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Alinaitwe L., Aturinda C.J., Lubega A., Kivali V., Bugeza J., Wainaina M., Richter M.H., Hoona J.J., Roesel K., Mayer-Scholl A., Cook E.A.J., Kankya C., Dürr S.

Cross-sectional serosurvey of *Leptospira* species among slaughter pigs, goats, and sheep in Uganda

(2024) PLoS Neglected Tropical Diseases, 18 (3), art. no. e0012055

DOI: 10.1371/journal.pntd.0012055

ABSTRACT: Introduction *Leptospira* are a group of bacteria, including pathogenic types that cause leptospirosis. In Uganda, *Leptospira* exposure has been reported in humans, with domesticated animals being speculated as the source. However, comparable evidence of *Leptospira* prevalence and circulating serovars/serogroups in animals is only documented for cattle, and dogs. Our study determined *Leptospira* seroprevalence, associated risk factors and serogroups circulating among slaughtered pigs, goats, and sheep in Uganda. Methods During an 11-month cross-sectional survey in selected slaughter facilities in three regions of Uganda, we collected blood from 926 pigs, 347 goats, and 116 sheep. The age, sex, breed, and origin of each sampled animal were noted. The samples were tested for anti-*Leptospira* antibodies using the microscopic agglutination test, based on a panel of 12 serovars belonging to 12 serogroups. Results *Leptospira* seroprevalence was 26.67% (247/926, 95%CI 23.92–29.61) among pigs, and 21.81% (101/463, 95%CI 18.29–25.80) in goats and sheep (small ruminants). *L. interrogans Australis* and *L. kirschneri Grippotyphosa* were the commonest serovars among pigs, as was *L. borgpetersenii Tarassovi* in small ruminants. Pigs sourced from the Eastern (Odds Ratio [OR] = 2.82, 95%CI 1.84–4.30) and Northern (OR = 3.56, 95%CI 2.52–5.02) regions were more likely to be seropositive, compared to those from the Central region. For small ruminants, being female (OR 2.74, 95% CI 1.69–4.57) and adult (OR 4.47, 95% CI 1.57– 18.80) was significantly more associated with *Leptospira* seropositivity. Conclusion/significance: Detection of a moderate seroprevalence, and several *Leptospira* serogroups among pigs, sheep, and goats from all regions of Uganda, supports existing reports in cattle and dogs, and implies widespread *Leptospira* exposure in domestic animals in Uganda. These findings may inform future programs for the control of leptospirosis in livestock in Uganda.

LANGUAGE OF ORIGINAL DOCUMENT: English

Boonciew P., Saisongkorh W., Brameld S., Thongpin M., Kurilung A., Krangvichian P., Niyomtham W., Patarakul K., Phichitraslip T., Hampson D.J., Prapasarakul N.

Improved Antibody Detection for Canine Leptospirosis: ELISAs Modified Using Local *Leptospira* Serovar Isolates from Asymptomatic Dogs

(2024) *Animals*, 14 (6), art. no. 893

DOI: 10.3390/ani14060893

ABSTRACT: Leptospirosis is a zoonotic disease of significant concern for human and animal health, with domestic animals, including dogs, acting as reservoirs for human infection. Serology is widely used for leptospirosis diagnosis, even though the standard microscopic agglutination test (MAT) using a panel of serovars lacks specificity and can lead to detection limitations in certain regions. In this study, we aimed to develop an antibody detection tool for dogs using an indirect enzyme-linked immunosorbent assay (ELISA) with a set of local serovar isolates, including Paidjan, Dadas, and Mini, to enhance the accuracy of leptospirosis surveillance in our region. The specificity and sensitivity of various antigen preparations, namely leptospiral whole-cell protein (WCP), total membrane protein (TMP), and outer membrane protein (OMP), were assessed using sera from infected and non-infected dogs, as well as negative puppy sera. Leptospirosis diagnosis was supported using a genus-specific nested polymerase chain reaction test on all collected sera. Protein

preparations were validated using SDS-PAGE and Western blotting analysis. In the results, the standard MAT failed to detect antibodies in any of the dogs confirmed as being infected using PCR and isolation, highlighting its limitations. In contrast, the OMP-based ELISAs using local isolates of *Leptospira* serovars gave positive results with sera from all infected dogs, and negative results with sera from all dogs from non-endemic areas. IgG titres of infected and unvaccinated dogs from endemically affected areas were significantly higher than those in non-endemic regions. Using the OMP-based IgG/ELISAs with the local serovar Dadas resulted in higher specificity and lower sensitivity than when using the WCP- and TMP-based IgG/ELISAs. Agreement analysis revealed fair and moderate concordance between OMP-based IgG/ELISAs and PCR results, whereas slight and fair agreement was observed between OMP-based ELISAs and the MAT. Overall, the modified OMP-based IgG/ELISAs, utilising relevant local serovar isolates from dogs, demonstrated improved accuracy in detecting leptospirosis in the study area, overcoming the limitations of the MAT. This study highlights the importance of identifying and incorporating these local circulating serovar isolates into serological techniques for leptospirosis diagnosis and surveillance.

LANGUAGE OF ORIGINAL DOCUMENT: English

Torres A.E.P., Bolivar-Lozano S.A., Faccini-Martínez Á.A.

Diffuse alveolar hemorrhage as a presentation of severe anicteric leptospirosis

(2024) *Revista da Sociedade Brasileira de Medicina Tropical*, 57, art. no. e00905-2024

DOI: 10.1590/0037-8682-0582-2023

LANGUAGE OF ORIGINAL DOCUMENT: English

Win T.Z., Han S.M., Edwards T., Maung H.T., Brett-Major D.M., Smith C., Lee N.

Antibiotics for treatment of leptospirosis

(2024) *Cochrane Database of Systematic Reviews*, 2024 (3), art. no. CD014960

DOI: 10.1002/14651858.CD014960.pub2

ABSTRACT: Background: Leptospirosis is a disease transmitted from animals to humans through water, soil, or food contaminated with the urine of infected animals, caused by pathogenic *Leptospira* species. Antibiotics are commonly prescribed for the management of leptospirosis. Despite the widespread use of antibiotic treatment for leptospirosis, there seems to be insufficient evidence to determine its effectiveness or to recommend antibiotic use as a standard practice. This updated systematic review evaluated the available evidence regarding the use of antibiotics in treating leptospirosis, building upon a previously published Cochrane review. Objectives: To evaluate the benefits and harms of antibiotics versus placebo, no intervention, or another antibiotic for the treatment of people with leptospirosis. Search methods: We identified randomised clinical trials following standard Cochrane procedures. The date of the last search was 27 March 2023. Selection criteria: We searched for randomised clinical trials of various designs that examined the use of antibiotics for treating leptospirosis. We did not impose any restrictions based on the age, sex, occupation, or comorbidities of the participants involved in the trials. Our search encompassed trials that evaluated antibiotics, regardless of the method of administration, dosage, and schedule, and compared them with placebo or no intervention, or compared different antibiotics. We included trials regardless of the outcomes reported. Data collection and analysis: During the preparation of this review, we adhered to the Cochrane methodology and used Review Manager. The primary outcomes were all-cause mortality and serious adverse events (nosocomial infection). Our secondary outcomes were quality of life, proportion of people with adverse

events considered non-serious, and days of hospitalisation. To assess the risk of bias of the included trials, we used the RoB 2 tool, and for evaluating the certainty of evidence we used GRADEpro GDT software. We presented dichotomous outcomes as risk ratios (RR) and continuous outcomes as mean differences (MD), both accompanied by their corresponding 95% confidence intervals (CI). We used the random-effects model for all our main analyses and the fixed-effect model for sensitivity analyses. For our primary outcome analyses, we included trial data from the longest follow-up period. Main results: We identified nine randomised clinical trials comprising 1019 participants. Seven trials compared two intervention groups and two trials compared three intervention groups. Amongst the trials comparing antibiotics versus placebos, four trials assessed penicillin and one trial assessed doxycycline. In the trials comparing different antibiotics, one trial evaluated doxycycline versus azithromycin, one trial assessed penicillin versus doxycycline versus cefotaxime, and one trial evaluated ceftriaxone versus penicillin. One trial assessed penicillin with chloramphenicol and no intervention. Apart from two trials that recruited military personnel stationed in endemic areas or military personnel returning from training courses in endemic areas, the remaining trials recruited people from the general population presenting to the hospital with fever in an endemic area. The participants' ages in the included trials was 13 to 92 years. The treatment duration was seven days for penicillin, doxycycline, and cephalosporins; five days for chloramphenicol; and three days for azithromycin. The follow-up durations varied across trials, with three trials not specifying their follow-up periods. Three trials were excluded from quantitative synthesis; one reported zero events for a prespecified outcome, and two did not provide data for any prespecified outcomes. Antibiotics versus placebo or no intervention. The evidence is very uncertain about the effect of penicillin versus placebo on all-cause mortality (RR 1.57, 95% CI 0.65 to 3.79; I² = 8%; 3 trials, 367 participants; very low-certainty evidence). The evidence is very uncertain about the effect of penicillin or chloramphenicol versus placebo on adverse events considered non-serious (RR 1.05, 95% CI 0.35 to 3.17; I² = 0%; 2 trials, 162 participants; very low-certainty evidence). None of the included trials assessed serious adverse events. Antibiotics versus another antibiotic. The evidence is very uncertain about the effect of penicillin versus cephalosporin on all-cause mortality (RR 1.38, 95% CI 0.47 to 4.04; I² = 0%; 2 trials, 348 participants; very low-certainty evidence), or versus doxycycline (RR 0.93, 95% CI 0.13 to 6.46; 1 trial, 168 participants; very low-certainty evidence). The evidence is very uncertain about the effect of cefotaxime versus doxycycline on all-cause mortality (RR 0.18, 95% CI 0.01 to 3.78; 1 trial, 169 participants; very low-certainty evidence). The evidence is very uncertain about the effect of penicillin versus doxycycline on serious adverse events (nosocomial infection) (RR 0.62, 95% CI 0.11 to 3.62; 1 trial, 168 participants; very low-certainty evidence) or versus cefotaxime (RR 1.01, 95% CI 0.15 to 7.02; 1 trial, 175 participants; very low-certainty evidence). The evidence is very uncertain about the effect of doxycycline versus cefotaxime on serious adverse events (nosocomial infection) (RR 1.01, 95% CI 0.15 to 7.02; 1 trial, 175 participants; very low-certainty evidence). The evidence is very uncertain about the effect of penicillin versus cefotaxime (RR 3.03, 95% CI 0.13 to 73.47; 1 trial, 175 participants; very low-certainty evidence), versus doxycycline (RR 2.80, 95% CI 0.12 to 67.66; 1 trial, 175 participants; very low-certainty evidence), or versus chloramphenicol on adverse events considered non-serious (RR 0.74, 95% CI 0.15 to 3.67; 1 trial, 52 participants; very low-certainty evidence). Funding: Six of the nine trials included statements disclosing their funding/supporting sources and three trials did not mention funding source. Four of the six trials mentioning sources received funds from public or governmental sources or from international charitable sources, and the remaining two, in addition to public or governmental sources, received support in the form of trial drug supply directly from pharmaceutical companies. Authors' conclusions: As the certainty of evidence is very low, we do not know if antibiotics provide

little to no effect on all-cause mortality, serious adverse events, or adverse events considered non-serious. There is a lack of definitive rigorous data from randomised trials to support the use of antibiotics for treating leptospirosis infection, and the absence of trials reporting data on clinically relevant outcomes further adds to this limitation.

