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alerts us to the importance of monitoring and control of these pathogens in the veterinary hospital environment, which can be easily carted to in patients, may cause infections related to health care, as well as colonize humans live in these places.

MI-0689

Identification and molecular typing of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) in water from dairy goat farms.

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Paratuberculosis or Johne's disease, infectious chronic inflammatory bowel disease, that may affect ruminants by ingestion of water, colostrum and contaminated food, whose etiologic agent is *Mycobacterium avium* ssp. *paratuberculosis* (MAP). Infected goats have progressive weight loss and diarrhea may or may not be present. The agent is eliminated mainly in feces and milk contaminating soil and water. The aim of the study was detecting and typify MAP in water for human and animal consumption in 10 dairy goat's farms, from Zona da Mata, Minas Gerais State, Brazil, important producing region of goat milk. Techniques used were microbiological culture, PCR, RE-PCR and sequencing. MAP was identified in 50% of water samples for animal consumption and 30% in the ones for human consumption. Amongst the animal samples, bacteria were detected in viable form in four of the five positive samples. Restriction enzyme- IS1311 was performed, which showed that all isolates were type C (cattle). These results support possible involvement of water as MAP's transmission via, contributing to the maintenance agent in the herd. The zoonotic potential, associated with economic and production losses, shows the importance of researching the agent in the aquatic environment. This is the first report on the isolation and typify of MAP in water from dairy goats' farms in Brazil.

MI-0690

The bacterial multi-resistance in domiciled animals in São Paulo city.

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Dogs and cats are considered active members of Brazilian families. The tenderness relationship increased contact between animals and their owners what permitted to share physical space and instruments. Therefore animals carrying multi-resistant bacteria can disseminate of such agents or its resistance genes. This work aimed to describe the bacterial multi resistance in isolates from distinct samples obtained from domiciled dogs and cats that have veterinary assistance. The descriptive and retrospective study involved 2459 samples originated from several regions of São Paulo city during 2015. The disc diffusion method was performed according to CLSI standards (2013) and resistance markers were the BLEE detection in Enterobacteriaceae, oxacillin (1 µg) disc-resistance and MLSB+ phenotype in the *Staphylococcus intermedius* group (SIG) and the Imipenem (10µg) disc-resistance in the *Pseudomonas aeruginosa* strains. The urine isolates analysis reveal the *Escherichia coli* and ESBL producing *Klebsiella* spp prevalence were 22% and 42%, respectively. Furthermore 20% of ESBL+ *Klebsiella* spp strains showed cross resistance to other five antimicrobial drugs classes which means the double of the *E. coli* resistance. The SIG were isolated in 75,5% from skin and otic samples. Among skin infections the MLSB phenotype was detected in almost 42% of the isolates and together with β-lactamic resistance in 11,5% of the isolates. In addition 16% of these strains revealed cross resistance to other five antimicrobial drugs classes such as fluoroquinolones (92%) and cotrimoxazol (88%). The SIG isolates obtained from otic samples did not reveal increased resistance to β-lactamic (5%) although 37,5% of oxacillin-resistant strains were also resistant to other five antimicrobial drugs classes, such as aminoglycosides (87,5%), fluoroquinolones (87,5%) and cotrimoxazol (94%). A imipenem resistance was seen in 33,5% among the *P. aeruginosa* cutaneous samples. Another relevant data was that 16,5% of tested strains displayed resistance to both aminoglycosides and fluoroquinolones. The results revealed that multi-resistance is a current issue amongst bacteria that cause distinct animal infections and this should always be considered by the veterinarian when selecting an empiric therapeutic choice. The authors observed that β-lactamic resistance is more significant amongst gram negative bacteria and when facing ESBL+ *Klebsiella* spp strains the treatment options became sparse. In the treatment of SIG infections the β-lactamic drugs still can be good therapeutic options although the use of macrolides, lincosamides and fluoroquinolones should only be done after disc-diffusion test results. The understanding of the bacterial agent as well as its resistance profile is fundamental in order to prevent that multi-resistant strains continue to be selected and eventually shared.

