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della Lombardia e dell'Emilia – Romagna “Bruno Ubertini”
Centro di Referenza Nazionale per la Leptospirosi**

BOLLETTINO BIBLIOGRAFICO

Edizione n. 2024/02

Marzo – Aprile 2024

Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia – Romagna “Bruno Ubertini”

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Thielen B.K., Holzbauer S., Templen B., Schafer I.J., Artus A., Galloway R., Ireland M., Femrite T., Schleiss M.R.

Case Report: Locally Acquired Leptospirosis in a Minnesota Boy and His Dog

(2024) American Journal of Tropical Medicine and Hygiene, 110 (1), pp. 123 - 126

DOI: 10.4269/ajtmh.23-0291

ABSTRACT: Leptospirosis affects numerous animal species, including domestic dogs, but documented transmission to humans is rare. Here, we describe epidemiologically linked cases in a 12-year-old Minnesota boy and his pet dog. While human leptospirosis is often thought of as a disease of tropical locations, this case report describes a rare documented example of local transmission in the northern United States, a region historically not perceived to be at high risk of *Leptospira* species transmission to humans. This case highlights an unusual presentation, with facial nerve palsy, underappreciated epidemiological risks, and diagnostic challenges of this reemerging infection.

LANGUAGE OF ORIGINAL DOCUMENT: English

Zida S., Kania D., Bolloré K., Bandaogo O., Pisoni A., Dicko A., Tinto B., Traoré J., Perre P.V.D., Ouédraogo H.G., Tuillon E.

Leptospirosis Cases among Outpatients with Non-Malaria Fever Attending Primary Care Clinics during the Rainy Season in Bobo Dioulasso, Burkina Faso

(2024) American Journal of Tropical Medicine and Hygiene, 110 (1), pp. 127 - 132

DOI: 10.4269/ajtmh.23-0044

ABSTRACT: Leptospirosis is presumably an important cause of non-malarial fever in West Africa. In this study, outpatients consulting in primary care clinics during the rainy season were tested for leptospirosis, and clinical characteristics associated with leptospirosis cases were explored. Patients with fever $\geq 39^{\circ}\text{C}$ were recruited in nine primary health care centers in Bobo Dioulasso (Burkina Faso). Diagnosis of malaria was ruled out using a rapid diagnostic test (RDT; SD Bioline MalariaVR). Leptospirosis cases were defined as patients who tested positive for *Leptospira* IgM (Leptocheck-WB RDT and *Leptospira* IgM ELISA assay, Panbio) or DNA in plasma (LipL32 polymerase chain reaction [PCR]). Among 350 patients, 202 tested positive for malaria and were excluded, and 148 met the eligibility criteria and were included. Among these, 26 subjects were considered to be leptospirosis cases: 23 tested positive for *Leptospira* IgM (15.5%) and three tested positive by PCR (2.2%). Headaches, abdominal symptoms, and myalgia were frequently reported without any difference between leptospirosis cases and negative cases. Cough was more frequently observed among subjects testing positive for leptospirosis ($P = 0.02$). Water exposure, presence of a skin injury, and walking barefoot were associated with a *Leptospira*-positive test. All leptospirosis cases recovered without sequelae. A significant portion of outpatients with non-malarial febrile illness during the rainy season in Burkina Faso had epidemiological factors associated with leptospirosis and tested positive for *Leptospira*. The favorable outcome of leptospirosis cases was reassuring; this could be due in particular to the young age of the patients.

LANGUAGE OF ORIGINAL DOCUMENT: English

Harran E., Kuntz G., Decors A., Bourhy P., Auffret A., Bigeard C., Cherel D., Kodjo A., Le Dréan E., Lejas C., Lequeux G., Pilard M.-A., Pivette M., Guillois Y., Ayrat F.

Tracking potential *Leptospira* sources following human cases of leptospirosis: A One Health approach applied to an ecosystem in Brittany, France

(2024) One Health, 18, art. no. 100726

DOI: 10.1016/j.onehlt.2024.100726

ABSTRACT: Pathogenic *Leptospira* can cause leptospirosis: a widespread, potentially fatal bacterial zoonosis whose risk is mediated by the soil and water features, animal host distributions, meaning the local ecosystem. When human cases of leptospirosis occur, it is challenging to track down their source because ecosystem-level epidemiological knowledge on *Leptospira* is needed. Between 2016 and 2019 in a focal riparian ecosystem, the human population experienced an outbreak and successive cases of leptospirosis attributable to *L. kirschneri* and *L. interrogans*. The epidemiological investigation was carried out using the One Health approach, as described in international health guidelines. As a first step in this process, we investigated leptospiral carriage in the main animal hosts found in the region. We sampled 143 nutrias, 17 muskrats, and 10 Norway rats using convenient trapping. DNA was extracted from their kidneys, lungs, and urine and subjected to real-time PCR (RT-PCR) targeting the *Leptospira* 16S rDNA and *lfb1* genes. In the farms along the river's stretch of interest, we sampled serum from 439 cattle and used a microscopic agglutination test to detect the presence of antibodies against *Leptospira*. Urine samples were concomitantly obtained from 145 cattle and were used in two analyses: RT-PCR targeting the *Leptospira* 16S rDNA gene and *Leptospira* culturing. We found th, wt rodents were the most likely source of the *L. interrogans* behind the human cases. The cattle tested negative for *Leptospira* DNA but positive for antibodies against the serogroups implicated in the human cases. We failed to identify the potential source of the *L. kirschneri* responsible for several human cases of leptospirosis. Our results call for further clarification of the *Leptospira* maintenance community, which may comprise known maintenance hosts, such as rodents, as well as taxa not commonly considered to be maintenance hosts but that can still spread *Leptospira*. The resulting research network will collaboratively conduct future eco-epidemiological surveys to illuminate the leptospirosis risks faced by humans and animals within ecosystems.

LANGUAGE OF ORIGINAL DOCUMENT: English

Dinkar A., Singh J., Yadav M.

Leptospirosis Associated Digital Gangrene of Lower Extremities: Two Cases and Review of Literature

(2024) Infectious Disorders - Drug Targets, 24 (5), art. no. e220124225941, pp. 1 - 5

DOI: 10.2174/0118715265256882231128074609

ABSTRACT: Background: Leptospirosis is the most common zoonotic illness worldwide, caused by pathogenic spirochete bacteria called *Leptospira*. It is clinically presented with mild to moderate in most cases. However, sometimes, the course may be severe with multiorgan dysfunction. Case Presentation: We present two rare cases of Leptospirosis with peripheral dry gangrene of the lower extremities. A 25-year-old male, farmer by occupation without any significant past medical history had been diagnosed with a case of Leptospirosis that complicated to digital gangrene on 15 days of illness during hospitalization. Another 21-year-old male student was admitted for leptospiro-sis and developed digital gangrene on 19 days of illness. All clinical findings were resolved on the steroid. Conclusion: Apart from a high index of suspicion and awareness of unusual manifestations, serology plays a vital role in making an accurate and quick diagnosis to initiate appropriate therapy.

LANGUAGE OF ORIGINAL DOCUMENT: English

Hamond C., LeCount K., Anderson T., Putz E.J., Stuber T., Hicks J., Camp P., van der Linden H., Bayles D.O., Schlater L.K., Nally J.E.