LANGUAGE OF ORIGINAL DOCUMENT: English

Farman M., Jamil S., Nisar K.S., Akgul A.

Mathematical study of fractal-fractional leptospirosis disease in human and rodent populations dynamical transmission

(2024) Ain Shams Engineering Journal, 15 (3), art. no. 102452

DOI: 10.1016/j.asej.2023.102452

ABSTRACT: In both industrialized and developing nations, leptospirosis is one of the most underdiagnosed and under-reported diseases. It is known that people are more likely to contract a disease depending on their employment habits and the environment they live in, which varies from community to community. The absence of global data for morbidity and mortality has contributed to leptospirosis' neglected disease status even though it is a life-threatening illness and is widely acknowledged as a significant cause of pulmonary hemorrhage syndrome. This study aims to examine the impact of rodent-borne leptospirosis on the human population by constructing and evaluating a compartmental mathematical model using fractional-order differential equations. The model considers both the presence of disease-causing agents in the environment and the rate of human infection resulting from interactions with infected rodents and the environment. Through this approach, the research investigates the dynamics and implications of leptospirosis transmission in the context of human-rodent interactions and environmental factors. We create a fractal-fractional model using the mittag-leffler kernel. The positivity and boundedness of solutions are first discussed. The model equilibria and fundamental reproduction number are then presented. With the use of the Lyapunov function method, the solutions are subjected to global stability analysis. The fixed-point theory is used to derive the fractional-order model's existence and uniqueness. Solutions are produced using a two-step Lagrange polynomial in the generalized form of the Mittag-Leffler kernel to explore the effect of the fractional operator with numerical simulations, which shows the influence of the sickness due to the effect of different parameters involved. Such a study will aid in the development of control strategies to combat the disease in the community and an understanding of the behavior of the *Leptospira* virus.

LANGUAGE OF ORIGINAL DOCUMENT: English

Adewole M.O., Abdullah F.A., Ali M.K.M.

Dynamics of leptospirosis in human and rodent populations: A multiscale modeling approach

(2024) Journal of Biological Systems

DOI: 10.1142/S0218339024500220

ABSTRACT: Leptospirosis is a bacterial infection prevalent in many tropical regions, caused by the genus *Leptospira*. Humans contract the disease by coming in contact with contaminated environments. This study proposes a deterministic mathematical model that links the within-host and between-host dynamics of leptospirosis and investigates its properties. The model's parameters were estimated by fitting it to real-life data using the "Isqcurvefit" package in MATLAB. The study employs global sensitivity analysis using Latin hypercube sampling with a partial rank correlation coefficient index and uses Pontryagin's maximum principle

to identify cost-effective solutions for time-dependent intervention strategies to suppress the bacteria transmission within a specific period. The results of the study showed that bacteria replication within human and rodent hosts is the major driver of the overall dynamics of leptospirosis and therefore controlling the prevalence of the disease by focusing on the epidemiology components is necessary but will not be effective if the intra-host dynamics of the bacteria within rodent hosts and human hosts are not attentively considered.
LANGUAGE OF ORIGINAL DOCUMENT: English

Baharom M., Ahmad N., Hod R., Ja'afar M.H., Arsad F.S., Tangang F., Ismail R., Mohamed N., Mohd Radi M.F., Osman Y.

Environmental and Occupational Factors Associated with Leptospirosis: A Systematic Review

(2024) *Heliyon*, 10 (1), art. no. e23473

DOI: 10.1016/j.heliyon.2023.e23473

ABSTRACT: Background: Leptospirosis is a neglected emerging zoonotic disease with a profound public health impact worldwide with higher burden of disease in resource-poor countries. The environmental and occupational exposures contribute to human and animal transmission, but the interaction was less explored. A deeper understanding of the critical environmental and occupational drivers in different contexts will provide useful information for disease control and prevention measures. Objective: This review aimed to summarize the potential environmental and occupational risk factors associated with leptospirosis infection. Methods: Four databases (Scopus, Web of Science, Ovid MEDLINE, EBSCOhost) were searched for articles published from 2012 to 2021. Eligible articles were assessed using a checklist for assessing the quality of the studies. The quality of the articles was assessed based on the laboratory diagnosis approach and statistical analysis method. Results: A total of 32 studies were included in this systematic review. Water-related risk factors such as natural water as the primary water source (AOR 1.8–18.28), water-related recreational activities (AOR 2.36–10.45), flood exposure (AOR 1.54–6.04), contact with mud (AOR 1.57–4.58) and stagnant water (AOR 2.79–6.42) were associated with increased risk of leptospirosis. Infrastructural deficiencies such as un-plastered house walls and thatched houses presented a higher risk (AOR 2.71–5.17). Living in low-lying areas (AOR 1.58–3.74), on clay loam soil (OR 2.72), agricultural land (OR 2.09), and near rubber tree plantations (AOR 11.65) is associated with higher risk of leptospirosis. Contact with rats (AOR 1.4–3.5), livestock (AOR 1.3–10.4), and pigs (AOR 1.54–7.9) is associated with an increased risk of leptospirosis. Outdoor workers (AOR 1.95–3.95) and slaughterhouse workers (AOR 5.1–7.5) have higher risk of leptospirosis. Conclusion: The environmental and occupational components related to water, infrastructure, landscape, agriculture, and exposed animals play an essential role in leptospirosis transmission. The magnitude of those risk factors differs with geographical region, climate factor, urbanization and population growth, and the country's socioeconomic status.

LANGUAGE OF ORIGINAL DOCUMENT: English

Petakh P., Oksenykh V., Kamyshnyi O.

Exploring *Leptospira interrogans* FDAARGOS_203: Insights into AMR and Anti-Phage Defense

(2024) *Microorganisms*, 12 (3), art. no. 546

DOI: 10.3390/microorganisms12030546

ABSTRACT: *Leptospira*, which are known to be important disease-causing agents transmitted between animals and humans, result in significant illness and, in some cases, significant death in human populations.

This purpose of this study was to examine the genomic structure of *Leptospira interrogans* serovar Copenhageni strain FDAARGOS_203 to identify the specific genetic factors that contribute to antimicrobial resistance (AMR) and defense against phages. The genome, consisting of two contigs totaling 4,630,574 base pairs, underwent thorough examination for protein-coding sequences, transfer RNA genes, and ribosomal RNA genes. A total of twenty-two antibiotic resistance genes that specifically target essential cellular processes such as cell wall synthesis, DNA replication, and protein synthesis have been identified. Significant among these were *gidB*, *gdpD*, and *ggsA*, each involved in separate aspects of antibiotic resistance. In addition, the investigation explored the defense mechanisms of bacteriophages, revealing the presence of defense islands that contain a range of anti-phage systems, including RM_Type_IV, PrrC, Borvo, CAS_Class1-Subtype-IC, and CAS_Class1-Subtype-IB. This comprehensive genomic analysis enhances our understanding of the molecular mechanisms that determine *Leptospira*'s ability to adapt to various environments. The identified genetic factors linked to AMR and defense against phages not only enhance our scientific comprehension, but also provide a basis for focused interventions to reduce the impact of leptospirosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Sohm C., Willixhofer D., Fasching E., Waldner K., Deitzer N., Steiner J., Jöbstl J., Schleicher C., Schwarz M., Fuchs R., Bourhy P., Käsbohrer A., Wittek T., Firth C., Steinparzer R., Desvars-Larrive A.

First isolation and genotyping of pathogenic *Leptospira* spp. from Austria

(2024) Scientific Reports, 14 (1), art. no. 4467

DOI: 10.1038/s41598-024-53775-w

ABSTRACT: Leptospirosis is a globally distributed zoonotic disease. The standard serological test, known as Microscopic Agglutination Test (MAT), requires the use of live *Leptospira* strains. To enhance its sensitivity and specificity, the usage of locally circulating strains is recommended. However, to date, no local strain is available from Austria. This study aimed to isolate circulating *Leptospira* strains from cattle in Austria to enhance the performances of the routine serological test for both humans and animals. We used a statistical approach combined with a comprehensive literature search to profile cattle with greater risk of leptospirosis infection and implemented a targeted sampling between November 2021 and October 2022. Urine and/or kidney tissue were sampled from 410 cattle considered at higher risk of infection. Samples were inoculated into EMJH-STAFF culture media within 2–6 h and a real-time PCR targeting the *lipL32* gene was used to confirm the presence/absence of pathogenic *Leptospira* in each sample. Isolates were further characterised by core genome multilocus sequence typing (cgMLST). Nine out of 429 samples tested positive by PCR, from which three isolates were successfully cultured and identified as *Leptospira borgpetersenii* serogroup Sejroe serovar Hardjobovis, cgMLST cluster 40. This is the first report on the isolation and genotyping of local zoonotic *Leptospira* in Austria, which holds the potential for a significant improvement in diagnostic performance in the country. Although the local strain was identified as a cattle-adapted serovar, it possesses significant zoonotic implications. Furthermore, this study contributes to a better understanding of the epidemiology of leptospirosis in Europe.

LANGUAGE OF ORIGINAL DOCUMENT: English

Ferreira L.C.A., Filho L.F.A.F., Cosate M.R.V., Sakamoto T.

Genetic structure and diversity of the *rfb* locus of pathogenic species of the genus *Leptospira*

(2024) Life Science Alliance, 7 (6), art. no. e202302478

DOI: 10.26508/lsa.202302478

ABSTRACT: Leptospirosis is caused by pathogenic strains of the genus *Leptospira* and is considered the most widespread zoonotic bacterial disease. The genus is characterized by the large number of serology variants, which challenges developing effective serotyping methods and vaccines with a broad spectrum. Because knowledge on the genetic basis of the serological diversity among leptospires is still limited, we aimed to explore the genetic structure and patterns of the *rfb* locus, which is involved in the biosynthesis of lipopolysaccharides, the major surface antigen that defines the serovar in leptospires. Here, we used genomic data of 722 pathogenic samples and compared the gene composition of their *rfb* locus by hierarchical clustering. Clustering analysis showed that the *rfb* locus gene composition is species-independent and strongly associated with the serological classification. The samples were grouped into four well-defined classes, which cluster together samples either belonging to the same serogroup or from different serogroups but sharing serological affinity. Our findings can assist in the development of new strategies based on molecular methods, which can lead to better tools for serological identification in this zoonosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Hagedoorn N.N., Maze M.J., Carugati M., Cash-Goldwasser S., Allan K.J., Chen K., Cossic B., Demeter E., Gallagher S., German R., Galloway R.L., Habuš J., Rubach M.P., Shiokawa K., Sulikhan N., Crump J.A.

