling: This allows farmers to immediately build milking groups and to maintain the correct milking order. Milk sample analysis becomes easier, faster, more objective, and suitable for routine application. Additionally, all steps of the analytical procedure are suitable for automation, from sample preparation to the final qPCR reaction. This allows for the first time the implementation of sanitation programs at a broader, regional level, instead of being limited to the herd level.

Effects of dexamethasone and opsonized Mycoplasma bovis on bovine neutrophil function in vitro. H. A. Alabdullah*, L. K. Fox1, J. M. Gay1, G. M. Barrington1, and R. H. Mealey2,
The objective was to determine if in vitro glucocorticoids treatment of bovine neutrophils would impair their function to phagocytize and kill opsonized M. bovis. We hypothesized that in vitro treatment of bovine neutrophils by glucocorticoids impairs phagocytosis of opsonized M. bovis compared with non-treated neutrophils and such impairment would be a function of M. bovis strain differences. Neutrophils isolated from 20 mid-lactation cows were treated with 5 × 10−4 M dexamethasone (TX) or non-treated (CX). After treatment neutrophil function included: percentage reduction in log_{10} of M. bovis cfu/mL, percentage of phagocytizing neutrophils, phagocytized M. bovis per neutrophil, and killed M. bovis per neutrophil were quantified by incubating one of TX (NDM1–4) or CX (NM1–4) neutrophils group with one of 4 opsonized M. bovis strains. Least squares means of all neutrophil groups were contrasted using linear mixed-effects models. Overall means ± SEM for the dependent variables of percentage reduction in log_{10} of M. bovis cfu/mL, percentage phagocytizing neutrophils, phagocytized M. bovis per neutrophil, and killed M. bovis per neutrophil were: 17 ± 1.19, 69 ± 1.48, 8.3 ± 1.23, and 1.57 ± 0.67 for control neutrophils and 14 ± 1.3, 34 ± 1.4, 2.6 ± 0.82, and 0.59 ± 0.53 for neutrophils treated with dexamethasone respectively. Effects due to strain, treatment, and their interaction on neutrophil function measured by the number of phagocytized M. bovis per neutrophil and number of killed M. bovis per neutrophil were different (P < 0.05). However, there was no strain by treatment interaction effect on percentage reduction in log_{10} of M. bovis cfu/mL or strain and strain by treatment interaction effects associated with the dependent variable of percentage phagocytizing neutrophils. Dexamethasone consistently decreased all neutrophil function tested (P < 0.0001). These findings might explain in part the association of stressful events with subsequent outbreaks of Mycoplasma bovis associated bovine diseases.

Key Words: dexamethasone, Mycoplasma bovis, neutrophil function


Galectins (Gal) are a family of proteins that bind to β-galactoside sugars found on parts of other proteins, either on the cells’ surface or in the extracellular matrix. There are 15 galectin protein subtypes that all share the characteristic of carbohydrate recognition. Galectins are known to have an impact on immuno-modulation and are involved in uterine immunoregulation during pregnancy. The aim of this study was to evaluate the expression of Galectins in cow blood and identify their modulation during their periparturient period. We hypothesized that fold changes in galectin expression is dependent on the periparturient period (close-up and c+7) and also the health of the animal. Fold change ≥2 is considered significant. With the use of Primer-Blast from NCBI, galectin 1, 2, 3, 4, 7, 8, 9, 12 (forward and reverse) were sequenced for use in this project. Blood was taken 2 weeks close to calving (close up), and 7 d after calving(c+7) at Michigan State University dairy farm and shipped in Paxgene tubes for analysis (n = 20). Total RNA was isolated, reverse-transcribed to cDNA, and then used in real-time PCR experiments with the above primers and β-actin as the control. Fold change in transcript abundance was calculated using the Livak method. Where ΔΔCt = (Target genes_{c+7} - βactin_{c+7}) - ΔCt (Target genes_{close-up} - βactin close-up). Fold change = 2^(-ΔΔCt). In non-pregnant cows, all 8 galectins tested were expressed in bovine blood. In periparturient cows, only 1, 2, 3 and 4 were expressed. Galectins 1, and 3 were expressed in both close-up and c+7 samples. Galectin 4 was expressed before parturition. Galectin 2 was expressed after parturition. All genes tested were expressed in cow blood at varying levels. Galectin 1 was upregulated after calving (Fold change = 2.4). Further studies are needed to determine the role of galectins and factors that affect their expression in blood during the periparturient period.