Isolation and characterization of saprophytic and pathogenic strains of *Leptospira* from water sources in the Midwestern United States

(2024) *Frontiers in Water*, 6, art. no. 1278088

DOI: 10.3389/frwa.2024.1278088

ABSTRACT: The genus *Leptospira* is a diverse and unique group of bacteria comprising multiple saprophytic and pathogenic species, which survive and persist in suitable moist environments. Pathogenic species cause human and animal leptospirosis, a global and neglected zoonotic disease. Disease transmission occurs by exposure to contaminated water and moist soil environments or by contact with domestic animals and wildlife acting as reservoir hosts that shed *Leptospira* via urine. Here, we describe the unexpected diversity of saprophytic and pathogenic species of *Leptospira* isolated from water in the Midwestern United States. Samples were collected by volunteers in 11 counties in Iowa from water sources, including puddles, sewage, creeks, ponds, lakes, and rivers, during the summer of 2021. One hundred and five water samples were tested by culture for the presence of saprophytic and pathogenic species and by lipL32 qPCR specific for the detection of pathogens; 82 (78.1%) were culture positive and five (4.8%) were positive by lipL32 qPCR. Whole genome sequencing of isolates cultured from water samples identified 10 species of saprophytes, namely *L. montravelensis*, *L. kemamanensis*, *L. bandrabouensis*, *L. bourretii*, *L. bouyouniensis*, *L. chreensis*, *L. ellinghausenii*, *L. terpstrae*, *L. yanagawae*, and *L. abararensis*, as well as three novel saprophytic species. Whole genome sequencing also identified two novel pathogenic species. The remaining cultures comprised mixed populations of saprophytic species and six comprised a mixture of saprophytic and pathogenic species. One of these mixed cultures was enriched to select for a clonal isolate of pathogenic *Leptospira*, strain WS101.C1, which was classified as *L. interrogans* serogroup Djasiman serovar Djasiman. Cumulatively, 9.5% (10/105) of water samples were positive for pathogenic *Leptospira*. This study emphasizes the diversity of *Leptospira* present in water sources in the Midwestern United States and provides unique opportunities to explore the geographic diversity and evolution of this genus. The identification of known and novel pathogenic species circulating in local water sources highlights their potential usefulness as diagnostic antigens, as well as the role of water in the transmission of infection to human and animal populations. Integrating knowledge on human, animal, and environmental health is essential to control and predict risk for zoonoses.

LANGUAGE OF ORIGINAL DOCUMENT: English

Liu Y.-H., Chen Y.-H., Chen C.-M.

Fulminant Leptospirosis Presenting with Rapidly Developing Acute Renal Failure and Multiorgan Failure

(2024) *Biomedicines*, 12 (2), art. no. 435

DOI: 10.3390/biomedicines12020435

ABSTRACT: Leptospirosis, caused by pathogenic spirochetes of the *Leptospira* genus, is a common zoonosis in tropical and subtropical regions and can lead to an epidemic following heavy rainfall or flooding. The primary reservoirs of *Leptospira* include rodents, wild animals, dogs, cats, amphibians, and others, but the brown rat (*Rattus norvegicus*) remains the main source of human Leptospirosis. Humans are often accidental hosts and they can be infected through cuts, abrasions, mucosa, conjunctiva, or by ingesting contaminated water. The clinical manifestation of leptospirosis can vary from mild, nonspecific symptoms to a fatal outcome involving

liver and renal failure, pulmonary hemorrhage, meningitis, and septic shock. The severity of fatal outcomes is likely to be due to virulence factors, host susceptibility, and epidemiological conditions. *L. interrogans* are associated with high-risk individuals, particularly patients older than 60 years of age in clinical settings. The current case study showed a foreign worker who presented with rapidly deteriorating clinical signs of fever, jaundice, impaired consciousness, and oliguric acute renal failure. Drawing from our experience, it is advisable to consider the possibility of leptospirosis diagnosis in patients who show clinical symptoms such as fever, hepatic failure with jaundice, and acute renal failure. This is particularly important for those individuals with a prior history of pathogen exposure. This case study had a strong suspicion of leptospirosis, which was confirmed by the microscopic agglutination test (MAT) and, later, the patient's recovery following treatment. LANGUAGE OF ORIGINAL DOCUMENT: English

Caballero Méndez L.C., González Londoño L.M., Gómez Ruíz J.C., Escobar Herrera M.J., Mazo M.M., Franco-Montoya L.N.

Molecular determination of *Leptospira* spp., street and shelters dogs from the Coffee Region of Colombia [Molekularno određivanje *Leptospira* spp. u uličnim psima i psima iz skloništa u kolumbijskoj Regiji kave]

(2024) Veterinarska Stanica, 55 (5), pp. 527 - 535

DOI: 10.46419/vs.55.5.2

ABSTRACT: Leptospirosis is considered a zoonotic disease with a substantial impact on animal and human health. It is distributed in tropical and subtropical climates, which improves the survival of these bacteria for a long time, affecting domestic and wild animals that act as a reservoir. Canine leptospirosis has obtained great clinical relevance, due to the susceptibility of this species to infection and the frequent exposure to leptospirosis from the environment. Canines from the street and animal shelters constitute a high-risk population due to the proximity to sources of infection. This paper describes a cross-sectional study that involves sampling dogs from shelters located in the departments of Risaralda, Valle del Cauca, and Caldas, known as the Coffee Region, located in the centre-west of Colombia. Blood samples were taken from 140 canines and analysed in the laboratory of the Veterinary Medicine and Animal Science, Technological University of Pereira. DNA was extracted, and the LipL32 gene was amplified by conventional PCR. A 15% prevalence for *Leptospira* sp. was found in dogs from the Coffee region. No correlation was found between the variables such as sex, age, origin, and socioeconomic status. However, a tendency for infection was observed with several cases of diagnosis in female dogs older than six years in low strata. This study constitutes the first report of canine leptospirosis in this region of Colombia, which will allow the design of strategies aiming to mitigate the disease in this region.

LANGUAGE OF ORIGINAL DOCUMENT: English

Andityas M., Nuraini D.M., Sota P., Loong S.K., Sripta B., Sukon P., Tangkawattana P., Tangkawattana S.

Feline leptospirosis prevalence worldwide: A systematic review and meta-analysis of diagnostic approaches

(2024) Veterinary World, 17 (2), pp. 255 - 272

DOI: 10.14202/vetworld.2024.255-272

ABSTRACT: Background and Aim: Leptospirosis in felids (domestic and wild cats) presents an ongoing challenge in our understanding. Numerous studies have reported the detection of *Leptospira* spp. in these feline populations, highlighting their potential as zoonotic carriers. This systematic review and meta-analysis

aimed to provide insight into the global prevalence of leptospirosis in domestic and wild cats. **Materials and Methods:** We conducted extensive searches across five databases (PubMed, Scopus, Web of Science, Science Direct, and Google Scholar) following the Preferred Reporting Items for Systematic Reviews and Meta-analyses Protocols guidelines. Random-effect meta-analyses were performed using R software version 4.3.0 to estimate pooled prevalence rates. Subgroup meta-analyses were conducted based on continents, diagnostic methods, sample types, and wildcat genera. **Results:** A total of 71 articles on leptospirosis in domestic cats and 23 articles on leptospirosis in wild cats met the eligibility criteria. Our findings indicated a significantly higher pooled seroprevalence of leptospirosis in domestic cats compared with infection prevalence (9.95% [95% confidence interval (CI), 7.60%–12.54%] vs. 4.62% [95% CI, 2.10%–7.83%], $p = 0.01$). In contrast, no significant difference was observed in pooled seroprevalence and infection prevalence among wild cats (13.38% [95% CI, 6.25%–21.93%] vs. 2.9% [95% CI, 0.00%–18.91%], $p = 0.21$). A subgroup meta-analysis of domestic cats revealed significant differences in seroprevalence across continents, sample types, and diagnostic methods. On the contrary, wild cats had no significant differences in any of the subgroups. **Conclusion:** *Leptospira* spp. have evidently been exposed to both domestic and wild cats, highlighting their potential roles as reservoir hosts for leptospirosis. These findings highlight the importance of considering felids as a possible public health threat.

LANGUAGE OF ORIGINAL DOCUMENT: English

Kumari P., Yadav S., Sarkar S., Satheeshkumar P.K.

Cleavage of cell junction proteins as a host invasion strategy in leptospirosis

(2024) Applied Microbiology and Biotechnology, 108 (1), pp. 1 - 14

DOI: 10.1007/s00253-023-12945-y

ABSTRACT: Infection and invasion are the prerequisites for developing the disease symptoms in a host. While the probable mechanism of host invasion and pathogenesis is known in many pathogens, very little information is available on *Leptospira* invasion/pathogenesis. For causing systemic infection *Leptospira* must transmigrate across epithelial barriers, which is the most critical and challenging step. Extracellular and membrane-bound proteases play a crucial role in the invasion process. An extensive search for the proteins experimentally proven to be involved in the invasion process through cell junction cleavage in other pathogens has resulted in identifying 26 proteins. The similarity searches on the *Leptospira* genome for counterparts of these 26 pathogenesis-related proteins identified at least 12 probable coding sequences. The proteins were either extracellular or membrane-bound with a proteolytic domain to cleave the cell junction proteins. This review will emphasize our current understanding of the pathogenic aspects of host cell junction-pathogenic protein interactions involved in the invasion process. Further, potential candidate proteins with cell junction cleavage properties that may be exploited in the diagnostic/therapeutic aspects of leptospirosis will also be discussed. **Key points:** • The review focussed on the cell junction cleavage proteins in bacterial pathogenesis • Cell junction disruptors from *Leptospira* genome are identified using bioinformatics • The review provides insights into the therapeutic/diagnostic interventions possible.