Global distribution of *Leptospira* serovar isolations and detections from animal host species: A systematic review and online database

(2024) *Tropical Medicine and International Health*, 29 (3), pp. 161 - 172

DOI: 10.1111/tmi.13965

ABSTRACT: Objectives: *Leptospira*, the spirochaete causing leptospirosis, can be classified into >250 antigenically distinct serovars. Although knowledge of the animal host species and geographic distribution of *Leptospira* serovars is critical to understand the human and animal epidemiology of leptospirosis, current data are fragmented. We aimed to systematically review the literature on animal host species and geographic distribution of *Leptospira* serovars to examine associations between serovars with animal host species and regions and to identify geographic regions in need of study. Methods: Nine library databases were searched from inception through 9 March 2023 using keywords including *Leptospira*, animal, and a list of serovars. We sought reports of detection of *Leptospira*, from any animal, characterised by cross agglutinin absorption test, monoclonal antibody typing, serum factor analysis, or pulsed-field gel electrophoresis to identify the serovar. Results: We included 409 reports, published from 1927 through 2022, yielding data on 154 *Leptospira* serovars. The reports included data from 66 (26.5%) of 249 countries. Detections were from 144 animal host species including 135 (93.8%) from the class Mammalia, 5 (3.5%) from Amphibia, 3 (2.1%) from Reptilia, and 1 (0.7%) from Arachnida. Across the animal host species, *Leptospira* serovars that were detected in the largest number of animal species included *Grippotyphosa* (n = 39), *Icterohaemorrhagiae* (n = 29), *Pomona* (n = 28), *Australis* (n = 25), and *Ballum* (n = 25). Of serovars, 76 were detected in a single animal host species. We created an online database to identify animal host species for each serovar by country. Conclusions: We found that many countries have few or no *Leptospira* serovars detected from animal host species and that many serovars were detected from a single animal species. Our study highlights the importance of efforts to identify animal host species of leptospirosis, especially in places with a high incidence of human leptospirosis. We provide an updated resource for leptospirosis researchers.

LANGUAGE OF ORIGINAL DOCUMENT: English

Batey R., Nilon P., Page S.W., Browning G.F., Norris J.M.

Antimicrobial prescribing guidelines for sheep

(2024) Australian Veterinary Journal, 102 (4), pp. 103 - 142

DOI: 10.1111/avj.13310

LANGUAGE OF ORIGINAL DOCUMENT: English

Noh M.A., Masri S.N., Zulkapli A., Mohd Ali M.R., Amran F.

Leptospira infection and carrier survey on rats from wet market areas in Kuala Lumpur, Malaysia

(2024) Journal of Vector Borne Diseases, 61 (1)

DOI: 10.4103/0972-9062.383644

ABSTRACT: Background & objectives: Leptospirosis is an important zoonotic infection that has caused significant mortality and morbidity worldwide. This disease is endemic in Malaysia and as a developing tropical country, leptospirosis is concerning as it threatens Malaysian public health and the country's economic sectors. However, there is limited information on leptospirosis in Malaysia, especially regarding leptospiral seroepidemiology among carriers in Malaysia. Therefore, more epidemiological information on the source of the disease and reservoir are needed for better disease control and source intervention. The objectives of this study are to gather information on Leptospira infection and the carrier status of rats captured from selected wet markets of Kuala Lumpur metropolitan city in Malaysia. Methods: Live rat trappings were performed in four major wet markets in Kuala Lumpur, namely, Pudu, Chow Kit, Datuk Keramat, and Petaling Street. Animal samplings were performed for 12 months in 2017, where blood and kidney samples were collected and tested for anti-leptospiral antibodies via Microscopic Agglutination Test (MAT) and pathogenic Leptospira screening via Polymerase Chain Reaction (PCR) amplification of flxB gene. Results: MAT showed that 34.7% (n = 50/144) of the captured rats were positive for anti-leptospiral antibody of which the most prominent serovar was Malaya followed by a local strain, IMR LEP 175. In parallel, 50 rats were also positive for pathogenic Leptospira DNA. Interpretation & conclusion: This study showed that there are persistent Leptospira infections among rats in Kuala Lumpur wet markets and these rats are important reservoir hosts for the bacteria.

LANGUAGE OF ORIGINAL DOCUMENT: English

Hsu S.-H., Yang H.-Y., Chang C.-C., Tsai S.-K., Li C., Chang M.-Y., Ko Y.-C., Chou L.-F., Tsai C.-Y., Tian Y.-C., Yang C.-W.

Blocking pathogenic Leptospira invasion with aptamer molecules targeting outer membrane LipL32 protein

(2024) Microbes and Infection, art. no. 105299

DOI: 10.1016/j.micinf.2024.105299

ABSTRACT: This study aimed to develop aptamers targeting LipL32, a most abundant lipoprotein in pathogenic Leptospira, to hinder bacterial invasion. The objectives were to identify high-affinity aptamers through SELEX and evaluate their specificity and inhibitory effects. SELEX was employed to generate LipL32 aptamers (L32APs) over 15 rounds of selection. L32APs' binding affinity and specificity for pathogenic Leptospira were assessed. Their ability to inhibit LipL32-ECM interaction and Leptospira invasion was investigated. Animal studies were conducted to evaluate the impact of L32AP treatment on survival rates, Leptospira colonization, and kidney damage. Three L32APs with strong binding affinity were identified. They

selectively detected pathogenic *Leptospira*, sparing non-pathogenic strains. L32APs inhibited LipL32-ECM interaction and *Leptospira* invasion. In animal studies, L32AP administration significantly improved survival rates, reduced *Leptospira* colonies, and mitigated kidney damage compared to infection alone. This pioneering research developed functional aptamers targeting pathogenic *Leptospira*. The identified L32APs exhibited high affinity, pathogen selectivity, and inhibition of invasion and ECM interaction. L32AP treatment showed promising results, enhancing survival rates and reducing *Leptospira* colonization and kidney damage. These findings demonstrate the potential of aptamers to impede pathogenic *Leptospira* invasion and aid in recovery from *Leptospira*-induced kidney injury.

LANGUAGE OF ORIGINAL DOCUMENT: English

Kędzierska-Mieszkowska S., Kędzierska B., Potrykus K.

LIC_12757 from the pathogenic spirochaete *Leptospira interrogans* encodes an autoregulated ECF σ E-type factor

(2024) *Veterinary Microbiology*, 293, art. no. 110092

DOI: 10.1016/j.vetmic.2024.110092

ABSTRACT: ECF (extracytoplasmic function) σ factors, members of the σ 70-family, are the largest class of alternative σ factors which are stimulated in the presence of specific signals and direct RNA polymerase to transcribe a defined subset of genes. Thanks to them, bacterial pathogens can effectively reprogram their gene expression and, consequently, survive in the host and establish infection in a relatively short time. The number of ECF σ factors encoded within bacterial genomes is different depending on a given species and it reflects the likelihood that these bacteria will encounter harsh environmental conditions. The genome of *L. interrogans*, a zoonotic pathogen responsible for leptospirosis, is predicted to encode 11 ECF σ E-type factors, but none of them have been characterized biochemically to date and their functions are still unknown. Here, we focused on one of the leptospiral ECF σ factors, namely LIC_12757, which was previously found to be up-regulated at elevated temperatures and may be related to the expression of *clpB* encoding an important *L. interrogans* virulence factor. We report cloning of the coding sequence of the LIC_12757 gene, its expression with the pET system and biochemical characterization of LIC_12757. By performing EMSA and in vitro transcription assays, we provide strong evidence that LIC_12757 indeed functions as a transcriptional factor that enables RNA polymerase to bind to the specific σ E-type promoter and to initiate transcription. Interestingly, we demonstrate that LIC_12757 is autoregulated at the transcriptional level. Our study is a first step towards determining key aspects of LIC_12757 function in pathogenic *Leptospira*.

LANGUAGE OF ORIGINAL DOCUMENT: English

de Oliveira N.R., Maia M.A.C., Santos F.D.S., Seixas Neto A.C.P., Oliveira Bohn T.L., Dellagostin O.A.

Evaluation of protective efficacy, serological responses, and cytokine modulation induced by polyvalent *Leptospira* vaccines in hamsters

(2024) *Comparative Immunology, Microbiology and Infectious Diseases*, 108, art. no. 102159

DOI: 10.1016/j.cimid.2024.102159

ABSTRACT: Whole-cell inactivated vaccines (bacterins) are the only licensed vaccines available for leptospirosis prevention and control, especially in domestic and farm animals. However, despite their widespread use, inconsistencies in their efficacy have been reported. Because immunity induced by bacterins is mainly mediated by antibodies against leptospiral lipopolysaccharides, the involvement of cellular responses

is not well-known. The aim of this study was to investigate the efficacy and characterize the humoral and cellular immune responses induced by whole-cell inactivated leptospirosis bacterin formulations containing serovars Bratislava, Canicola, Copenhageni, Grippotyphosa, Hardjoprajitno, and Pomona. For the potency test, hamsters were immunized with one dose of polyvalent bacterins (either commercial or experimental) and then challenged with a virulent Pomona strain. Serological (MAT and IgM and IgG-ELISA) and cellular (cytokine transcription in blood evaluated by RT-qPCR) analyses were performed. The results revealed that vaccination with either bacterin formulation was able to protect 90–100% of the hamsters infected with the Pomona serovar, although most of the surviving animals remained as renal carriers. Specific agglutinating antibodies and significant levels of IgM, IgG, and IgG2 ($P < 0.05$) that were able to react with the six serovars present in the vaccine formulations were produced, indicating that the vaccines can potentially provide immunity against all strains. The protective immunity of these vaccines was mainly mediated by balanced a Th1/Th2 response, characterized by increased IFN- γ , IL-10 and IL- α transcription. These data support the importance of characterizing immunological responses involved in bacterin efficacy and investing in the improvement of these vaccine formulations.

LANGUAGE OF ORIGINAL DOCUMENT: English

Paim M.G., Rivas B.B., Sebastião G.A., Kaefer K., Rodrigues R.O., Mayer F.Q., Nunes L.N., Costa F.V.A.D.
Investigation of anti-*Leptospira* spp. antibodies and leptospiruria in cats attended to a veterinary teaching hospital in southern Brazil

(2024) Comparative Immunology, Microbiology and Infectious Diseases, 107, art. no. 102138

DOI: 10.1016/j.cimid.2024.102138

ABSTRACT: Leptospirosis is a bacterial zoonosis that affects both humans and animals worldwide. Currently, it is known that cats may be susceptible to infection. This study aims to investigate the presence of anti-*Leptospira* spp. antibodies and leptospiruria in cats, using Microscopic Agglutination Test (MAT) and Real-time Polymerase Chain Reaction (PCR) techniques, respectively. A total of 76 cats, undergoing comprehensive anamnesis, general physical examination, and complementary exams were included in the investigation. Among the 76 cats tested, 9.2% (7/76) exhibited the presence of anti-*Leptospira* spp. antibodies, while *Leptospira* spp. DNA was detected in at 1.3% (1/76) of the evaluated urine samples. No significant associations were observed between the serological and molecular diagnostic results and the assessed variables, including clinical data and laboratory results of cats testing positive. This study provides insight into the occurrence of *Leptospira* spp. infection and leptospiruria in cats treated at a veterinary teaching hospital in southern Brazil.

LANGUAGE OF ORIGINAL DOCUMENT: English

Ulsenheimer B.C., dos Santos M.Y., Della Flora B., Matarrita D.A.R., de Avila Botton S., Von Laer A.E., Pereira D.I.B., Figuera R.A., Tonin A.A.