Key Words: bovine blood, periparturient, galectin gene expression

189 Pegbovigrastim affected gene expression in neutrophils of transition cows indicating increased neutrophil function. A. Heiser, S. LeBlanc*, and S. McDougall. AgResearch, Palmerston North, New Zealand, 2Ontario Veterinary College, University of Guelph, Guelph, ON, Canada, 3Cognosco, AnexaFVC, Morrinsville, New Zealand.

Treatment of transition cows with granulocyte colony stimulating factor (G-CSF) has been shown to increase neutrophil count and function. It was hypothesized that prepartum under-nutrition may reduce the effect of a commercial recombinant bovine G-CSF product (pegbovigrastim; IMR). Hence this study was undertaken to test the effect of under-nutrition and IMR treatment on gene expression in neutrophils. Pasteure-fed cows (n = 99) in New Zealand were blocked by calving date and BCS and randomly assigned in a 2 × 2 factorial design to be fed prepartum to exceed energy requirements or restricted to 85% of energy requirements. Half of the animals in each group were injected with IMR or saline at approximately 7 d before expected calving and again on the day of calving. Blood samples were collected 7 d post-calving (D-7) and samples from blood, uterus and milk were on D4 and D7 after calving. Gene expression analysis was performed for 21 genes using Nanostring. Effects of time and IMR treatment were observed but feeding did not affect gene expression. On average, cows showed higher expression of almost all selected genes at D4 compared with D-7 including genes for migration and inflammation markers (L-selectin, ICAM-1 and TLR 2 and 4; P < 0.05) indicating an ongoing neutrophil response to the hormonal and metabolic stresses of the parturition and postpartum infections. IMR treatment enhanced the effect by further increasing expression of ICAM1 and TLR2 (P < 0.05) suggesting increased neutrophil efficiency. In uterine fluid and to a lesser degree in milk IMR lowered expression of migration markers and increased expression of genes for other neutrophil functions, including myeloperoxidase, FAS, and caspases 2 and 9 (P < 0.05) potentially increasing neutrophil effectiveness. IMR treatment resulted in significant increases in the expression of genes involved in inflammation, phagocytosis, respiratory burst, degranulation, and apoptosis/survival of neutrophils in blood, uterine fluid and milk, and also migration of blood neutrophils.

Key Words: transition cow, neutrophil, pegbovigrastim

188 Changes in galectin gene expression in bovine blood during the periparturient period. E. Asiajah1, S. Adjei-Fremah1, K. Ekwemalo1, M. Worku1, L. Sordillo2, and J. Gandy2. 1North Carolina A&T State University, Greensboro, NC, 2Michigan State University, East Lansing, MI.

Galectins (Gal) are a family of proteins that bind to β-galactoside sugars found on parts of other proteins, either on the cells’ surface or in the extracellular matrix. There are 15 galectin protein subtypes that all share the characteristic of carbohydrate recognition. Galectins are known to have an impact on immuno-modulation and are involved in uterine immunoregulation during pregnancy. The aim of this study was to evaluate the expression of Galectins in cow blood and identify their modulation during their periparturient period. We hypothesized that fold changes in galectin expression is dependent on the periparturient period (close-up and c+7) and also the health of the animal. Fold change ≥2 is considered significant. With the use of Primer-Blast from NCBI, galectin 1, 2, 3, 4, 7, 8, 9, 12 (forward and reverse) were sequenced for use in this project. Blood was taken 2 weeks close to calving (close up), and 7 d after calving(c+7) at Michigan State University University dairy farm and shipped in Paxgene tubes for analysis (n = 20). Total RNA was isolated, reverse-transcribed to cDNA, and then used in real-time PCR experiments with the above primers and β-actin as the control. Fold change in transcript abundance was calculated using the Livak method. Where ΔΔCt = (Target genes_{c+7} - βactin_{c+7}) - ΔCt (Target genes_{close-up} - βactin close-up). Fold change = 2^(-ΔΔCt). In non-pregnant cows, all 8 galectins tested were expressed in bovine blood. In periparturient cows, only 1, 2, 3 and 4 were expressed. Galectins 1, and 3 were expressed in both close-up and c+7 samples. Galectin 4 was expressed before parturition. Galectin 2 was expressed after parturition. All genes tested were expressed in cow blood at varying levels. Galectin 1 was upregulated after calving (Fold change = 2.4). Further studies are needed to determine the role of galectins and factors that affect their expression in blood during the periparturient period.