LANGUAGE OF ORIGINAL DOCUMENT: English

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

Antibiotic prophylaxis for leptospirosis

(2024) Cochrane Database of Systematic Reviews, 2024 (3), art. no. CD014959

DOI: 10.1002/14651858.CD014959.pub2

ABSTRACT: Background: Leptospirosis is a global zoonotic and waterborne disease caused by pathogenic *Leptospira* species. Antibiotics are used as a strategy for prevention of leptospirosis, in particular in travellers and high-risk groups. However, the clinical benefits are unknown, especially when considering possible treatment-associated adverse effects. This review assesses the use of antibiotic prophylaxis in leptospirosis and is an update of a previously published review in the Cochrane Library (2009, Issue 3). Objectives: To evaluate the benefits and harms of antibiotic prophylaxis for human leptospirosis. Search methods: We identified randomised clinical trials through electronic searches of the Cochrane Hepato-Biliary Group Controlled Trials Register, CENTRAL, MEDLINE, Embase, LILACS, Science Citation Index Expanded, and other resources. We searched online clinical trial registries to identify unpublished or ongoing trials. We checked reference lists of the retrieved studies for further trials. The last date of search was 17 April 2023. Selection criteria: We included randomised clinical trials of any trial design, assessing antibiotics for prevention of leptospirosis, and with no restrictions on age, sex, occupation, or comorbidity of trial participants. We looked for trials assessing antibiotics irrespective of route of administration, dosage, and schedule versus placebo or no intervention. We also included trials assessing antibiotics versus other antibiotics using these criteria, or the same antibiotic but with another dose or schedule. Data collection and analysis: We followed Cochrane methodology. The primary outcomes were all-cause mortality, laboratory-confirmed leptospirosis regardless of the presence of an identified clinical syndrome (inclusive of asymptomatic cases), clinical diagnosis of leptospirosis regardless of the presence of laboratory confirmation, clinical diagnosis of leptospirosis confirmed by laboratory diagnosis (exclusive of asymptomatic cases), and serious adverse events. The secondary outcomes were quality of life and the proportion of people with non-serious adverse events. We assessed the risk of bias of the included trials using the RoB 2 tool and the certainty of evidence using GRADE. We presented dichotomous outcomes as risk ratios (RR) and continuous outcomes as mean difference (MD), with their 95% confidence intervals (CI). We used a random-effects model for our main analyses and the fixed-effect model for sensitivity analyses. Our primary outcome analyses included trial data at the longest follow-up. Main results: We identified five randomised clinical trials comprising 2593 participants that compared antibiotics (doxycycline, azithromycin, or penicillin) with placebo, or one antibiotic compared with another. Four trials assessed doxycycline with different durations, one trial assessed azithromycin, and one trial assessed penicillin. One trial had three intervention groups: doxycycline, azithromycin, and placebo. Three trials assessed pre-exposure prophylaxis, one trial assessed postexposure prophylaxis, and one did not report this clearly. Four trials recruited residents in endemic areas, and one trial recruited soldiers who experienced limited time exposure. The participants' ages in the included trials were 10 to 80 years. Follow-up ranged from one to three months. Antibiotics versus placebo. Doxycycline compared with placebo may result in little to no difference in all-cause mortality (RR 0.15, 95% CI 0.01 to 2.83; 1 trial, 782 participants; low-certainty evidence). Prophylactic antibiotics may have little to no effect on laboratory-confirmed leptospirosis, but the evidence is very uncertain (RR 0.56, 95% CI 0.25 to 1.26; 5 trials, 2593 participants; very low-certainty evidence). Antibiotics may result in little to no difference in the clinical diagnosis of leptospirosis regardless of laboratory confirmation (RR 0.76, 95% CI 0.53 to 1.08; 4 trials, 1653 participants; low-certainty evidence) and the clinical diagnosis of leptospirosis with laboratory confirmation (RR 0.57, 95% CI 0.26 to 1.26; 4 trials, 1653 participants; low-certainty evidence). Antibiotics compared with placebo may increase non-serious adverse events, but the evidence is very uncertain (RR 10.13, 95% CI 2.40 to 42.71; 3 trials, 1909 participants; very

low-certainty evidence). One antibiotic versus another antibiotic. One trial assessed doxycycline versus azithromycin but did not report mortality. Compared to azithromycin, doxycycline may have little to no effect on laboratory-confirmed leptospirosis regardless of the presence of an identified clinical syndrome (RR 1.49, 95% CI 0.51 to 4.32; 1 trial, 137 participants), on the clinical diagnosis of leptospirosis regardless of the presence of laboratory confirmation (RR 4.18, 95% CI 0.94 to 18.66; 1 trial, 137 participants), on the clinical diagnosis of leptospirosis confirmed by laboratory diagnosis (RR 4.18, 95% CI 0.94 to 18.66; 1 trial, 137 participants), and on non-serious adverse events (RR 1.12, 95% CI 0.36 to 3.48; 1 trial, 137 participants), but the evidence is very uncertain. The certainty of evidence for all the outcomes was very low. None of the five included trials reported serious adverse events or assessed quality of life. One study is awaiting classification. Funding. Four of the five trials included statements disclosing their funding/supporting sources, and the remaining trial did not include this. Three of the four trials that disclosed their supporting sources received the supply of trial drugs directly from the same pharmaceutical company, and the remaining trial received financial support from a governmental source. Authors' conclusions: We do not know if antibiotics versus placebo or another antibiotic has little or have no effect on all-cause mortality or leptospirosis infection because the certainty of evidence is low or very low. We do not know if antibiotics versus placebo may increase the overall risk of non-serious adverse events because of very low-certainty evidence. We lack definitive rigorous data from randomised trials to support the use of antibiotics for the prophylaxis of leptospirosis infection. We lack trials reporting data on clinically relevant outcomes.

LANGUAGE OF ORIGINAL DOCUMENT: English

Maksimović Z., Babić S., Zahirović A., Rifatbegović M.

Seroprevalence of leptospirosis among stray dogs in Bosnia and Herzegovina

(2024) Comparative Immunology, Microbiology and Infectious Diseases, 109, art. no. 102171

DOI: 10.1016/j.cimid.2024.102171

ABSTRACT: Leptospirosis is a (re) emerging zoonosis that occurs worldwide. This study aimed to assess seroprevalence of leptospirosis and to identify the most common reactive serovars and risk factors for seropositivity in apparently healthy stray dogs of unknown vaccination status in the Sarajevo region of Bosnia and Herzegovina. Positive microscopic agglutination test titres ($\geq 1:25$) were detected in 3.87% (156/4028) of samples and most of the sera reacted against one serovar (85.9%). Dogs were most commonly reactive to Canicola (40.4%) and Hardjo (33.3%), followed by Pomona (15.4%) Tarassovi (14.7%), Icterohaemorrhagiae (8.3%), Grippotyphosa (5.8%), Bratislava (1.3%) and Saxkoebing (0.6%). Dogs older than one year had higher odds of seropositivity compared to younger dogs. The seropositivity was higher in spring and autumn than in summer. These results advocate for the need of a control strategy for this zoonosis in the country, which should include sero-surveillance, monitoring, and the inclusion of additional serovars in the testing.

LANGUAGE OF ORIGINAL DOCUMENT: English

Nascimento Filho E.G., Vieira M.L., Dias M., Mendes M.A., Sanchez F.B., Setubal J.C., Heinemann M.B., Souza G.O., Pimenta D.C., Nascimento A.L.T.O.