Detection of pathogenic *Leptospira* spp. in unconventional pets

(2024) Comparative Immunology, Microbiology and Infectious Diseases, 108, art. no. 102158

DOI: 10.1016/j.cimid.2024.102158

ABSTRACT: Leptospirosis is a disease caused by *Leptospira* spp. responsible for considerable impacts on the public and animal health. In the past two decades, non-domesticated species of pets (unconventional pets) have become popular. However, the role of these unconventional pets on maintaining diseases still unclear.

Therefore, the objective of this study was to survey the presence of *Leptospira* spp. DNA in unconventional pets. Samples of kidney tissues from 29 animals belonging to the Mammalia class (including Orders Carnivora, Lagomorpha and Rodentia) were analyzed for the presence of the gene lipL32. As a result, DNA of pathogenic *Leptospira* spp. from specie *L. interrogans* was detected in four (13,80%) of the analyzed samples: three from *Oryctolagus cuniculus* and one from *Mesocricetus auratus*. This study highlights the importance of epidemiological surveillance of leptospirosis, as it identified in species of unconventional pets, that may possibly act as reservoirs of *Leptospira* spp.

LANGUAGE OF ORIGINAL DOCUMENT: English

Laptev S., Pimenov N., Pozyabin S., Ivanyuk V., Marzanova S., Permyakova K., Selina M.

Predicting Leptospirosis Outcomes in Dogs with the Simplified Acute Physiology Score

(2024) *Advancements in Life Sciences*, 11 (1), pp. 173 - 181

ABSTRACT: Background: Leptospirosis is a serious infectious disease affecting dogs, caused by the spirochete bacterium *Leptospira*. Understanding the prognosis and severity of the disease is essential for effective clinical management. This study aimed to assess the use of the PIRO and SAPS scales in predicting the outcome of leptospirosis in dogs. Methods: The study involved 24 dogs diagnosed with leptospirosis and a control group of 22 healthy dogs. Clinical assessments were conducted, and scores on the PIRO and SAPS scales were assigned within 24 hours of admission. Statistical analyses, including correlation and regression, were employed to evaluate the relationship between scale scores and disease outcomes. Results: In dogs with leptospirosis, SAPS scale scores exhibited a strong positive correlation with disease outcomes, indicating a robust association. Scores on the SAPS scale were associated with the severity of the disease, with specific score ranges indicative of a moderate, severe, or fatal outcome. The PIRO scale also demonstrated a substantial correlation with SAPS scores and disease prognosis. In cases where the immune system was compromised, protective mechanisms activated with a delay, increasing the risk of fatality. Conclusion: The PIRO and SAPS scales provide valuable tools for assessing the severity and predicting the outcome of leptospirosis in dogs. These scales offer clinicians a means to promptly evaluate the risk of physiological disruptions and sepsis complications in dogs with leptospirosis, ultimately aiding in clinical decision-making and treatment planning.

LANGUAGE OF ORIGINAL DOCUMENT: English

David S., Sophia I., Anbazhagan S., Karikalan M., Saravanan R., Viswas K.N., Thomas P., Chaudhuri P.

Outer membrane vesicles as nanovaccine candidates against pathogenic *Leptospira* in experimental Guinea pig model

(2024) *Biologicals*, 86, art. no. 101764

DOI: 10.1016/j.biologicals.2024.101764

ABSTRACT: *Leptospira interrogans* serovar Hardjo is a long slender bacterium of size 0.1–0.3 µm × 5–50 µm. It is one of the major causes of bovine leptospirosis and is of economic importance because of the reproductive failure, still birth, abortion, and reduced productivity in cattle. It is also a zoonotic disease-causing infection in humans characterized by headaches, fever, chills, sweats and myalgia, lethargy, aching joints, pulmonary haemorrhages, and death in severe cases. Control of the disease involves antibiotic therapy, management and vaccination, of which immunization is the cheapest and effective means of disease prevention. The present study was developed to isolate and characterize the outer membrane

vesicles of *Leptospira interrogans* serovar Hardjo and to evaluate their vaccine potential in guinea pig model. The OMVs were isolated from the culture by sonication and ultracentrifugation. In transmission electron microscopy, the isolated OMVs appeared as small spherical structures of 50–200 nm size. In Western blot and indirect ELISA, antibodies specific to OMVs were observed as indicative of a good humoral immune response elicited by *L. interrogans* serovar Hardjo OMV. The OMV-based *Leptospira* vaccine was able to prevent kidney lesions and renal colonization compared to the control and bacterin vaccinated group as proven by histopathology and PCR.

LANGUAGE OF ORIGINAL DOCUMENT: English

Orozco M.M., Argibay H.D., Minatel L., Signorelli Nuñez G., Arnica D., Blanco P., Figni I., Caimi K.

Marsh deer (*Blastocerus dichotomus*) as a new host for *Leptospira borgpetersenii* in Argentina [El ciervo de los pantanos *Blastocerus dichotomus*) como un nuevo hospedador de *Leptospira borgpetersenii* en Argentina]

(2024) *Mastozoologia Neotropical*, 31 (1), art. no. e0969

DOI: 10.31687/saremMN.24.31.01.15.e0969

ABSTRACT: Leptospirosis is a worldwide re-emerging zoonosis caused by bacteria of the genus *Leptospira*. All mammals are potentially susceptible to pathogenic *Leptospira*, while certain species can act as reservoirs of the bacterium, whose main route of transmission is water. The marsh deer (*Blastocerus dichotomus*) is a wetland-dependent native cervid distributed in the Paraná-Paraguay River and influence areas. During the last decades, its populations have undergone mortality episodes of multifactorial origin. Since wetlands constitute favorable scenarios for the transmission of *Leptospira*, we investigated the occurrence of this agent in 12 marsh deer from the subpopulation of the Paraná Delta in Argentina, categorized as “Endangered”. DNA was extracted from urine and/or kidney samples, and characterization was performed at the species level by PCR amplification of the 16S rRNA gene. An aliquot of urine and serial dilutions of kidney macerates were seeded in a semisolid EMJH medium spiked with 5-Fluorouracil, and isolation was achieved in a kidney sample. *Leptospira borgpetersenii* was detected in two samples (one from urine and one from kidney), constituting the first report in marsh deer. Our findings add a new species as the host of *L. borgpetersenii*, whose circulation in wildlife has been little studied in the region. Further studies are needed to determine the transmission patterns of this bacterium in wildlife, evaluate its pathogenicity in marsh deer and other wild species, and explore the existence of reservoirs in natural areas.

LANGUAGE OF ORIGINAL DOCUMENT: English

Suwannin P., Jangpatarapongsa K., Polpanich D., Alhibshi A., Errachid A., Elaissari A.

Enhancing leptospirosis control with nanosensing technology: A critical analysis

(2024) *Comparative Immunology, Microbiology and Infectious Diseases*, 104, art. no. 102092

DOI: 10.1016/j.cimid.2023.102092

ABSTRACT: Leptospirosis is a serious health problem in tropical areas; thus, animals shed leptospirae in the environment. Humans are accidental hosts infected through exposure to contaminating bacteria in the environment. One health strategy can be applied to protect and eliminate leptospirosis because this cooperates and coordinates activities between doctors, veterinarians, and ecologists. However, conventional methods still have limitations. Therefore, the main challenges of leptospirosis control are the high sensing of detection methods to screen and control the pathogens. Interestingly, nano sensing combined with a

leptospirosis detection approach can increase the sensitivity and eliminate some limitations. This article reviews nanomaterial development for an advanced leptospirosis detection method, e.g., latex beads-based agglutination test, magnetic nanoparticles enrichment, and gold-nanoparticles-based immunochromatographic assay. Thus, nanomaterials can be functionalized with biomolecules or sensing molecules utilized in various mechanisms such as biosensors. Over the last decade, many biosensors have been developed for *Leptospira* spp. pathogen and others. The evolution of biosensors for leptospirosis detection was designed for high efficiency and might be an alternative tool. In addition, the high-sensing fabrications are useful for leptospires screening in very low levels, for example, soil or water from the environment.

LANGUAGE OF ORIGINAL DOCUMENT: English

Garcia-Lopez M., Lurier T., Bouilloud M., Pradel J., Tatard C., Sepulveda D., Anfray G., Dussert J., Bourhy P., Charbonnel N., Djelouadji Z.

Prevalence, genetic diversity and ecoepidemiology of pathogenic *Leptospira* species in small mammal communities in urban parks Lyon city, France

(2024) PLoS ONE, 19 (4 April), art. no. e0300523

DOI: 10.1371/journal.pone.0300523

ABSTRACT: Rodents are recognized as the main reservoirs of *Leptospira* spp. Rats, in particular, serve as hosts for the widely predominant *Leptospira interrogans* serovar Icterohaemorrhagiae, found worldwide. Several studies have shown the importance of other reservoirs, such as mice or hedgehogs, which harbor other leptospires' serovars. Nevertheless, our knowledge of circulating *Leptospira* spp. in reservoirs other than rats remains limited. In this context, we proposed an eco-health approach to assess the health hazard associated with leptospires in urban green spaces, where contacts between human/small mammals and domestic animals are likely. We studied the prevalence, the diversity of circulating strains, and epidemiology of pathogenic *Leptospira* species in small terrestrial mammal communities (rodents and shrews), between 2020-2022, in two parks in Lyon metropolis, France. Our study showed a significant carriage of *Leptospira* spp. in small terrestrial mammals in these parks and unveiled a global prevalence rate of 11.4%. Significant variations of prevalence were observed among the small mammal species (from 0 to 26.1%), with *Rattus norvegicus* exhibiting the highest infection levels (26.1%). We also observed strong spatio-temporal variations in *Leptospira* spp. circulation in its reservoirs. Prevalence seems to be higher in the peri-urban park and in autumn in 2021 and 2022. This is potentially due to differences in landscape, abiotic conditions and small mammal communities' composition. Our study suggests an important public health relevance of rats and in a lesser extent of other rodents (*Apodemus* spp., *Clethrionomys glareolus* and *Mus musculus*) as reservoirs of *L. interrogans*, with rodent species carrying specific serogroups/serovars. We also emphasize the potential hazard associated between the shrew *Crocidura russula* and *L. kirschneri*. Altogether, these results improve our knowledge about the prevalence of leptospirosis in an urban environment, which is an essential prerequisite for the implementation of prevention of associated risks. © 2024 Garcia-Lopez et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

LANGUAGE OF ORIGINAL DOCUMENT: English

Muco E., Karruli A., Dajlani A., Zerja A., Bego A.