MI-0691

Absence of methicillin resistance in *Staphylococcus aureus* isolated from bovine mastitis in southeast Brazil.

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Bovine mastitis has major impact in the global dairy industry and *Staphylococcus aureus* is the main causative agent of this disease. Besides economic and animal health importance, there is also a potential implication for human health due to the zoonotic spread of *S. aureus*, especially methicillin resistant *S. aureus* (MRSA), and due to the extensive use of antibiotics in treatment and control of mastitis that might select resistant bacteria. This study aimed to identify phenotypic and genotypic resistance to methicillin, since MRSA is a potentially important veterinary pathogen and a known important public health concern. For this purpose, 380 strains of *S. aureus* were tested. All material came from rural properties around three states in southeast Brazil: Minas Gerais, São Paulo and Rio de Janeiro. Between 1994 and 2014, strains were identified by standard biochemical procedures and stored at -80°C. Species identification was confirmed by targeting of a specific sequence of the *S. aureus* thermonuclease *nuc* gene. In addition, susceptibility profile of each isolate was obtained by Kirby-Bauer disk diffusion method and

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all strains were submitted to PCR targeting of the *mecA* gene, the main responsible for methicillin-resistance. This study had prior clearance of the Ethics Committee for the Use of Animals (CEUA) of the Faculty of Veterinary Medicine of the University of São Paulo (protocol number 6323200215). Resistance was found in 60% (228/380) of the strains, most frequently to ampicillin with 55.3% (210/380), tetracycline with 13.7% (52/380) and erythromycin with 3.7% (14/380). Multidrug resistance was found in 15/380 strains (3.9%). None of the strains showed phenotypic resistance to oxacillin and ceftiofur and the *mecA* gene was absent in all the samples tested. There are few studies on the epidemiology of MRSA from bovine mastitis and detection of MRSA-ST398 isolates in Brazil occurred in only one heard. ST398 is a worldwide spread lineage, associated with farm animals and with community acquired MRSA in humans in some European countries. However, in other countries, such as the United States, although ST398 is present in livestock, transmission to humans does not seem to be important. In conclusion, to our knowledge this is the first study that attempts to understand time distribution of MRSA in bovines in Brazil, however MRSA was absent in the samples studied and does not appear to be of importance in the country. Further studies are necessary to confirm this bovine mastitis pathogen presence in herds and to assess its zoonotic potential.

MI-0692

Low frequency of anti- *Leptospira* spp. antibodies in dogs and small wild mammals in Pampa and Atlantic rainforest biomes from Rio Grande do Sul State, Brazil.

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Leptospirosis is a worldwide distributed anthrozoosis that affects a wide range of species, including domestic animals and man. Wild animals can participate in the epidemiological chain of the disease, mainly as reservoirs. Therefore, the aim of this study was to evaluate the frequency of anti- *Leptospira* spp. antibodies in wild animals and dogs. For this reason, 343 blood serum were analyzed, 192 of dogs and 151 of small mammals, more specifically rodents of the Cricetidae and Caviidae families and marsupials of the Didelphidae family. All material came from Pampa and Atlantic rainforest biomes of conservation areas and rural properties around these areas of three municipalities in Rio Grande do Sul state: Barra do Quaraí (Parque Estadual do Espinilho), Cerro Largo and Derrubadas (Parque Estadual do Turvo). Blood samples were collected by venipuncture of the cephalic in dogs and cardiac puncture in small mammals, and subsequently blood serum was obtained. The Microscopic Agglutination Test (MAT) was used against 23 serovars of *Leptospira* spp. The study had permit and prior clearance of the Ethics Committee for the Use of Animals (CEUA) of the Faculty of Veterinary Medicine of the University of São Paulo (protocol number 2908/2013) and the Chico Mendes Institute for Biodiversity (ICMBio) (protocol number 38502-1). From the total of dogs samples 9.89 % (19/192) were positive, with titers ranging from 100-3200. Evaluating only the most probable serovars, the predominance was of Australis (5/14), Cynopteri (4/14) and Butembo (2/14). A dog in the municipality of Derrubadas was positive for Pomona, the same serovar found in a wild animal in the same region. Among the small mammals, the prevalence was of 1.32 % (2/151). The two reagent wild animals were rodents Cricetidae family, an animal with titer 100 for the serovar Grippytophosa and another with titer 200 for Pomona, both belonging the municipality of Derrubadas. In Barra do Quaraí, the most probable serovar was Cynopteri and Australis in Cerro Largo. We can conclude that *Leptospira* spp. does not seem to be circulating in wild animals in the three regions studied and the frequency of seropositive *Leptospira* spp. in dogs was low.