Global proteome of the saprophytic strain *Leptospira biflexa* and comparative analysis with pathogenic strain *Leptospira interrogans* uncover new pathogenesis mechanisms

(2024) Journal of Proteomics, 297, art. no. 105125

DOI: 10.1016/j.jprot.2024.105125

ABSTRACT: *Leptospira* is a genus of bacteria that includes free-living saprophytic species found in water or soil, and pathogenic species, which are the etiologic agents of leptospirosis. Besides all the efforts, there are only a few proteins described as virulence factors in the pathogenic strain *L. interrogans*. This work aims to perform *L. biflexa* serovar Patoc1 strain Paris global proteome and to compare with the proteome database of pathogenic *L. interrogans* serovar Copenhageni strain Fiocruz L1–130. We identified a total of 2327 expressed proteins of *L. biflexa* by mass spectrometry. Using the Get Homologues software with the global proteome of *L. biflexa* and *L. interrogans*, we found orthologous proteins classified into conserved, low conserved, and specific proteins. Comparative bioinformatic analyses were performed to understand the biological functions of the proteins, subcellular localization, the presence of signal peptide, structural domains, and motifs using public softwares. These results lead to the selection of 182 low conserved within the saprophyte, and 176 specific proteins of *L. interrogans*. It is anticipated that these findings will indicate further studies to uncover virulence factors in the pathogenic strain. This work presents for the first time the global proteome of saprophytic strain *L. biflexa* serovar Patoc, strain Patoc1. Significance: The comparative analysis established an array of specific proteins in pathogenic strain that will narrow down the identification of immune protective proteins that will help fight leptospirosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Vijayachari P., Awaradi S., Siddaraju H.M., Nithin K., Veerendra S.S., Suresh Babu U., Punnam Chander M., Kartick C., Anwesh M., Sugunan A.P.

Survey of the present health & nutritional status of Shompen tribe of Great Nicobar Island

(2024) Indian Journal of Medical Research, 159 (1), pp. 35 - 42

DOI: 10.4103/ijmr.ijmr_3193_21

ABSTRACT: Background & objectives: Shompens are one of the two mongoloid tribes of Nicobar district. There is little information about their recent health status since the last survey which was conducted in 1998. Hence, a comprehensive health and nutritional survey was conducted in March 2017 to assess the changes. The survey was carried out by a joint team of various organizations including the ICMR-Regional Medical Research Centre and Tribal Welfare and Health Department both located in Port Blair. Methods: A detailed health and nutrition survey of the Shompen community was planned by deputing a field research team. The survey included demographic data, anthropometric data, clinical examination, screening for the markers of infectious diseases, respiratory pathogens, tuberculosis and haemoglobinopathies. Results: About half of the Shompen adults (both males and females) had a body mass index (BMI) of ≥ 23 . However, Shompen children had a good nutritional status with no child suffering from undernutrition. As per BMI for age, none of the children < 5 yr were under-nourished, while in the 5-17 yr group, 12 per cent of children were undernourished. Anaemia prevalence was about 48.3 per cent, with 54 per cent prevalence in females and 43.8 per cent in males. Fungal infection of the skin, acute respiratory infection and abdominal pain were the common morbidities observed. None had active pulmonary tuberculosis. Of 38 Shompens screened for IgG (immunoglobulin G) antibodies, 42.1 and 18.4 per cent were positive for measles and rubella, respectively. Seroprevalence of *Leptospira* was 35.5 per cent. The prevalence of hypertension was 13.2 per cent, whereas another 28.9 per cent were pre-hypertensive. Interpretation & conclusions: The population structure of the Shompen is not skewed and under nutrition was not widely prevalent among the children of < 5 yr. The other positive observations were the absence of malaria, filariasis and dengue. However, there was natural infection of measles and rubella. Fungal skin infection and intestinal parasitic infestations were widely prevalent. Although cardiovascular risk profile

was low, there were signs of emerging risk of over-weight, hypertension and dyslipidaemia. These together with the high prevalence of smokeless tobacco use may have a serious effect on the cardiovascular disease susceptibility of the Shompen population in the future.

LANGUAGE OF ORIGINAL DOCUMENT: English

Suárez-Galaz A., Reyes-Novelo E., Hernández-Betancourt S., Panti-May A., Estrella E., Sánchez-Montes S., Noh-Pech H., Lugo-Caballero C., Colunga-Salas P., Peláez-Sánchez R., Sosa-Escalante J., Herrera-Flores B.G., Rodríguez-Vivas R.I., Torres-Castro M.

Study on the relation of the characteristics of the capture sites with the *Leptospira* spp. occurrence in bats and rodents from Yucatan, Mexico

(2024) *Acta Tropica*, 249, art. no. 107072

DOI: 10.1016/j.actatropica.2023.107072

ABSTRACT: This study aims to describe the natural *Leptospira* occurrence in small mammals from Yucatan, Mexico, and to explore the relation between the characteristics of the capture sites and the *Leptospira* occurrence. Bats and rodents were captured in five sites of Yucatan state, and from them, a kidney fragment was collected that was used in the genomic DNA extraction. *Leptospira* DNA was identified by PCR targeting the 16S-rRNA and LipL32 genes. Additionally, a bioinformatic analysis was carried out to know the *Leptospira* species and was corroborated with a phylogenetic tree. The assemblage of small mammals was compound of 82 (51.2 %) bats and 78 (48.8 %) rodents. A global frequency (bats plus rodents) of *Leptospira* occurrence of 21.2 % (34/160) was observed; in bats, it was 21.9 % (18/82), and in rodents, 20.5 % (16/78). The phylogenetic trees based on LipL32 gene showed that the recovered sequences most closely resemble the species *L. borgpetersenii* and *L. noguchii*. The ordination of the capture sites with tropical deciduous forests as original vegetation is more related to the abundance of *Leptospira*-infected rodents. The ordination of the capture sites with tropical sub-deciduous forests as original vegetation is more related to the diversity of *Leptospira*-infected bat species. The canonical ordering of the capture sites is by the original vegetation type and the diversity and abundance of *Leptospira*-infected bat and rodent species.

LANGUAGE OF ORIGINAL DOCUMENT: English

Sayanthi Y., Susanna D.

Pathogenic *Leptospira* contamination in the environment: a systematic review

(2024) *Infection Ecology and Epidemiology*, 14 (1), art. no. 2324820

DOI: 10.1080/20008686.2024.2324820

ABSTRACT: Background: The pathogenic *Leptospira* is maintained in renal tubules of certain animals, mostly rodents, and excreted in the urine which can contaminate the environment. It is necessary to detect pathogenic *Leptospira* in environmental samples. Knowing the survival of *Leptospira* in the environment (water and soil) can provide an overview of where and how they can be transmitted to humans. Objective: Therefore, this study aimed to provide a systematic overview of pathogenic *Leptospira* presence in water and soil environment, the various species of pathogenic *Leptospira* that are harmful for human, and the ability to survive using a systematic review method. Methods: The search process used four databases: PubMed, Science Direct, Scopus, and ProQuest. Furthermore, the articles sought were published from 2000 to July 2021, and 38 were analysed. Results: The pathogenic *Leptospira* contamination in water was higher in urban areas, while soil samples were higher in rural areas. Various pathogenic *Leptospira* detected in the environment were *L.*

alstonii, L. kmetyi, L. noguchii, and L. interrogans. Those pathogenic *Leptospira* can survive in water at 4–30°C and at pH < 7; in soil, it can survive at a humidity of < 20% and a pH < 6. Conclusion: Urban and rural areas have the same risk for leptospirosis disease because pathogenic *Leptospira* (P1).

LANGUAGE OF ORIGINAL DOCUMENT: English

Sharma A., Singh M., Kumar P., Thakur S.D., Sharma A.

An investigation on infectious etiologies of bovine abortions in Northern Western Himalayan region of Himachal Pradesh

(2024) Indian Journal of Animal Sciences, 94 (4), pp. 325 - 328

DOI: 10.56093/ijans.v94i4.130222

ABSTRACT: This study was conducted to ascertain infectious etiologies of bovine abortions in Northern Western Himalayan region of Himachal Pradesh. Overall, 16.77% (27/161) serum samples were positive for antibodies to at least one bovine abortion-causing pathogen. The overall prevalence was highest for BHV-1 (8.07%) followed by *Chlamydia* (3.11%), *B. abortus* (2.48%), *T. gondii* (1.86%), *Leptospira* (0.62%), and *C. albicans* (0.62%). None of the tested samples was positive for *C. burnetii* and *Aspergillus*. The occurrence of bovine abortions was higher (51.85%) in the second trimester of gestation followed by the third (44.44%) and first trimester (3.70%). In comparison to previous studies, we recorded a lower prevalence of infectious etiologies of bovine abortions. Hence, it is important to investigate the role of the noninfectious etiologies of bovine abortions such as hormonal (progesterone insufficiency), nutritional (negative energy balance, feedstuff containing anti-nutritional factors) and miscellaneous causes including poor animal management, toxin infestation, and twin pregnancies.