Severe murine typhus complicated by multiple organ dysfunctions: A case report

(2024) Caspian Journal of Internal Medicine, 15 (1), pp. 188 - 192

DOI: 10.22088/cjim.15.1.23

ABSTRACT: Background: Rickettsioses are infectious diseases which are caused by intracellular bacteria which belong to the family Rickettsiaceae. This zoonosis endemically prefers tropical and subtropical regions of which the Mediterranean is included. Murine typhus is a type of rickettsial disease that commonly presents with undulating fever, headache rash, chills, malaise, and myalgias. It can lead to complications such as multi-organ failure and has a lethality rate of <5% in such cases. Case Presentation: A 70-year-old male was hospitalized at the Unit of Infectious Diseases, Mother Teresa Hospital, Tirana, Albania in a comatose condition. He had a seven-day history of fever up to 39-40°C, headache, fatigue, anorexia, vomiting, cough, and myalgia. He was a farmer and had contact with animals. Upon admission, he had scleral hemorrhages, hepatosplenomegaly, jaundice, maculopapular rash over the trunk, abdomen, and palms of his hands as well as severe acidosis, depressed bicarbonate levels, alteration in liver, kidney, and pancreas function tests. He was urgently transferred to the Intensive care unit of the Infectious Diseases Department. He was hemodynamically unstable and was put immediately on vasoactive agents and mechanical ventilation. ELISA Rickettsia typhi IgM resulted positive. Supportive treatment along with antibiotics Levofloxacin and Ceftriaxone was initiated. However, the patient died on the 4th day of hospitalization and the 11th of the disease onset. Conclusion: Murine typhus should be included in the investigation of possible causes when dealing with patients presenting with fever and maculopapular rash complicated by multi-organ failure and coming from a typhus-endemic area, especially in the summer season. © 2024 Babol University of Medical Sciences. All rights reserved.

LANGUAGE OF ORIGINAL DOCUMENT: English

Zhao J., Pang B., Liu C., Wang X., Chen S., Feng H., Kou Z., Wu T., Xu C., Yang L.

Infections and Influencing Factors of Pathogens in Rattus norvegicus along the Zengjiang River in Guangzhou, China

(2024) Vector-Borne and Zoonotic Diseases, 24 (1), pp. 46 - 54

DOI: 10.1089/vbz.2023.0045

ABSTRACT: Background: Rattus norvegicus can carry and transmit various zoonotic pathogens. Some studies were conducted to investigate a few zoonotic pathogens in Guangzhou, China, but no coinfections were investigated or specifically mentioned. Studies on the infections and the influencing factors of various zoonotic pathogens in R. norvegicus along the Zengjiang River in Guangzhou have not been carried out. Materials and Methods: In this study, R. norvegicus was captured in November 2020 and September 2021 along the Zengjiang River, and was tested for Bartonella spp., Leptospira spp., Orientia tsutsugamushi, Borrelia burgdorferi, Hantavirus (HV), Ehrlichia spp., and severe fever with thrombocytopenia syndrome virus (SFTSV) by the RT-PCR. Logistic regression analysis was used to determine the impact of habitat and demographic factors on the infections and coinfections of the surveyed pathogens. Results: In 119 R. norvegicus, the detection rates of Bartonella spp., Leptospira spp., O. tsutsugamushi, B. burgdorferi, and HV were 46.2%, 31.9%, 5%, 0.8%, and 18.5%, respectively. Ehrlichia spp. and SFTSV were negative. The triple coinfection rate of Bartonella spp., Leptospira spp., and HV was 11.8%. In addition, the coinfection of Bartonella spp., Leptospira spp., and B. burgdorferi was 0.8%. Dual coinfection of Bartonella spp. and Leptospira spp.,

Leptospira spp. and HV, Bartonella spp. and O. tsutsugamushi, Leptospira spp. and O. tsutsugamushi, and HV and O. tsutsugamushi was 9.2%, 3.4%, 1.7%, 1.7%, and 0.8%, respectively. Infections of these pathogens in R. norvegicus were found in habitats of banana plantation, grassland, and bush. Weight affected the infection of Bartonella spp., Leptospira spp., or HV in R. norvegicus. Conclusions: R. norvegicus along the Zengjiang River not only carried various potentially zoonotic pathogens but also had a variety of coinfections. Surveillance of the density and pathogens in R. norvegicus should be strengthened to reduce the incidence of relevant zoonotic diseases.

LANGUAGE OF ORIGINAL DOCUMENT: English

de Oliveira M.C.F., Santos J.F.N., de Medeiros A.M.L.A., Castro V., Bezerra C.S., Alves C.J., de Azevedo **S.S., Santos C.S.A.B.**

Serological evidence of Leptospira spp. infection in livestock from indigenous villages in the Caatinga biome, Brazil [Evidência sorológica de infecção por Leptospira spp. em animais de produção de aldeias indígenas no bioma Caatinga, Brasil]

(2024) Ciencia Rural, 54 (5), art. no. e20230191

DOI: 10.1590/0103-8478cr20230191

ABSTRACT: Leptospirosis, a disease of significant economic impact on livestock and public health concern, may exhibit unique epidemiological characteristics in indigenous villages, particularly those located within semiarid climates such as the Caatinga biome in Brazil. This environment often presents conditions unfavorable for leptospire survival. This study conducted serological diagnoses of livestock in indigenous villages within the Caatinga biome, Northeastern Brazil. The survey was carried out in the Mãe Maria and Santa Helena indigenous villages, home to the Xukuru de Cimbres tribe, in the county of Pesqueira, Pernambuco State, Brazil, within the Caatinga biome. Blood samples were collected from cattle (n = 42), goats (n = 41), and sheep (n = 19). Out of the 102 samples tested, 73 (71.6%; 95% CI = 62.8%-80.3%) were seroreactive (cut-off ≥ 100). The seropositivity rates for cattle, goats, and sheep were 54.8%, 80.5%, and 89.5%, respectively. A statistically significant difference was observed in the proportion of seropositive animals between cattle and goats and cattle and sheep ($P < 0.05$). Icterohaemorrhagiae was identified as the most probable serogroup across all animal species. The study revealed that livestock in indigenous villages within the Caatinga biome are frequently exposed to leptospire. This finding underscores the importance of a One Health approach, emphasizing the need for comprehensive studies in areas where large human and animal populations coexist. Such studies are crucial for investigating zoonotic infections and for planning and implementing control measures against livestock-associated leptospirosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Griebsch C., Kirkwood N., Ward M.P., Norris J.M.

Serological evidence of exposure of healthy dogs to Leptospira in Sydney, New South Wales, Australia

(2024) Australian Veterinary Journal, 102 (4), pp. 215 - 221

DOI: 10.1111/avj.13315

ABSTRACT: In 2017, highly fatal canine leptospirosis emerged in Sydney, Australia. Based on results of microscopic agglutination testing (MAT), serovar Copenhageni appeared to be the most common causative serovar. Prior to this, no clinical cases had been reported since 1976. In a serosurvey of healthy dogs in Australian shelters in 2004, 2.4% of 431 New South Wales dogs had serological evidence of exposure to

Copenhageni, the most prevalent serovar. The aim of this study was to estimate the current prevalence of *Leptospira* exposure and associated serovars in healthy Sydney dogs, previously unvaccinated against *Leptospira*. Serum samples from 411 healthy dogs in leptospirosis hotspots and neighbouring suburbs were collected before vaccination. MAT for 23 serovars was performed at the WHO Leptospirosis Reference Laboratory in Queensland, Australia. The overall seroprevalence was 4.1% (17/411) with low titres (1/50–1/200) detected. Eleven dogs were from known leptospirosis hotspots. Eight dogs were known to hunt rodents. One dog had been in contact with a leptospirosis positive dog 1 year prior. Serovar Topaz was the most prevalent serovar (n = 5) followed by serovars Australis (n = 4), Copenhageni (n = 4), Djasiman (n = 2), Cynopteri (n = 1), Javanica (n = 1), Medanensis (n = 1), and Pomona (n = 1). In conclusion, serological evidence of exposure of dogs in Sydney to *Leptospira* is low, but apparently has increased since 2004. Positive titres to serovars not previously reported to cause disease in dogs could be due to low virulence of those serovars or cross-reactivity with other serovars.

LANGUAGE OF ORIGINAL DOCUMENT: English

Matiz-González J.M., Ballesteros-Ballesteros J.A., Hernández M., Mejorano-Fonseca J.A., Cuervo C., Faccini-Martínez Á.A., Hidalgo M., Pérez-Torres J., Silva-Ramos C.R.

Genetic diversity of P1/pathogenic *Leptospira* species hosted by bats worldwide

(2024) Zoonoses and Public Health

DOI: 10.1111/zph.13126

ABSTRACT: Introduction: Bats are a diverse group of mammals that have unique features allowing them to act as reservoir hosts for several zoonotic pathogens such as *Leptospira*. Leptospire have been classified into pathogenic, intermediate, and saprophytic groups and more recently into clades P1, P2, S1, and S2, being all the most important pathogenic species related to leptospirosis included within the P1/pathogenic clade. *Leptospira* has been detected from bats in several regions worldwide; however, the diversity of leptospire harboured by bats is still unknown. Aim: The aim of the present study was to determine the genetic diversity of *Leptospira* spp. harboured by bats worldwide. Methods: A systematic review was conducted on four databases to retrieve studies in which *Leptospira* was detected from bats. All studies were screened to retrieve all available *Leptospira* spp. 16S rRNA sequences from the GenBank database and data regarding their origin. Sequences obtained were compared with each other and reference sequences of *Leptospira* species and analysed through phylogenetic analysis. Results: A total of 418 *Leptospira* spp. 16S rRNA sequences isolated from 55 bat species from 14 countries were retrieved from 15 selected manuscripts. From these, 417 sequences clustered within the P1/pathogenic group, and only one sequence clustered within the P2/intermediate group. Six major clades of P1/pathogenic *Leptospira* spp. were identified, three of them composed exclusively of sequences obtained from bats. Conclusion: We identified that bats harbour a great genetic diversity of *Leptospira* spp. that form part of the P1/pathogenic clade, some of which are closely related to leptospirosis-associated species. This finding contributes to the knowledge of the diversity of leptospire hosted by bats worldwide and reinforces the role of bats as reservoirs of P1/pathogenic *Leptospira* spp.

LANGUAGE OF ORIGINAL DOCUMENT: English

Putz E.J., Fernandes L.G.V., Sarlo Davila K.M., Whitelegge J., Lippolis J.D., Nally J.E.

Proteomic profiles of *Leptospira borgpetersenii* serovar Hardjo strains JB197 and HB203 cultured at different temperatures

(2024) Journal of Proteomics, 295, art. no. 105106

DOI: 10.1016/j.jprot.2024.105106

ABSTRACT: Leptospirosis is a global zoonotic disease affecting humans, domestic, and wild animals. *Leptospira* are typically shed in the urine of reservoir hosts which persist in suitable environments where incidental host transmission occurs after direct contact with infected urine or contaminated environments. Interestingly, serologically identical *L. borgpetersenii* serovar Hardjo strains JB197 and HB203 show divergent disease severity in the hamster model; JB197 causes severe acute infection while HB203 causes persistent chronic infection. Historically, serovar Hardjo was limited to culture at 29 °C, but utilization of HAN media allows propagation from host tissues at 37 °C. Here, the proteome of strains JB197 and HB203 were characterized after culture from experimentally challenged hamsters at 29 °C and 37 °C. Comparative analyses of JB197 and HB203 samples cultured at 29 °C yielded 425 significantly differentially expressed (DE) proteins, while strains at 37 °C yielded 613 DE proteins including prominent outer membrane proteins and known virulence factors. In agreement, membrane protein GO terms were identified by STRING network analyses along with numerous metabolic KEGG pathways consistent with condition differences. Within strain, JB197 cultured at 29 °C vs 37 °C identified 529 DE proteins, while HB203 identified 524 DE proteins. Investigating differential protein profiles provide insights into strain specific behaviors with implications for better understanding host-pathogen interactions, disease transmission, and response to environmental conditions which can contribute to vaccine development, diagnostic improvement, and ultimately leptospirosis control. Significance: Leptospirosis is a devastating zoonotic disease affecting humans, wild and domestic animals around the globe. Different species and serovars of *Leptospira* can affect various animal host species differently; for instance, a serovar that is asymptomatic in the rat may cause severe disease in a dog or human. These differences in host response are not only found at the species and serovar level for *Leptospira*, but also at the strain level. A prime example comes from strains JB197 and HB203, both species *L. borgpetersenii*, both serovar Hardjo. Interestingly, JB197 causes a severe acute infection in the hamster while HB203 causes an asymptomatic chronic infection. Understanding these unique relationships between pathogen and host species is important, especially in the context of prevention technologies such as vaccine design, where the strain of *Leptospira* used as a bacterin might have different efficiencies in different hosts. In this study, proteomic profiles of strains JB197 and HB203 were analyzed, and results revealed diverse protein expression profiles of outer membrane proteins, as well as proteins functioning in motility and growth.