Key Words: bovine blood, periparturient, galectin gene expression

190 Effect of prepartum energy balance on neutrophil function following pegbovigrastim treatment in periparturient cows. S. McDougall1, S. LeBlanc2, and A. Hesier3. 1Cognosco, AnexaFVC, Morrinsville, New Zealand, 2Ontario Veterinary College, University of Guelph, Guelph, ON, Canada, 3AgResearch, Hopkirk Research Institute, Palmerston North, New Zealand.

Treatment with granulocyte colony stimulating factor (G-CSF) increases neutrophil (PMN) count and enhances PMN function in the periparturient cow. It was hypothesized that prepartum undernutrition may reduce the effect of a commercial recombinant bovine G-CSF product (pegbovigrastim; IMR) on PMN count and function. Hence this study
was undertaken to test the effect of undernutrition for one month before calving on the response to IMR. Cows (n = 99) on pasture in a research herd in New Zealand were blocked by expected calving date and BCS and randomly assigned in a 2 by 2 factorial design to be fed to exceed energy requirements prepartum (FULL), or restricted to approximately 85% of prepartum energy requirements (RES). At approximately 7 d before expected calving and on the day of calving, half the cows in each feed group were injected with IMR while the remaining half were injected with saline. Blood samples were collected pre-and post-calving for complete blood count, biochemistry and in vitro assessment of PMN function including phagocytosis, myeloperoxidase (MPO) release and oxidative burst. Energy restriction prepartum resulted in lower body weight (96.1 ± 0.4% vs 101.0 ± % of initial body weight for RES vs FULL cows at calving; P < 0.001), and a higher proportion of cows with elevated concentrations (i.e., > 0.4 mmol/L) of fatty acids (35/41 (85.4%) vs 23/41 (56.1%) elevated for RES vs FULL cows at 7 d before calving; P < 0.001). Treatment with IMR increased PMN count (9.8 ± 0.2 vs 3.9 ± 0.2 × 10^3/mL; P < 0.001). There was a time x IMR interaction (P < 0.001) for proportional release of MPO by PMN, with higher release at 4 d post-calving in IMR cows (0.80 (95%CI = 0.72–0.88) vs 0.59 (95%CI = 0.53–0.64)). There was no effect of prepartum energy restriction, nor energy restriction x IMR interactions for any of the white cell counts or functional tests. It is concluded that IMR treatment results in significant increases in PMN count, and enhances PMN function as indicated by increased MPO release. The response to IMR was not affected by restricted pre-partum energy intake.

**Key Words:** pegbovigrastim, energy balance, neutrophil function

191 **Epidemiology of bovine respiratory disease in pre-weaned dairy calves in California.** S. A. Dubrovsky*,1, A. L. Van Eenennaam1, B. M. Karle2, T. W. Lehenbauer3, 4, and S. S. Aly1, 4, 1Department of Animal Science University of California Davis, Davis, CA, 2University of California Cooperative Extension, Orland, CA, 3Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, CA, 4Veterinary Medicine Teaching and Research Center, School of Veterinary Medicine, University of California, Davis, Tulare, CA.

Bovine respiratory disease (BRD) is one of the leading causes of pre-weaning death in dairy heifers. The objective of this prospective cohort study was to characterize the epidemiology of BRD in preweaned dairy calves and to identify management practices that reduce the incidence of BRD. Calves were assigned to one of four groups based on management practices, calf records, location, and size. A total of 6,250 calves, ranging in size from 700 to 3,200 milking cows, in 6 counties across California’s Central Valley, were enrolled for at least one year. A total of 11,945 calves were born on the study dairy and followed from birth to weaning. Incidence of BRD was estimated using treatment records. A comprehensive calf management survey and prevalence estimate was performed by trained study personnel once every season. A shared frailty model was used to identify significant risk factors associated with first lactation 305 milk production in Holstein dairy calves. T. R. Dunn*,1, T. L. Ollivett2, D. L. Renaud3, and D. F. Kelton1, 1Department of Population Medicine, University of Guelph, Guelph, ON, Canada, 2Department of Medical Sciences, University of Wisconsin-Madison, School of Veterinary Medicine, Madison, WI.