LANGUAGE OF ORIGINAL DOCUMENT: English

Aymée L., Mendes J., Lilienbaum W.

Bovine Genital Leptospirosis: An Update of This Important Reproductive Disease

(2024) Animals, 14 (2), art. no. 322

DOI: 10.3390/ani14020322

ABSTRACT: Bovine leptospirosis is an important disease that affects the reproductive sphere. Due to its high relevance for the bovine production chain in a worldwide scenario, a better understanding of the disease is crucial to reduce its negative impacts. The main agents are strains from the Sejroe serogroup, such as Hardjo and Guaricura, which lead to renal and genital infection. The genital colonization causes a chronic, silent, and subclinical reproductive syndrome, called Bovine Genital Leptospirosis (BGL). Embryonic death, estrus repetition, subfertility, and abortions are the main signs of BGL condition in females. However, although leptospires have been identified in semen, the manifestation of BGL in bulls remains to be clarified. The recommended diagnosis of BGL includes a serologic screening of the herds using the microscopic agglutination test followed by PCR of genital samples (cervicovaginal mucus, uterine fragment, or semen), especially from animals with reproductive failures. After the identification of carriers, control is carried out considering three steps: antimicrobial treatment of the carriers, environmental and reproductive management, and herd vaccination. Systematic testing, quarantine of newly arrived animals, and usage of antimicrobials in semen diluents or embryo culture media are other sanitary approaches that are encouraged to improve the control of the syndrome. Herein we discuss protocols for an efficient diagnosis and preventive procedures of

BGL, which are fundamental to reducing the negative impact of the disease on cattle reproduction and its consequent economic hazards.

LANGUAGE OF ORIGINAL DOCUMENT: English

Hall T.A., Soepnel A.W., Addidle M.

A review of ten years of *Leptospira* serology and PCR testing

(2024) New Zealand Journal of Medical Laboratory Science, 78 (1), pp. 25 - 30

ABSTRACT: Objective: To evaluate the use of diagnostic *Leptospira* laboratory testing within the Midlands region of New Zealand and identify the most sensitive testing strategy. Method: *Leptospira* serology and polymerase chain reaction (PCR) testing performed within the Pathlab remit in 2013-2022 were reviewed by comparing methodologies and request origins to identify trends over time and evaluate the relative performance of serology and PCR testing. Results: 81% of the cases tested by both serology and PCR that were confirmed infections were detected by either blood PCR, urine PCR, or serology alone. No significant difference was observed between the detection rates of blood PCR and urine PCR. Serology was the most frequently requested methodology, though PCR testing quadrupled in 2017 and uptake has continued to increase since then, becoming the favoured methodology amongst hospital-based requestors in 2022. Appropriately timed paired serological testing was rarely performed. Conclusions: No single methodology can be relied on to consistently detect leptospirosis infections. Follow-up serology was under-utilised. A combination of PCR and serology testing was the most effective testing strategy.

LANGUAGE OF ORIGINAL DOCUMENT: English

Klink J.C., Rieger A., Wohlsein P., Siebert U., Obiegala A.

Vector-Borne and Zoonotic Pathogens in Raccoon Dogs (*Nyctereutes procyonoides*) and Raccoons (*Procyon lotor*) from Schleswig-Holstein, Germany

(2024) Pathogens, 13 (3), art. no. 270

DOI: 10.3390/pathogens13030270

ABSTRACT: Raccoon dogs (*Nyctereutes procyonoides*) and raccoons (*Procyon lotor*) are invasive alien species originating from East Asia and North America, respectively. They are discussed as vectors and reservoirs for various infectious diseases, including vector-borne and zoonotic pathogens, and are therefore a potential threat to human and domestic animal health, as well as to biodiversity and conservation. In the years 2021 and 2022, 110 raccoon dogs (*Nyctereutes procyonoides*) and 30 raccoons (*Procyon lotor*) were screened via qPCR for the presence of *Leptospira* spp., *Rickettsia* spp. and *Borrelia* spp. in the German federal state of Schleswig-Holstein as part of a health and risk assessment study. *Borrelia* spp. were confirmed in one raccoon dog and one raccoon, identified as *Borrelia afzelii* in the raccoon. *Leptospira* spp. were found in 21 (19.44%) raccoon dogs and 2 (6.90%) raccoons. In five raccoon dogs, *Leptospira* spp. were identified as *Leptospira borgpetersenii*, *Leptospira kirschneri* and *Leptospira interrogans*.

LANGUAGE OF ORIGINAL DOCUMENT: English

Senavirathna I., Jayasundara D., Warnasekara J., Matthias M.A., Vinetz J.M., Agampodi S.

Whole genome sequencing data of *Leptospira weilii* and *Leptospira kirschneri* isolated from human subjects of Sri Lanka

(2024) Data in Brief, 52, art. no. 109840

DOI: 10.1016/j.dib.2023.109840

ABSTRACT: Leptospirosis is a re-emerging zoonotic disease. This article reports the complete genome sequences of three novel strains of Genus *Leptospira*: two from the species *Leptospira weilii* (FMAS_RT1, FMAS_PD2) and one from *Leptospira kirschneri* (FMAS_PN5). These isolates were recovered from the blood samples of acute febrile patients in different geographical and climatic zones of Sri Lanka. High-quality genomic DNA was extracted from the three isolates in mid-log phase cultures. Whole genome sequencing was conducted using the PacBio Single Molecule Real-Time (SMRT) platform to identify the species, genome features, and novelty of the strains. The annotation was conducted using RAST (Rapid Annotation Using Subsystem Technology version 2.0) and the NCBI Prokaryotic Genome Annotation Pipeline. The genome sequences of three isolates have been deposited in the Mendeley data repository and the National Center for Biotechnology Information (NCBI) repository. This data will be useful for future researchers when conducting comparative genomic analysis, revealing the exact mechanism of pathogenesis of leptospirosis and developing molecular diagnostic tools for early detection.

LANGUAGE OF ORIGINAL DOCUMENT: English

Valente M., Bramugy J., Keddie S.H., Hopkins H., Bassat Q., Baerenbold O., Bradley J., Falconer J., Keogh R.H., Newton P.N., Picardeau M., Crump J.A.

Diagnosis of human leptospirosis: systematic review and meta-analysis of the diagnostic accuracy of the *Leptospira* microscopic agglutination test, PCR targeting *Lfb1*, and IgM ELISA to *Leptospira fainei* serovar Hurstbridge

(2024) BMC Infectious Diseases, 24 (1), art. no. 168

DOI: 10.1186/s12879-023-08935-0

ABSTRACT: Background: Leptospirosis is an underdiagnosed infectious disease with non-specific clinical presentation that requires laboratory confirmation for diagnosis. The serologic reference standard remains the microscopic agglutination test (MAT) on paired serum samples. However, reported estimates of MAT's sensitivity vary. We evaluated the accuracy of four index tests, MAT on paired samples as well as alternative standards for leptospirosis diagnosis: MAT on single acute-phase samples, polymerase chain reaction (PCR) with the target gene *Lfb1*, and ELISA IgM with *Leptospira fainei* serovar Hurstbridge as an antigen. Methods: We performed a systematic review of studies reporting results of leptospirosis diagnostic tests. We searched eight electronic databases and selected studies that tested human blood samples and compared index tests with blood culture and/or PCR and/or MAT (comparator tests). For MAT selection criteria we defined a threshold for single acute-phase samples according to a national classification of leptospirosis endemicity. We used a Bayesian random-effect meta-analysis to estimate the sensitivity and specificity of MAT in single acute-phase and paired samples separately, and assessed risk of bias using the Quality Assessment of Studies of Diagnostic Accuracy Approach- 2 (QUADAS-2) tool. Results: For the MAT accuracy evaluation, 15 studies were included, 11 with single acute-phase serum, and 12 with paired sera. Two included studies used PCR targeting the *Lfb1* gene, and one included study used IgM ELISA with *Leptospira fainei* serovar Hurstbridge as antigen. For MAT in single acute-phase samples, the pooled sensitivity and specificity were 14% (95% credible interval [CrI] 3–38%) and 86% (95% CrI 59–96%), respectively, and the predicted sensitivity and specificity were 14% (95% CrI 0–90%) and 86% (95% CrI 9–100%). Among paired MAT samples, the pooled sensitivity and specificity were 68% (95% CrI 32–92%) and 75% (95% CrI 45–93%) respectively, and the predicted sensitivity and specificity were 69% (95% CrI 2–100%) and 75% (2–100%). Conclusions: Based on

our analysis, the accuracy of MAT in paired samples was not high, but it remains the reference standard until a more accurate diagnostic test is developed. Future studies that include larger numbers of participants with paired samples will improve the certainty of accuracy estimates.