LANGUAGE OF ORIGINAL DOCUMENT: English

Verma A., Hunt J.

Novel leptospirosis research at Lincoln Memorial University

(2024) American Journal of Veterinary Research, 85 (2)

DOI: 10.2460/ajvr.23.12.0275

LANGUAGE OF ORIGINAL DOCUMENT: English

Aymée L., Lilenbaum W.

Comments on the sensitivity variation of serology to diagnose bovine leptospirosis: Facing the chronic infection

(2024) Preventive Veterinary Medicine, 224, art. no. 106136

DOI: 10.1016/j.prevetmed.2024.106136

LANGUAGE OF ORIGINAL DOCUMENT: English

Ricardo T., Azócar-Aedo L.I., Previtali M.A., Monti G.

Seroprevalence of pathogenic *Leptospira* serogroups in asymptomatic domestic dogs and cats: systematic review and meta-analysis

(2024) *Frontiers in Veterinary Science*, 11, art. no. 1301959

DOI: 10.3389/fvets.2024.1301959

ABSTRACT: Leptospirosis is a neglected zoonotic disease transmitted by contact with the urine of animals infected with pathogenic species of the bacteria *Leptospira* or by contact with environments contaminated with the bacteria. Domestic dogs and cats may act as reservoirs or as sentinels of environmental contamination with leptospires, posing a public health concern. There is a great diversity of leptospires, and one common way to classify them is into serogroups that provide some information on the host species they are associated with. The aims of this study were: (1) to quantitatively summarize the overall prevalence and serogroup-specific prevalence of antibodies against pathogenic leptospires in asymptomatic dogs and cats and (2) to identify environmental and host characteristics that may affect the prevalence. Three electronic databases and the reference lists of eligible articles were screened, for epidemiological studies conducted between the years 2012–2022. We estimated overall and serogroup-specific prevalence using three-level meta-analysis models and assessed potential sources of heterogeneity by moderator analysis and meta-regression. Eighty-four studies met the inclusion criteria (dog studies 66.7%, cat studies 26.2%, and both species 7.1%). There were significant differences between dogs and cats in the overall prevalence model ($P < 0.001$), but not in the serogroup-specific model ($P > 0.05$). In dogs, the prevalence of *Leptospira interrogans* serogroup Canicola was significantly higher than the other pathogenic serogroups ($P < 0.001$), while in cats there were no significant differences among serogroups ($P = 0.373$). Moderator analysis showed that the prevalence of *L. kirschneri* serogroup Grippotyphosa was significantly higher in stray/sheltered dogs than in domiciled dogs ($P = 0.028$). These results suggest that pathogenic serogroups associated with small mammals are circulating among asymptomatic pets and should be taken into account in the transmission cycle of leptospires, as well as in the standard MAT panel for diagnosis in dogs and cats. It also highlights the importance of including both dogs and cats as potential reservoirs when conducting eco-epidemiological studies in different geographical and ecological areas.

LANGUAGE OF ORIGINAL DOCUMENT: English

Hokmi A., Eshraghi S.S., Foroushani A.R., Abdollahpour G., Fard R.M.N.

Leptospirosis in Slaughterhouse Personnel: A Seroepidemiologic Study Using Microscopic Agglutination Test

(2024) *Applied Food Biotechnology*, 11 (1), art. no. e5

DOI: 10.22037/afb.v10i3.43527

ABSTRACT: Background and Objective: Meat can be contaminated by *Leptospira* species. This bacterial pathogen causes severe leptospirosis disease in humans and animals. The major aims of this study were to assess seroepidemiological prevalence of leptospirosis in employees of a slaughterhouse in Guilan Province, Iran, using microscopic agglutination test and further investigate the positive samples using nested polymerase chain reaction method. Material and Methods: In this study, 150 employees of a slaughterhouse in Guilan Province, Iran, were participated after completing written consents and personal questionnaires. This sample

size was calculated based on the mean prevalence of the pathogen in the region. After assessing sera of the participants for *Leptospira* antibody using microscopic agglutination test, urine samples were collected from the positive participant for further assessments using nested polymerase chain reaction. Results and Conclusion: Based on the results, microscopic agglutination test was positive for 10.7% of the participants. However, Nested-PCR was negative for the positive microscopic agglutination tests on sera collected from the participants with antibodies against *Leptospira* antigens. The current results demonstrate that *Leptospira* can occur in asymptomatic humans in slaughterhouses and highlight the high potential of the disease transmission to humans in the province. Therefore, further extended control and prevention measures for slaughterhouse workers are recommended to guarantee the food safety. Conflict of interest: The authors declare no conflict of interest.

LANGUAGE OF ORIGINAL DOCUMENT: English

Putri A., Charoenwisedsil R., Techavachara N., Imad H., Chinpraditsuk S., Thaipadungpanit J., Matsee W.

Severe leptospirosis with rhabdomyolysis in a traveller visiting Thailand

(2024) *Journal of Travel Medicine*, 31 (1), art. no. taad161

DOI: 10.1093/jtm/taad161

LANGUAGE OF ORIGINAL DOCUMENT: English

Suanes A., Macchi M.V., Fernández F., Salaberry X., Moreira C., Gil A.D.

Seroprevalence and herd-level associated factors of pathogenic *Leptospira* spp. circulating locally in dairy cattle in Uruguay

(2024) *Preventive Veterinary Medicine*, 223, art. no. 106097

DOI: 10.1016/j.prevetmed.2023.106097

ABSTRACT: Leptospirosis is a zoonotic disease of worldwide importance. In Uruguay, it is endemic in cattle and primarily affects people with occupational exposure to livestock. The aim of this study was to determine the national seroprevalence and associated factors of local pathogen *Leptospira* spp. in dairy cattle. A cross-sectional study was carried out. Herds were stratified by size (1–50, 51–250, and > 250 cattle), and up to 60 dairy cows per herd were randomly selected. A total of 4269 serum samples from 101 dairy herds were analyzed by microscopic agglutination test (MAT). A two-stage sampling design was used to estimate population seroprevalence of *Leptospira* spp. In order to determine the factors associated with the disease, herds with at least 1 seropositive animal were considered as case herds. Seroprevalence of *Leptospira* was 27.80% with a 95% CI [21.06, 34.54] at the animal level and 86.92% with a 95% CI [80.00, 93.75] at the herd level. The serology confirms the predominance of serogroups Sejroe and Pomona in our herd with the presence of incidental leptospire infection, in smaller proportion, but with a wide distribution at farm level. The population size and purchasing replacement of cows on dairy farms were associated with infection at farm level. The serologic studies confirmed that exposure to *Leptospira* spp. is endemic in our herds, and the spreading over dairy herds. Although the movement of purchased females and the size of the herd were associated with the disease, more studies should be conducted, to better understand the epidemiology of the disease and to highlight the possible risks to public health, especially in rural workers, farmers and veterinarians.

LANGUAGE OF ORIGINAL DOCUMENT: English

Beato-Benítez A., Cano-Terriza D., González M., Martínez R., Pérez-Cobo I., Ruano M.J., Guerra R., Mozos-Mora E., García-Bocanegra I.

Fatal leptospirosis in endangered Barbary macaques (*Macaca sylvanus*) kept in captivity: Assessing the role of sympatric rodents

(2024) *Veterinary Microbiology*, 291, art. no. 110028

DOI: 10.1016/j.vetmic.2024.110028

ABSTRACT: Between December 2020 and January 2021, an outbreak of acute mortality in endangered Barbary macaques (*Macaca sylvanus*) kept in captivity was detected in a zoo in Spain. The main findings observed in the two fatally affected animals at post-mortem evaluation were jaundice, renal tubular necrosis and interstitial nephritis. *Leptospira* spp. infection was confirmed by real time PCR (qPCR) in different tissues in both individuals. Analyses of *secY* gene from a positive individual showed 100% homology with a previously published sequence corresponding to *Leptospira interrogans* serovar Copenhageni. Free-living sympatric brown rats (*Rattus norvegicus*) from the affected zoo were also analyzed, and showed a prevalence and seroprevalence of *Leptospira* spp. of 18.2% (4/22; 95% CI: 2.1–34.3) and 41.9% (26/62; 95% CI: 29.7–54.2), respectively. We detected seropositive sera to five different serovars of *Leptospira* spp. (Copenhageni, Grippotyphosa, Pomona, Canicola and Hardjo) in the rodent population, with *L. Copenhageni* being the predominant one. This study describes for first time an outbreak of fatal leptospirosis in captive non-human primates in Europe. Our results show that Barbary macaques, an endangered species, are highly susceptible to *Leptospira* spp. infection, with sympatric wild rodents being the most likely reservoir animals involved in transmission in this outbreak. Our results suggest that rodent control could be an effective measure for minimizing exposure to *Leptospira* spp. in zoological collections. Given the potential implications for conservation, animal and public health, non-human primates and rodents should be included in surveillance programs for *Leptospira* spp. in zoos.

LANGUAGE OF ORIGINAL DOCUMENT: English

Howard M.

Acute kidney injury and liver disease in an American bulldog with suspected leptospirosis

(2024) *The Canadian veterinary journal = La revue veterinaire canadienne*, 65 (4), pp. 385 - 388

ABSTRACT: A 6-year-old spayed female American bulldog was brought to a veterinary clinic with a 3-day history of vomiting, lethargy, anorexia, icterus, hemorrhagic diarrhea, and oliguria. The dog's clinical signs, complete blood (cell) count, serum biochemistry, urinalysis, and diagnostic imaging were indicative of acute kidney injury and acute hepatopathy consistent with leptospirosis. Treatment for leptospirosis was initiated but, due to the dog's lack of response and progression of clinical signs, euthanasia was ultimately elected after 3 d of hospitalization. The dog tested negative for *Leptospira* spp. on ELISA; urine, blood, and tissue PCRs; and immunohistochemistry. This case demonstrates that confirmation of leptospirosis can be challenging, even in an animal with the expected clinical presentation. Therefore, limitations of the diagnostic tests available, as well as the possibility of other, less likely differential diagnoses such as toxicosis, must be considered.