Bovine respiratory disease (BRD) is a complex disease process and early diagnosis can be difficult because of inconsistent or absent clinical signs. Many reports emphasize the negative implications of clinical BRD. Diagnosing subclinical respiratory disease through thoracic ultrasonography has the potential to improve animal welfare and productivity. The objective of this cohort study was to determine if lung consolidation in young dairy calves was associated with a decline in first lactation milk production. A total of 215 female calves from 3 dairy herds in Southwestern Ontario were enrolled and assessed weekly during their first 8 weeks of life for evidence of lung consolidation (CON) through the use of thoracic ultrasonography (US) (Ibex Pro, Loveland, CO). Consolidation was measured within the first 10 intercostal spaces on both sides of the thorax, using gridlines on the screen of the US. Calves were considered CON positive if 3cm or more of consolidated lung was present. A multivariable linear regression model was used to identify significant risk factors associated with first lactation 305 milk production. In the study population, the following calfhood conditions were present: twins (4%; n = 8), diarrhea in the first 21 d of life (31%; n = 66), rib fractures (7%; n = 14), lung abscesses (3%; n = 6), and at least one diagnosis of CON (57%; n = 123). Overall, 7% (n = 15) of calves died, and 18% (n = 38) of animals were sold before the end of first lactation. For every one-month increase in age at first calving, milk production in first lactation increased by nearly 140 kg (P = 0.01). The presence of CON, at least once in the first 8 weeks of life, was associated with a 525kg decrease in first lactation 305 milk production (P = 0.027). These results indicate that lung consolidation during the first 56 d of life may have a possible long-term impact on dairy calves, manifested as reduced milk production during first lactation.

**Key Words:** lung consolidation, ultrasonography

193 **Associations between respiratory disease type and average daily gain in preweaned group-housed dairy calves.** M. C. Cramer*1 and T. L. Ollivett2, 1University of Wisconsin-Madison, Department of Dairy Science, Madison, WI, 2University of Wisconsin-Madison, School of Veterinary Medicine, Madison, WI.

The study objective was to determine associations between average daily gain (ADG) in dairy calves and 6 forms of respiratory disease (RESP), defined by combinations of clinical and thoracic ultrasound scores. Preweaned dairy calves (n = 280) on a commercial herd in Ohio, USA were enrolled at entry to an automated milk feeder barn and housed in groups of 13 ± 3 (mean ± stdev). Calves were 21 ± 6 d old at enrollment...
and were followed for 6 weeks. Twice weekly health exams included a clinical respiratory score (CRS), thoracic ultrasound score (USS), fecal score, and body weight. For the CRS, the nose, eyes, ears, cough, and rectal temperature were assigned a score (0–3) and was considered positive when at least 2 areas scored ≥2. The USS ranged from 0 (normal) to 5 (abnormal) based on the degree of lung consolidation. The CRS and USS were combined to create 6 RESP types: clinical lobular pneumonia (CLL; USS = 2, CRS+; n = 10), clinical lobar pneumonia (CL; USS ≥ 3, CRS+; n = 31), subclinical lobular pneumonia (SLL; USS = 2, CRS-; n = 82), subclinical lobar pneumonia (SCL; USS ≥ 3, CRS-; n = 88), upper respiratory tract disease (URT; USS < 2, CRS+; 40), and normal (USS < 2, CRS-; n = 29). A multivariable linear regression model was fit to determine if ADG was associated with RESP after controlling for sex, breed, and scours. A significant interaction existed between RESP and scours (P = 0.01). For calves without scours, ADG was significantly lower for CL (0.46kg) compared with SCL (0.69kg, P = 0.03), SLL (0.72kg, P = 0.008), and URT (0.79kg, P = 0.002); there was no difference in ADG among CL, CLL, or normal calves (P > 0.41). For scoursing calves, there was a tendency for lower ADG in URT calves (0.44kg) compared with SCL calves (0.70kg, P = 0.06); ADG did not differ among CL, CLL, SLL, or normal calves (P > 0.95). This research is the first step in understanding the impacts of types of RESP, identified with CRS and USS, on calf performance. Findings suggest that calves with clinical lobar pneumonia are most severely affected. Further research is needed to understand if these calves should be managed differently than calves with other types of respiratory disease.