LANGUAGE OF ORIGINAL DOCUMENT: English

Miyahara S., Mori H., Fukuda K., Ogawa M., Saito M.

Non-purulent myositis caused by direct invasion of skeletal muscle tissue by *Leptospira* in a hamster model

(2024) *Infection and Immunity*, 92 (2)

DOI: 10.1128/iai.00420-23

ABSTRACT: Myalgia is a common symptom of *Leptospira* infection in humans. Autopsies have reported that muscle tissue shows degeneration and necrosis of the myofibers and infiltration of inflammatory cells composed mainly of macrophages and lymphocytes. It remains unclear whether *Leptospira* directly infects the muscle and how the infiltrating inflammatory cells are involved in muscle fiber destruction. This study evaluated the relationship between histopathological changes and leptospiral localization in the muscle tissue of a hamster model. The influence of macrophages in skeletal muscle injury was also investigated, using selective depletion of macrophages by administration of liposomal clodronate. Hamsters infected subcutaneously with *Leptospira interrogans* serovar Manilae strain UP-MMC-SM showed myositis of the thighs adjacent to the inoculated area beginning at 6 days post-infection. The myositis was non-purulent and showed sporadic degeneration and necrosis of muscle fibers. The degeneration of myofibers was accompanied by aggregations of macrophages. Immunofluorescence staining revealed leptospirae surrounding the damaged muscle fibers. Subcutaneous injection of formalin-killed *Leptospira* or intraperitoneal injection of live *Leptospira* caused no myositis in hamster thighs. Liposomal clodronate treatment in infected hamsters reduced macrophage infiltration in muscle tissue without impacting bacterial clearance. Muscle necrosis was still observed in the infected hamsters treated with liposomal clodronate, and there was no significant change in serum creatine kinase levels compared to those in animals treated with liposomes alone. Our findings suggest that leptospiral invasion of muscle tissue from an inoculation site leads to the destruction of muscle fibers and causes non-purulent myositis, whereas the infiltrating macrophages contribute less to muscle destruction.

LANGUAGE OF ORIGINAL DOCUMENT: English

Jampasa S., Jikul B., Kreangkaiwal C., Khamcharoen W., Jesadabundit W., Waiwinya W., Saelim P., Phanbunmee T., Patarakul K., Chailapakul O.

Multiple signaling probe-based ultrasensitive electrochemical DNA sensor integrated with NFC-enabled smartphone to diagnose leptospirosis

(2024) *Sensors and Actuators B: Chemical*, 406, art. no. 135411

DOI: 10.1016/j.snb.2024.135411

ABSTRACT: Leptospirosis, caused by pathogenic *Leptospira*, is a worldwide zoonotic disease. Due to the non-specific symptoms and low concentrations of leptospiral DNA in the blood of patients during the acute phase of leptospirosis, the development of effective biosensors for its detection remains a challenge. Here we introduced a multiple signaling probe-based electrochemical DNA sensor (E-DNA) that integrates near-field communication (NFC) with portable smartphones, enabling ultrasensitive and on-site detection of leptospiral DNA in clinical samples. Unlike conventional sandwich-hybridization assays which employ a single signaling

probe, our E-DNA sensor used multiple signaling probes labeled with gold nanoparticles (AuNPs-DNA) to amplify the electrochemical signal in the presence of trace DNA targets. Hybridization between the first capture probe, coated on a magnetic bead, and the DNA target was pre-concentrated in a reaction tube. Subsequent conjugation with AuNPs-DNA significantly enhanced the gold current response. Both the increasing number of the AuNPs-DNAs and the capture probe binding sequences improved the signal by approximately 2.6-fold. This proposed sensor architecture achieved a sensitivity of 43 copies/mL, as a limit of detection (LOD), with a broad linearity ranging from 10^2 to 10^6 copies/mL. Its specificity in clinical samples was verified by real-time polymerase chain reaction (real-time PCR). Integration of the NFC with a smartphone renders this E-DNA sensor portable for on-site diagnosis of leptospirosis. Our work provides practical guidelines for designing sensitive E-DNA sensors, especially when DNA targets are present at low concentrations.

LANGUAGE OF ORIGINAL DOCUMENT: English

Sreevalsan T.V., Chandra R.

Relevance of Polymerase Chain Reaction in Early Diagnosis of Leptospirosis

(2024) Indian Journal of Critical Care Medicine, 28 (3), pp. 290 - 293

DOI: 10.5005/jp-journals-10071-24649

ABSTRACT: Aim and background: Leptospirosis is common in India, especially in the southern states. Mortality is high among untreated cases. Diagnosis of leptospirosis remains a challenge in India as polymerase chain reaction (PCR), which is more sensitive than Immunoglobulin M (IgM) is not widely available. This study aimed to find out the difference in diagnostic yield with PCR and IgM in early leptospirosis. Materials and methods: This retrospective, single-center study included 67 adults with laboratory-confirmed leptospirosis (IgM, PCR, or both) who presented within 7 days of symptom onset and were admitted to the intensive care unit (ICU). The difference in the diagnostic yield with PCR and IgM ELISA was studied. Results: About 77.6% of the patients tested positive by PCR and 55.2% tested positive by IgM. There was a statistically significant difference in the detection of leptospirosis by PCR and IgM (p -value = 0.036). In the subgroup of patients who presented within 3 days of onset of symptoms, PCR positivity was 90.32% whereas IgM positivity was only 25.8%. Conclusion: Our study showed that the sensitivity of leptospira PCR is significantly higher than IgM in the first week of illness. It also showed that among the subset of patients who died, a majority were detected only by PCR. Since PCR is not widely available, leptospirosis remains underdiagnosed and mortality from the same is underestimated. Polymerase chain reaction, if routinely done along with IgM for all suspected cases of leptospirosis that present within the first week of illness helps in prompt diagnosis and treatment.

LANGUAGE OF ORIGINAL DOCUMENT: English

Ji Z., Jian M., Su X., Pan Y., Duan Y., Ma W., Zhong L., Yang J., Song J., Wu X., Gao L., Ma W., Kong J., Li B., Chen J., Liu M., Fan Y., Peng L., Dong Y., Bao F., Liu A.

Efficacy and safety of antibiotics for treatment of leptospirosis: a systematic review and network meta-analysis

(2024) Systematic Reviews, 13 (1), art. no. 108

DOI: 10.1186/s13643-024-02519-y

ABSTRACT: Background: Leptospirosis, an important zoonotic bacterial disease, commonly affects resource-poor populations and results in significant morbidity and mortality worldwide. The value of antibiotics in leptospirosis remains unclear, as evidenced by the conflicting opinions published. Methods: We conducted a

search in the PubMed, Web of Science, and Cochrane Library databases for studies. These studies included clinical trials and retrospective studies that evaluated the efficacy or safety of antibiotics for leptospirosis treatment. The primary outcomes assessed were defervescence time, mortality rate, and hospital stays. Subgroup analyses were performed based on whether there were cases involving children and whether there were cases of severe jaundice. Safety was defined as the prevalence of adverse events associated with the use of antibiotics. p scores were utilized to rank the efficacy of the antibiotics. Results: There are included 9 randomized controlled trials (RCTs), 1 control trial (CT), and 3 retrospective studies (RS) involving 920 patients and 8 antibiotics. Six antibiotics resulted in significantly shorter defervescence times compared to the control, namely cefotaxime (MD, - 1.88; 95% CI = - 2.60 to - 1.15), azithromycin (MD, - 1.74; 95% CI = - 2.52 to - 0.95), doxycycline (MD, - 1.53; 95% CI = - 2.05 to - 1.00), ceftriaxone (MD, - 1.22; 95% CI = - 1.89 to - 0.55), penicillin (MD, - 1.22; 95% CI = - 1.80 to - 0.64), and penicillin or ampicillin (MD, - 0.08; 95% CI = - 1.01 to - 0.59). The antibiotics were not effective in reducing the mortality and hospital stays. Common adverse reactions to antibiotics included Jarisch–Herxheimer reaction, rash, headache, and digestive reactions (nausea, vomiting, diarrhea, abdominal pain, and others). Conclusions: Findings recommend that leptospirosis patients be treated with antibiotics, which significantly reduced the leptospirosis defervescence time. Cephalosporins, doxycycline, and penicillin are suggested, and azithromycin may be a suitable alternative for drug-resistant cases.