LANGUAGE OF ORIGINAL DOCUMENT: English

Uduwawala H., Manamperi A., Gunaratna G.P.S., Karunanayake L., Ceruti A., El Wahed A.A., Fernando L., Premaratna R., Hapugoda M.

Detection of pathogenic *Leptospira* with rapid extraction followed by recombinase polymerase amplification (RPA) and quantitative polymerase chain reaction (qPCR) assay-A comprehensive study from Sri Lanka

(2024) PLoS ONE, 19 (3 March), art. no. e0295287

DOI: 10.1371/journal.pone.0295287

ABSTRACT: Leptospirosis is the most widespread zoonosis in the world. The disease is more prevalent in tropical regions where the majority of developing countries are located. Leptospirosis is considered a protean manifestation zoonosis with severity of the disease ranging from a mild febrile illness to a severe and life-threatening illness. Clinical symptoms of leptospirosis overlap with other tropical febrile illnesses. Early, rapid, and definitive diagnosis is important for effective patient management. Since Polymerase Chain Reaction (PCR)-based assays are not readily available in most clinical settings, there is a need for an affordable, simple, and rapid diagnostic test. Quantitative PCR (qPCR) and Recombinase Polymerase Amplification (RPA) were implemented at the Faculty of Medicine, University of Kelaniya, and a prospective study to evaluate RPA for diagnosis of acute phase of leptospirosis was conducted. Results indicate that RPA and qPCR were positive in 81% (98/121) of the total positive and acute clinical samples. Of the 81 positive MAT confirmed patients 60 (74%) and 53 (65%) were positive with qPCR and RPA respectively. Retrospective evaluation revealed a high diagnostic accuracy (sensitivity-70% and specificity-87%) of RPA compared to MAT as the reference gold standard. Results further suggest that there is no significant difference between the two assays, qPCR and RPA-SwiftX ($P = 0.40$). Laboratory procedures for the extraction and detection by qPCR in the laboratory have been optimized to obtain results within 6 hours. However, the RPA-SwiftX method under field conditions took 35 minutes. The RPA-SwiftX method could replace the qPCR which shows similar sensitivity and specificity. Therefore, RPA established under the current study presents a powerful tool for the early and rapid diagnosis of leptospirosis at point-of-care.

LANGUAGE OF ORIGINAL DOCUMENT: English

Jin Y., Lan W., Chen X., Liu W., Luo W., Chen S.

A rare case of anti-DPPX encephalitis combined with neuroleptospirosis

(2024) BMC Neurology, 24 (1), art. no. 34

DOI: 10.1186/s12883-024-03538-x

ABSTRACT: Background: Neuroleptospirosis and anti-dipeptidyl-peptidase-like protein 6 (DPPX) encephalitis are both very rare and have only been reported in the form of respective case reports. There are no reports of anti-DPPX encephalitis combined with neuroleptospirosis in the literature. We reported the first case of neuroleptospirosis combined with elevated DPPX antibodies in serum and cerebrospinal fluid (CSF). Case presentation: A previously healthy 53-year-old Chinese male farmer with a history of drinking raw stream water and flood sewage exposure was brought to the hospital due to an acute onset of neuropsychiatric symptoms. No fever or meningeal irritation signs were detected on physical examination. Routine laboratory investigations, including infection indicators, leukocyte and protein in CSF, electroencephalogram and gadolinium-enhanced magnetic resonance imaging of the brain, all revealed normal. While metagenomic next-generation sequencing (mNGS) identified the DNA genome of *Leptospira interrogans* in the CSF. Anti-DPPX antibody was detected both in blood and in CSF. A diagnosis of neuroleptospirosis combined with autoimmune

encephalitis associated with DPPX-Ab was eventually made. He resolved completely after adequate amount of penicillin combined with immunotherapy. Conclusion: We highlight that in patients with acute or subacute behavioral changes, even in the absence of fever, if the most recent freshwater exposure is clear, physicians should pay attention to leptospirosis. Due to the low sensitivity of routine microscopy, culture, polymerase chain reaction and antibody testing, mNGS may have more advantages in diagnosing neuroleptospirosis. As autoimmune encephalitis can be triggered by various infections, neuroleptospirosis may be one of the causes of autoimmune encephalitis. Since neuronal antibody measurements themselves are not that common in neuroleptospirosis, future studies are needed to determine whether the detection of anti-DPPX antibodies is a rare event in leptospirosis. Early identification of autoimmune encephalitis and timely administration of immunotherapy may lead to a better outcome.

LANGUAGE OF ORIGINAL DOCUMENT: English

Kamaruzaman I.N.A., Staton G.J., Ainsworth S., Carter S.D., Evans N.J.

Characterisation of Putative Outer Membrane Proteins from *Leptospira borgpetersenii* Serovar Hardjo-Bovis Identifies Novel Adhesins and Diversity in Adhesion across Genomospecies Orthologs

(2024) *Microorganisms*, 12 (2), art. no. 245

DOI: 10.3390/microorganisms12020245

ABSTRACT: Leptospirosis is a zoonotic bacterial disease affecting mammalian species worldwide. Cattle are a major susceptible host; infection with pathogenic *Leptospira* spp. represents a public health risk and results in reproductive failure and reduced milk yield, causing economic losses. The characterisation of outer membrane proteins (OMPs) from disease-causing bacteria dissects pathogenesis and underpins vaccine development. As most leptospire pathogenesis research has focused on *Leptospira interrogans*, this study aimed to characterise novel OMPs from another important genomospecies, *Leptospira borgpetersenii*, which has global distribution and is relevant to bovine and human diseases. Several putative *L. borgpetersenii* OMPs were recombinantly expressed, refolded and purified, and evaluated for function and immunogenicity. Two of these unique, putative OMPs (rLBL0972 and rLBL2618) bound to immobilised fibronectin, laminin and fibrinogen, which, together with structural and functional data, supports their classification as leptospiral adhesins. A third putative OMP (rLBL0375), did not exhibit saturable adhesion ability but, together with rLBL0972 and the included control, OmpL1, demonstrated significant cattle milk IgG antibody reactivity from infected cows. To dissect leptospire host–pathogen interactions further, we expressed alleles of OmpL1 and a novel multi-specific adhesin, rLBL2618, from a variety of genomospecies and surveyed their adhesion ability, with both proteins exhibiting divergences in extracellular matrix component binding specificity across synthesised orthologs. We also observed functional redundancy across different *L. borgpetersenii* OMPs which, together with diversity in function across genomospecies orthologs, delineates multiple levels of plasticity in adhesion that is potentially driven by immune selection and host adaptation. These data identify novel leptospiral proteins which should be further evaluated as vaccine and/or diagnostic candidates. Moreover, functional redundancy across leptospire surface proteins together with identified adhesion divergence across genomospecies further dissect the complex host–pathogen interactions of a genus responsible for substantial global disease burden.

LANGUAGE OF ORIGINAL DOCUMENT: English

Paul A., Sarma V., Choudhury P.D., Pegu G., Sarma K., Sarma A., Saikia L.

Scrub Typhus- An Underestimated Infectious Disease Attributable to Community Acquired Acute Kidney Injury

(2024) Indian Journal of Microbiology, 64 (1), pp. 133 - 140

DOI: 10.1007/s12088-023-01137-x

ABSTRACT: Acute Kidney Injury (AKI) associated with Scrub typhus is an emerging health problem which is more common in the tropics including India. This study intended to find out the occurrence of Scrub typhus among the Community Acquired Acute Kidney Injury patients in a tertiary care hospital in Assam, North East India. AKI patients with acute febrile illness admitted to Gauhati Medical College and Hospital, Guwahati, Assam were included in the study and demographic characteristics along with clinical features were recorded. The detection of Scrub typhus was done by IgM Enzyme Linked Immunosorbent Assay (ELISA) test (Optical Density > 0.5) and polymerase chain reaction (PCR) analysis. Routine haematological and biochemical tests were performed. Molecular characterization of *Orientia tsutsugamushi* was done followed by phylogenetic analysis. The Graph Pad Prism software 9 was used for statistical analysis. Out of 221 AKI patients admitted to hospital, 45 patients (20.4%) were confirmed to be Scrub typhus positive and among them, 4 cases were co-infected with leptospirosis. Majority of Scrub typhus positive AKI patients were in Stage I (82.2%) under KDIGO guideline. "Karp" was the predominant circulating serotype. The study showed cases of Scrub typhus associated Acute Kidney Injury was high and mortality was 11.1%. Hence, in this region, further studies need to be done with large number of population and more emphasis need to be given on differential diagnosis. LANGUAGE OF ORIGINAL DOCUMENT: English

Rodríguez-Rodríguez V., Castro-Cordero A., Calderón-Rangel A., Martínez-Ibarra E., Yasnot M., Agudelo-Flórez P., Monroy F.P.

Acute human leptospirosis in a Caribbean region of Colombia: From classic to emerging risk factors

(2024) Zoonoses and Public Health, 71 (1), pp. 107 - 119

DOI: 10.1111/zph.13089

ABSTRACT: Background: Leptospirosis is a zoonosis of worldwide incidence, with a broad spectrum of health risk factors. Aim: The objective was to determine risk factors associated with acute human leptospirosis and to explore predictive variables of risk to human leptospirosis. Methods: The study was carried out in the Department of Córdoba, in the north of Colombia. We conducted a longitudinal prospective descriptive study with non-probabilistic sampling, which included 339 patients suspected of leptospirosis. Positive cases were confirmed by MAT and PCR. The determination of social and environmental risk factors was done with a survey on epidemiological and environmental variables to establish an association between cases of leptospirosis and risk factors as well as predictive variables. Results: We found 19.8% (67/339) cases of acute leptospirosis, and the seroprevalence was 27.1% (92/339). The most frequent serogroups were Sejroe, Australis, Pomona, Batavie, Pyrogenes and Grippotyphosa. We identified the following risk factors: age between 10 and 19 years (OR = 2.571; 95% CI); pig ownership (OR = 2.019; 95% CI); bathing or recreational activities in lake/lagoon (OR = 3.85; 95% CI) and in dams (OR = 3.0; 95% CI); floodings 30 days before the onset of symptoms (OR = 2.019; 95% CI), and a mean temperature of 28°C (p 0.044; 95%CI). As significant predictor variables, we identified age (10–19 years), bathing or recreational activities in the lake/lagoon, and flooding 30 days before symptoms were again evidenced. This region presents classic risk factors (pig ownership) and emerging environmental risk factors (recreational practice or bathing in a lake/lagoon and flooding 30 days before the

onset of symptoms), and demographic factors such as young age (10–19 years). Conclusions: These factors are also predictors of human cases of acute leptospirosis and provide contextual information on environmental and public health that should be considered for epidemiological surveillance in this endemic area.

LANGUAGE OF ORIGINAL DOCUMENT: English

Ioannou A.D.F., Tai C., Labato M.A., Butty E.M.