MI-0693

Bases moleculares de la resistencia a los antibióticos betalactámicos en *Escherichia coli* aisladas de *Leucophaeus pipixcan* (gaviota de Franklin) en la costa de Antofagasta.

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Las bacterias resistentes a los antibióticos no sólo constituyen un problema que concierne a los hospitales, sino que también existe una gran preocupación por su presencia en el medio ambiente, especialmente en animales domésticos y silvestres. Uno de ellos, lo constituyen las aves migratorias que albergan en su intestino bacterias resistentes a los antibióticos y que tienen una migración de miles de kilómetros. En ellas se han detectado cepas de *Escherichia coli* productoras de betalactamasas de espectro extendido (BLEE). La gaviota de Franklin (*Leucophaeus pipixcan*) habita en la frontera de Canadá y Estados Unidos y durante el invierno del hemisferio norte viaja por las costas del Pacífico y llega hasta Chile, incluyendo Antofagasta (noviembre a abril de cada año). En este estudio se investiga la presencia de *E. coli* multiresistentes a los antibióticos y se determina la existencia de cepas productoras de BLEE albergadas en el intestino de *L. pipixcan* en la costa de Antofagasta. Se tomaron muestras fecales recién emitidas por las gaviotas y se sembraron en agar MacConkey en forma convencional y también, en placas con 8 µg/ml de cefotaxima. Las cepas de *E. coli* se identificaron por pruebas bioquímicas y la susceptibilidad a los antibióticos por técnica de difusión por discos. En las cepas resistentes a cefotaxima se evaluó la presencia de BLEE por métodos fenotípicos, los genes *bla*_{CTX-M}, *bla*_{TEM} y *bla*_{SHV} por PCR y la identificación de los tipos enzimáticos por secuenciación de los amplicones de la PCR. También, se estudiaron los genotipos prevalentes por campo pulsado (PFGE). En los aislados se identificaron 91 cepas de *E. coli* con una elevada resistencia a los antibióticos beta-lactámicos como ampicilina, cefadroxilo y cefotaxima (100%), cefuroxima (98%), aztreonam (69%) y ceftazidima (49%). Además, se observó resistencia a las quinolonas (72-100%), tetraciclina (70%) y cotrimoxazol (73%). Frente a los aminoglicósidos, macrólidos, cloranfenicol y nitrofurantoina mostraron una elevada susceptibilidad y con un 100% a los carbapenemes. Se observó multiresistencia que fluctuó entre 5 y 11 antibióticos simultáneamente. En un 94% de las cepas, la amplificación reconoció al gen *bla*_{CTX-M}, en un 55,2% al gen *bla*_{TEM} y no detectó el gen *bla*_{SHV}. Diversos tipos enzimáticos fueron identificados por secuenciación; CTX-M-15 (53,7%), CTX-M-22 (23,9%), CTX-M-2 (13,4%) y CTX-M-1 (9%) de los aislados. La mayoría de las cepas productoras de CTX-M-15 estaban asociadas al elemento de inserción *ISEcp1* por el análisis bioinformático. En relación al gen *bla*_{TEM} se encontraron los tipos TEM-1 (28/75,7%), TEM-40 (5/13,5%) y TEM-195 (1/2,7%). En los ensayos de electroforesis de campo pulsado (PFGE) se detectó una gran diversidad genética y con un clon prevalente (25,5%). Estos hallazgos sugieren que las gaviotas

LIBRO DE RESUMENES

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**REUNIÓN DE LA SOCIEDAD LATINOAMERICANA DE TUBERCULOSIS Y
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