LANGUAGE OF ORIGINAL DOCUMENT: English

Hamer M., Watanabe O., Saraullo V., Ortega F., Sánchez C., Martínez M., Brihuega B., Grune Loffler S.

Optimization and comparative analysis of LAMP and PCR techniques for the detection of leptospiral DNA in Golden Syrian hamsters

(2024) Veterinary Research Communications, 48 (1), pp. 103 - 111

DOI: 10.1007/s11259-023-10183-1

ABSTRACT: Leptospirosis is a zoonotic disease with significant public health and economic impact worldwide. Rapid and accurate diagnosis is essential for effective prevention and treatment. This study optimized a loop-mediated isothermal amplification (LAMP) assay using BFo isothermal DNA polymerase with different colorimetric indicators. LAMP was able to detect DNA from pathogenic and intermediate leptospires, while non-pathogenic leptospires and other non-leptospiral microorganisms were negative. LAMP assay combined with calcein showed a tenfold higher limit of detection (1 ng of leptospiral DNA per reaction) than LAMP combined with hydroxynaphthol blue or end-point PCR lipL32 (10 ng of DNA per reaction). Animal samples were collected from infected and non-infected Golden Syrian hamsters (*Mesocricetus auratus*) to evaluate and compare the performance of LAMP and PCR. These techniques showed a substantial agreement according to Cohen's kappa statistic, being both useful techniques for detecting leptospiral DNA in clinical samples. Overall, this study demonstrates that the LAMP assay is a sensitive, specific, rapid, and simple tool for the detection of leptospiral DNA. It has the potential to facilitate the diagnosis of leptospirosis, particularly in low-income regions with limited diagnosis resources.

LANGUAGE OF ORIGINAL DOCUMENT: English

Selim A., Marzok M., Gattan H.S., Abdelhady A., Salem M., Hereba A.M.

Seroprevalence and associated risk factors for bovine leptospirosis in Egypt

(2024) Scientific Reports, 14 (1), art. no. 4645

DOI: 10.1038/s41598-024-54882-4

ABSTRACT: Leptospirosis is caused by pathogenic bacteria of the genus *Leptospira* and is one of causative agents of reproductive problems leading to negative economic impact on bovine worldwide. The goal of this study was to investigate the seroprevalence of *Leptospira* spp. in cattle in some governorates of Egypt's Nile Delta and assess the risk factors for infection. A total of 410 serum samples were collected from cattle and examined using microscopic agglutination test. The overall seroprevalence was 10.2% and the most prevalent serovars were Icterohaemorrhagiae, Pomona and Canicola. In addition, the potential risk factors were associated *Leptospira* spp. infection were age, herd size, history of abortion, presence of dogs and rodent control. Thus, leptospirosis is common in dairy cattle in the Nile Delta and the presence of rodents in feed and dog-accessible pastures increases the risk of *Leptospira* spp. infection among animals.

LANGUAGE OF ORIGINAL DOCUMENT: English

Her R., Crespin L., Etougbétché J., Groud K., Gnononfoun M., Chapron A., Evenamia C., Houéménou G., Lurier T., Cappelle J., Dobigny G., Ayral F.

Seroprevalence and renal carriage of pathogenic *Leptospira* in livestock in Cotonou, Benin

(2024) *Veterinary Medicine and Science*, 10 (3), art. no. e1430

DOI: 10.1002/vms3.1430

ABSTRACT: Background: Leptospirosis is a zoonotic disease. It is particularly prevalent in tropical countries and has major consequences for human and animal health. In Benin, the disease's epidemiology remains poorly understood, especially in livestock, for which data are lacking. Objectives: To characterise *Leptospira* seroprevalence and locally circulating serogroups in livestock from Cotonou and to estimate the prevalence of *Leptospira* renal carriage in cattle. Methods: We conducted a cross-sectional study in February 2020 during which livestock were sampled at an abattoir and in an impoverished city district. We analysed blood samples from 279 livestock animals (i.e. cattle, sheep, goats and pigs) using the microscopic agglutination test. Additionally, samples of renal tissue from 100 cattle underwent 16s rRNA (*rrs*) real-time PCR analysis. Results: For the 131 cattle, 85 sheep, and 50 goats tested, seroprevalence was 18% (95% confidence interval [CI] [12%, 26%]), 9% (95% CI [4%, 17%]) and 2% (95% CI [0%, 9%]), respectively, and most of the seropositive animals were associated with 1:100 titres. All 13 pigs were seronegative. *Leptospira* DNA was found in the renal tissue of 10% (95% CI [5%, 18%]) of the cattle tested (n = 100). *Leptospira borgpetersenii* was the main species present (n = 7), but *Leptospira interrogans* (n = 2) and *Leptospira kirschneri* (n = 1) were also detected. Various serogroups (Canicola, Grippotyphosa, Sejroe, Icterohaemorrhagiae, Pomona, Pyrogenes, Australis and Autumnalis) were detected using microscopic agglutination test without a clear predominance of any of them. Conclusions: These results suggest that abattoir workers and people living in close contact with livestock in poor urban areas are exposed to the risk of *Leptospira* infection.

LANGUAGE OF ORIGINAL DOCUMENT: English

Balcázar L., Azócar-Aedo L., Barrera V., Meniconi G., Muñoz V., Valencia-Soto C.

Detection of Antibodies for Pathogenic *Leptospira* in Wild Mammals and Birds from Southern Chile—First Record of Seropositivity in a Guiña (*Leopardus guigna*)

(2024) *Animals*, 14 (4), art. no. 601

DOI: 10.3390/ani14040601

ABSTRACT: Leptospirosis is a neglected bacterial zoonotic disease of worldwide distribution that is present in different animal species. This epidemiological study determined the seroprevalence of pathogenic *Leptospira* spp. in animals at a wildlife rehabilitation center in Puerto Montt, southern Chile, by sampling 60 animals belonging to three classes (birds, mammals, and reptiles). Diagnosis was performed using the microscopic agglutination test with a panel of eight serovars and serogroups. The results showed that 15 animals had anti-*Leptospira* antibodies, obtaining a seroprevalence of 25.00%, with *Leptospira borgpetersenii* serogroup Tarassovi presenting reactivity in 13 of the seropositive animals. Among the classes of mammals, chilla foxes (*Lycalopex griseus*) and pudus (*Pudu puda*) were seropositive. A guiña (*Leopardus guigna*) was also seropositive, which was described for the first time in mammals. Among the classes of birds, choroy parrots (*Enicognathus leptorhynchus*), bandurrias (*Theristicus melanopis*), and Magellanic penguins (*Spheniscus magellanicus*) were seropositive. Routine examinations to diagnose leptospirosis, perform epidemiological surveillance, and apply prevention and control measures are necessary, and additional research focusing on the One Health approach to explore the epidemiological role of different wild animal species in the maintenance and transmission of leptospirosis at the local and global levels are recommended. LANGUAGE OF ORIGINAL DOCUMENT: English

Arbour M., Brosseau M., Marchand-Senécal X.

Severe leptospirosis after a rat bite in an urban setting

(2024) CMAJ. Canadian Medical Association Journal, 196 (2), pp. E47 - E48

DOI: 10.1503/cmaj.231218

LANGUAGE OF ORIGINAL DOCUMENT: English

Bonhomme D., Santecchia I., Escoll P., Papadopoulos S., Vernel-Pauillac F., Boneca I.G., Werts C.