Retrospective evaluation of 22 dogs with leptospirosis treated with extracorporeal renal replacement therapies (2018-2021)

(2024) Journal of Veterinary Internal Medicine, 38 (2), pp. 1051 - 1059

DOI: 10.1111/jvim.16998

ABSTRACT: Background: Outcomes of dogs with acute kidney injury secondary to leptospirosis (AKI-L) treated using renal replacement therapies (RRT) are poorly characterized. Hypothesis/Objectives: Describe survival to discharge, short (≤ 30 days) and long-term (≥ 6 months) outcomes of AKI-L dogs receiving RRT and determine if there is a significant difference in maximum blood urea nitrogen (maxBUN), maximum creatinine (maxCr), maximum bilirubin (maxBili) and the number of body systems affected between survivors and non-survivors. Animals: Twenty-two client-owned dogs with AKI-L receiving RRT. Methods: Retrospective medical record review of dogs with AKI-L that received RRT between 2018 and 2021. Results: Sixteen of 22 (73%) dogs survived to discharge. Of the survivors, 13 (81%) were alive >30 days from discharge and 12 (75%) were alive at 6 months from discharge. Factors significantly higher in non-survivors included number of body systems affected (survivors: 1 (19%), 2 (50%), 3 (25%) and 4 (6%) vs non-survivors: 3 (33.3%), and 4 (66.7%); $P = .01$) and median maxBili (survivors: 1.9 mg/dL; range, 0.1-41.6 vs non-survivors: 21.0 mg/dL; range, 12.3-38.9; $P = .02$). There was no significant difference in median maxBUN (survivors: 153.0 mg/dL; range, 67-257 vs non-survivors: 185.5 mg/dL; range, 102-218; $P = .44$) and median maxCr (survivors: 9.8 mg/dL; range, 6.2-15.9 vs non-survivors: 9.8 mg/dL; range, 8.4-13.5; $P = .69$) between survivors and non-survivors. Conclusions and Clinical Importance: Regardless of azotemia severity, dogs with AKI-L receiving RRT have a good survival rate to discharge. The number of body systems affected and hyperbilirubinemia might be associated with worse outcomes

LANGUAGE OF ORIGINAL DOCUMENT: English

Senavirathna I., Jayasundara D., Warnasekara J., Kappagoda C., Agampodi S.

Levels of Cytokines in Leptospirosis Patients with Different Serovars and rfb Locus

(2024) Journal of Interferon and Cytokine Research, 44 (2), pp. 80 - 93

DOI: 10.1089/jir.2023.0091

ABSTRACT: Leptospirosis has a wide spectrum of clinical manifestations ranging from mild to severe disease. The cytokine response is considered one of the key drivers for this varying manifestation. The different cytokine response observed in patients with leptospirosis could be due to the variation of infecting serovars. Since the rfb locus codes for the lipopolysaccharide synthesis of the bacterial cell wall, which also determines the serovar, this locus may play a role in driving a specific cytokine response in the host. We investigated 12 commonly used cytokine profiles in serum samples of culture, microscopic agglutination test (MAT), or polymerase chain reaction (PCR)-positive patients with leptospirosis. The sequences of the rfb locus in culture-positive samples were generated from whole genome sequencing and serovar status was drawn from original data published. Isolated cultures were subjected to whole genome sequencing using the PacBio RS II system,

and the resulting data were used to determine the species. The recovered genomic data were annotated with the Rapid Annotation using Subsystem Technology (RAST) subsystem, and the rfb locus was extracted. The cytokine analysis was carried out using the Qiagen human ELISA kit. Eighteen samples were found to be positive by culture, while the other 7 samples were positive by PCR or MAT. Infections from *Leptospira interrogans* serovar Autumnalis (5), Pyrogens (3), Icterohaemorrhagiae (1) *Leptospira borgpetersenii* (all 7 samples clustered in same clonal group with serovar status not determined), *Leptospira weilii* (1 with serovar status not determined), and *Leptospira kirschneri* serovar Grippotyphosa (1) were included in the analysis. Three patients [infected with *Leptospira interrogans* serovar Autumnalis (2) and Pyrogens (1)] and 2 MAT-positive patients (highest titer against serovar Bratislava of *L.interrogans*) were reported to have severe clinical manifestations, while the rest had mild to moderate symptoms. Although the serum cytokine concentration of patients with severe clinical manifestation was comparatively higher, a statistically significant difference was observed only for interleukin (IL)-1b ($P < 0.05$). IL-10/tumor necrosis factor-alpha (TNF- α) ratio was high in patients with severe complications. In general, patients infected with *L. interrogans* showed higher concentration of cytokines compared to *L. borgpetersenii*.

LANGUAGE OF ORIGINAL DOCUMENT: English

Blanco R.M., dos Santos Lima E., de Haro G.N., Kamikawa C.M., Blanco R.M., Vincentini A.P., Romero E.C.
Comparative analysis of a novel N-butanol-prepared antigen vs thermo-resistant and sonicated antigens for human leptospirosis detection

(2024) Letters in Applied Microbiology, 77 (1), art. no. ovae004

DOI: 10.1093/lambio/ovae004

ABSTRACT: The diagnosis of human leptospirosis is mainly based on serological assays. Since the extraction by N-butanol has only been studied as an antigen for the diagnosis of cattle leptospirosis, this study aimed to investigate the feasibility of the N-butanol preparation for the diagnosis of human leptospirosis and compare it with sonicated and thermo-resistant antigens in IgM dot-blot test. Paired serum samples from 147 laboratory-confirmed leptospirosis cases were tested. The control group consisted of 148 serum samples from healthy individuals and nonleptospirosis cases. N-butanol antigens from serovar Copenhageni (ButC3) and serovar Patoc (ButP3) showed reactivity with antileptospiral antibodies from patients with confirmed leptospirosis. In the acute phase, sensitivities of IgM dot-blot assay with ButC3 and ButP3 antigens were 47.6% and 51.0%, respectively. In the convalescent phase, sensitivities were 95.9% (ButC3) and 93.2% (ButP3), and no significant differences were observed among the IgM dot-blot tests with other antigens. The specificity of the IgM dot-blot test with ButC3 antigen was good (92.6%), but with ButP3 (83.1%), it was significantly lower than with the other tests. The IgM dot-blot test described in this study is simple to perform and presents reliable visual results. Antigens prepared by N-butanol proved to be valuable diagnostic markers of leptospirosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Guzmán D.A., Diaz E., Sáenz C., Álvarez H., Cueva R., Zapata-Ríos G., Prado-Vivar B., Falconí M., Pearson T., Barragan V.

Domestic dogs in indigenous Amazonian communities: Key players in *Leptospira* cycling and transmission?

(2024) PLoS neglected tropical diseases, 18 (4), pp. e0011671

DOI: 10.1371/journal.pntd.0011671

ABSTRACT: BACKGROUND: Leptospirosis is the world's most common zoonotic disease. Mitigation and control rely on pathogen identification and understanding the roles of potential reservoirs in cycling and transmission. Underreporting and misdiagnosis obscure the magnitude of the problem and confound efforts to understand key epidemiological components. Difficulties in culturing hamper the use of serological diagnostics and delay the development of DNA detection methods. As a result, especially in complex ecosystems, we know very little about the importance of different mammalian host species in cycling and transmission to humans. **METHODOLOGY/PRINCIPAL FINDINGS:** We sampled dogs from five indigenous Kichwa communities living in the Yasuní National Park in the Ecuadorian Amazon basin. Blood and urine samples from domestic dogs were collected to assess the exposure of these animals to *Leptospira* and to identify the circulating species. Microscopic Agglutination Tests with a panel of 22 different serovars showed anti-leptospira antibodies in 36 sampled dogs (75%), and 7 serogroups were detected. Two DNA-based detection assays revealed pathogenic *Leptospira* DNA in 18 of 19 dog urine samples (94.7%). Amplicon sequencing and phylogenetic analysis of 16S rRNA and SecY genes from 15 urine samples revealed genetic diversity within two of three different *Leptospira* species: *noguchii* (n = 7), *santarosai* (n = 7), and *interrogans* (n = 1). **CONCLUSIONS/SIGNIFICANCE:** The high prevalence of antibodies and *Leptospira* DNA provides strong evidence for high rates of past and current infections. Such high prevalence has not been previously reported for dogs. These dogs live in the peridomestic environment in close contact with humans, yet they are free-ranging animals that interact with wildlife. This complex web of interactions may explain the diverse types of pathogenic *Leptospira* observed in this study. Our results suggest that domestic dogs are likely to play an important role in the cycling and transmission of *Leptospira*. Future studies in areas with complex ecoepidemiology will enable better parsing of the significance of genotypic, environmental, and host characteristics.

LANGUAGE OF ORIGINAL DOCUMENT: English

Gajdov V., Jokic G., Savic S., Zekic M., Blazic T., Rajkovic M., Petrovic T.

Genotyping of *Leptospira* spp. in wild rats leads to first time detection of *L. kirshneri* serovar Mozdok in Serbia

(2024) *Frontiers in Microbiology*, 15, art. no. 1379021

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ABSTRACT: Introduction: This study aimed to investigate the prevalence and molecular characterization of *Leptospira* species in Belgrade, Serbia, an area where this disease is underexplored. Specifically, the study sought to employ molecular and multilocus sequence typing analyses to fill the gap in understanding the diversity and distribution of *Leptospira* species within the region. **Methods:** A comprehensive molecular analysis was conducted on kidney samples obtained from Norway rats (*Rattus norvegicus*) in the urban environment. The study utilized molecular diagnostic techniques including real-time PCR targeting the *lipL32* gene and performing sequence-based typing schemes utilizing *adk*, *icdA*, *lipL32*, *lipL41*, *rrs2*, and *secY* genes. These methodologies were applied to ascertain the presence and characterize different *Leptospira* species and serovars, respectively. **Results:** The findings revealed the presence of two *Leptospira* species and three separate serovars in the Belgrade area. This study identified the presence of *L. kirshneri* serovar Mozdok in Serbia for the first time, a significant discovery previously undocumented in the region. This pioneering investigation sheds light on the molecular diversity and prevalence of *Leptospira* species in Serbia. **Discussion:** The study underscores the importance of employing molecular typing methods to gain insights into the

epidemiology and characterization of *Leptospira* species. These findings significantly contribute to both local and global perspectives on leptospirosis epidemiology, providing vital insights for the development of effective control strategies and interventions. Summary: In our recent study, we explored the presence and performed molecular typing of the *Leptospira* species, the bacteria responsible for leptospirosis, in wild rats in Serbia. This was the first time such a study was conducted in the region. Leptospirosis is a serious disease that affects both animals and humans, often transmitted through contact with water contaminated by infected animals. Our focus was on understanding which types of *Leptospira* were present in these animals. Excitingly, we discovered a particular strain of *Leptospira*, known as *L. kirshneri* serovar Mozdok, for the first time in Serbia. This finding is significant because it sheds light on the presence and spread of different *Leptospira* serovars in Serbia. It also raises awareness about the potential health risks associated with this serovar, which was previously unknown in the area. Our work fits into a broader context of disease surveillance and public health. By identifying the types of *Leptospira* present in a specific region, we can better understand the risks to public health and take steps to prevent and control the spread of leptospirosis. This discovery is not just important for scientists studying infectious diseases; it has real implications for public health officials, veterinarians, and anyone concerned with preventing and treating leptospirosis. Our findings highlight the need for ongoing monitoring of *Leptospira* in wildlife and synanthropic fauna, to protect both animal and human health. Copyright LANGUAGE OF ORIGINAL DOCUMENT: English