**Key Words:** bovine respiratory disease (BRD), calf, ultrasound

194 **Time lost to disease in dairy cattle: Associations between two consecutive lactations.** P. Bacigalupo-Sanguesa1, C. McConnel2, F. Garry1, J. Lombard1, and P. Pinedo6, 1Department of Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO, 2Department of Veterinary Clinical Sciences, College of Veterinary Medicine, Washington State University, Pullman, WA, 3USDA-APHIS-VS-Center for Epidemiology and Animal Health, Fort Collins, CO, 4Department of Animal Sciences, College of Agricultural Sciences, Colorado State University, Fort Collins, CO.

The objective of this study was to evaluate the association between days lost due to specific diseases and total days lost due to disease in 2 consecutive lactations using a new measure called the disease-adjusted lactation (DALact). The DALact is a health measure that incorporates morbidity and removal (death or culling) into a single time-based summary measure and it represents a new approach for assessing the impact of diseases in a lactation. Health and removal data were obtained from a Colorado dairy with approximately 1,400 lactating cows. Multiparous cows (n = 805) that calved, were sold, or died from July 1, 2015, through June 30, 2016, were selected. Individual cow health data were collected the previous lactation. Health events included calving injury, displaced abomasum, diarrhea, hypocalcemia, ketosis, lameness, mastitis, metritis, musculoskeletal injuries, pneumonia, and retained placenta. All cow-level data were imported into SAS for validation, calculation of DALact, and analysis. The DALact was calculated adding the Days Lost due to Premature Death or Culling (DLRD) and the Days Lost due to Illness (DLI). DLRD was calculated as the difference between the average completed lactation days in milk for the herd and the days in milk at culling or death for individual cows. The DLI was the product of the number of cases of each disease multiplied by established disability weights and estimated disease durations (days) for a specific disease. The association between DALacts in 2 consecutive lactations was evaluated using PROC GLM. P-values < 0.05 were considered significant. Positive significant associations (P < 0.001) were found between DALacts in 2 consecutive lactations for lameness and mastitis. Similarly, the total DALacts in 2 consecutive lactations were also significantly associated (P < 0.001). Identification of diseases and reasons for removal that significantly affect time lost during 2 consecutive lactations will help producers focus management and preventive measures on diseases having the greatest impact on future productivity and wellbeing.

**Key Words:** dairy cattle, disease, DALact

195 **Metagenomic analysis of fecal microbiomes in cattle infected with Mycobacterium avium ssp. paratuberculosis.** N. Indugu, D. Pitta, B. Bhukya, B. Vecchiarelli, M.-E. Fecteau, and R. Sweeney, University of Pennsylvania, School of Veterinary Medicine, New Bolton Center, PA.

Johne’s disease (JD) is a chronic gastrointestinal infection of cattle caused by *Mycobacterium avium ssp. paratuberculosis* (MAP). We hypothesized that cattle naturally infected with MAP acquire gastrointestinal dysbiosis which may play a role in the pathogenesis of JD. To this end, we compared the fecal microbiomes of 20 naturally infected fecal samples (positive group), 10 JD-negative herd mates (exposed group) and 10 JD-negative cows from a MAP-free herd (negative group). Metagenomic DNA libraries were constructed and sequenced on Ion Torrent platform and assembled using NextGENe (V2) program. Phylogenetic assignments and functional annotations of assembled contigs were performed with RefSeq and COGs database respectively using MG-RAST Server. Bray-Curtis dissimilarity distance based analysis showed significant differences (P < 0.05; PERMANOVA) between positive, exposed and negative groups. Taxonomic annotations revealed the abundance of bacteria at up to 85%. Although the same phylotypes were commonly present among all 3 groups, their relative abundance varied (P < 0.05; Wilcoxon), particularly in the positive group. Notably, Actinobacteria was highly abundant (30% of the total bacteria) in the positive group, whereas it constituted less than 1% in the other groups. Further, only a small proportion of sequences (100 sequences; 0.002%) were detected as MAP sequences in the positive group, but were not detected in the other 2 groups. Functional annotations showed the abundance of metabolism pathways at up to 25% of gene content. Among metabolic pathways, gene sequences associated with energy production, amino acid metabolism, lipid metabolism, mineral metabolism and secondary metabolites biosynthesis were significantly higher (P < 0.05; Wilcoxon) in the MAP positive group compared with the other 2 groups. While elevated lipid pathways in the MAP positive group denotes that MAP relies heavily on lipid-based substrates such as cholesterol for its growth. An increase in other metabolic pathways probably denotes adaptation mechanisms of MAP in the host.

**Key Words:** fecal-microbiome, Johne’s disease, MAP