Leptospiral lipopolysaccharide dampens inflammation through upregulation of autophagy adaptor p62 and NRF2 signaling in macrophages

(2024) Microbes and Infection, 26 (3), art. no. 105274

DOI: 10.1016/j.micinf.2023.105274

ABSTRACT: *Leptospira interrogans* are pathogenic bacteria responsible for leptospirosis, a worldwide zoonosis. All vertebrates can be infected, and some species like humans are susceptible to the disease whereas rodents such as mice are resistant and become asymptomatic renal carriers. Leptospire are stealth bacteria that are known to escape several immune recognition pathways and resist killing mechanisms. We recently published that leptospire may survive intracellularly in and exit macrophages, avoiding xenophagy, a pathogen-targeting form of autophagy. Interestingly, the latter is one of the antimicrobial mechanisms often hijacked by bacteria to evade the host immune response. In this study we explored whether leptospire subvert the key molecular players of autophagy to facilitate infection. We showed in macrophages that leptospire triggered a specific accumulation of autophagy-adaptor p62 in puncta-like structures, without altering autophagic flux. We demonstrated that *Leptospira*-induced p62 accumulation is a passive mechanism depending on the leptospiral virulence factor LPS signaling via TLR4/TLR2. p62 is a central pleiotropic protein, also mediating cell stress and death, via the translocation of transcription factors. We demonstrated that *Leptospira*-driven accumulation of p62 induced the translocation of transcription factor NRF2, a key player in the anti-oxidant response. However, NRF2 translocation upon *Leptospira* infection did not result as expected in antioxidant response, but dampened the production of inflammatory mediators such as iNOS/NO, TNF and

IL6. Overall, these findings highlight a novel passive bacterial mechanism linked to LPS and p62/NRF2 signaling that decreases inflammation and contributes to the stealthiness of leptospires.

LANGUAGE OF ORIGINAL DOCUMENT: English

Thibeaux R., Genthon P., Govan R., Selmaoui-Folcher N., Tramier C., Kainiu M., Soupé-Gilbert M.-E., Wijesuriya K., Goarant C.

Rainfall-driven resuspension of pathogenic *Leptospira* in a leptospirosis hotspot

(2024) *Science of the Total Environment*, 911, art. no. 168700

DOI: 10.1016/j.scitotenv.2023.168700

ABSTRACT: Leptospirosis is a zoonosis caused by *Leptospira* bacteria present in the urine of mammals. *Leptospira* is able to survive in soils and can be resuspended during rain events. Here, we analyzed the pathogenic *Leptospira* concentration as a function of hydrological variables in a leptospirosis hot spot. A total of 226 samples were collected at the outlet of a 3 km² watershed degraded by ungulate mammals (deer and feral pigs) and rats which are reservoirs for leptospirosis. Water samples collected at the beginning of a rain event following a dry period contained high concentrations of pathogenic *Leptospira*. The concentration was generally correlated with the water level and the suspended matter concentration (SMC) during the main flood event. A secondary peak of pathogenic *Leptospira* was sometimes detected after the main flood and in slightly turbid waters. Lastly, the pathogenic *Leptospira* concentration was extremely high at the end of a wet season. The pathogenic *Leptospira* concentrations could not be explained by a linear combination of hydrological variables (e.g. the rainfall, water level, SMC and soil moisture). However, nonlinear machine learning models of rainfall data only provided a fair fit to the observations and explained 75 % of the variance in the log₁₀-transformed pathogenic *Leptospira* concentration. A comparison of identical machine learning models for the water level, SMC and pathogenic *Leptospira* concentration showed that the residual error in the *Leptospira* concentration was due to not only the small dataset but also the intrinsic characteristics of the signal. Our results support the hypothesis whereby pathogenic *Leptospira* survive at different depths in soils and superficial river sediments (depending on their water saturation) and are transferred to surface water during erosion. These results might help to refine leptospirosis warnings given to the local population. Future research should be focused on larger watersheds in more densely populated areas.

LANGUAGE OF ORIGINAL DOCUMENT: English

Soro S.D., Lattard V., Kodjo A., Benoît E., Chatron N.

Structural investigation of vitamin K epoxide reductase domain-containing protein in *Leptospira* species: a potential target for the development of new leptospirosis treatments as an alternative to antibiotics

(2024) *Journal of Biomolecular Structure and Dynamics*

DOI: 10.1080/07391102.2024.2302925

ABSTRACT: Leptospirosis is a worldwide zoonosis caused by the motile bacterium *Leptospira*. This disease can cause hemorrhagic symptoms, multi-visceral and renal failures, resulting in one million cases and approximately 60,000 deaths each year. The motility of *Leptospira* is highly involved in its virulence and is ensured by the presence of two flagella in the periplasm. Several proteins that require the formation of disulfide bridges are essential for flagellar function. In *Leptospira*, these redox reactions are catalysed by the vitamin K epoxide reductase domain-containing protein (VKORdcp). The aim of the present work was to study the

conservation of VKORdcp among *Leptospira* species and its interactions with putative substrates and inhibitor. Our results evidenced the presence of ten amino acids specific to either pathogenic or saprophytic species. Furthermore, structural studies revealed a higher affinity of the enzyme for vitamin K1 quinone, compared to ubiquinone. Finally, characterisation of the binding of a potential inhibitor revealed the involvement of some VKORdcp amino acids that have not been present in the human enzyme, in particular the polar residue D114. Our study thus paves the way for the future development of *Leptospira* VKORdcp inhibitors, capable of blocking bacterial motility. Such molecules could therefore offer a promising therapeutic alternative to antibiotics, especially in the event of the emergence of antibiotic-resistant strains. Communicated by Ramaswamy H. Sarma.

LANGUAGE OF ORIGINAL DOCUMENT: English

Kuhnert P., Brodard I., Ackermann S., Schierack P., Jores J.

Serological and molecular detection as well as typing of *Leptospira* spp. in foxes, raccoons, and other wild carnivores in North-Eastern Germany, 2021–2022

(2024) *Heliyon*, 10 (1), art. no. e23268

DOI: 10.1016/j.heliyon.2023.e23268

ABSTRACT: Leptospirosis is a worldwide zoonosis caused by pathogenic *Leptospira* spp. While the latter are reported from various mammal hosts such as humans, dogs, or rodents, less is known about their presence in wild carnivores. We therefore investigated the presence of *Leptospira* spp. in foxes, raccoons, badgers, raccoon dogs, and martens in North-Eastern Germany. Kidney, urine, and blood specimens obtained from legally hunted or road-killed animals were tested by real-time PCR and by serogroup specific antibody detection for the presence of *Leptospira* spp. Additionally, kidney and urine specimens were tested by real-time PCR for the presence of *Brucella* spp. and *Francisella tularensis*, with all being negative for these two zoonotic pathogens. *Leptospira* spp. were detected by PCR in 12.6 % (n = 21/166) and serologically in 26.2 % (n = 53/202) of tissue and serum samples, respectively. Antibodies to 15 different serogroups were identified with Javanica (n = 25) and Bataviae (n = 12) being predominant. A high sero-prevalence of 34.0 % and 18.6 % in foxes and raccoons, respectively, and the presence of ST17 associated with human and animal leptospirosis indicates a reservoir and the zoonotic potential of these wild animals.

LANGUAGE OF ORIGINAL DOCUMENT: English

Yang Q.-F., Shu C.-M., Ji Q.-Y.

Diagnosis of pulmonary hemorrhagic leptospirosis complicated by invasive pulmonary aspergillosis complemented by metagenomic next-generation sequencing: a case report

(2024) *Frontiers in Medicine*, 11, art. no. 1365096

DOI: 10.3389/fmed.2024.1365096

ABSTRACT: Background: Leptospirosis is a bacterial zoonosis with variable clinical manifestations. Pulmonary diffuse hemorrhagic leptospirosis often occurs rapidly and, when not promptly diagnosed and treated, it can be life-threatening. *Aspergillus flavus* is an opportunistic fungus that is commonly seen in immunosuppressed patients. Invasive pulmonary aspergillosis also progresses rapidly. This case study describes a patient with severe pneumonia caused by pulmonary hemorrhagic leptospirosis combined with invasive pulmonary aspergillosis. We have found almost no clinical reports to date on these two diseases occurring in the same patient. Case presentation: A 73-year-old male arrived at our hospital complaining of

fever, general malaise, and hemoptysis that had lasted 4 days. The patient was initially diagnosed with severe pneumonia in the emergency department, but he did not respond well to empiric antibiotics. Subsequently, the patient's condition worsened and was transferred to the ICU ward after emergency tracheal intubation and invasive ventilator. In the ICU, antibacterial drugs were adjusted to treat bacteria and fungi extensively. Although the inflammatory indices decreased, the patient still had recurrent fever, and a series of etiological tests were negative. Finally, metagenomic next-generation sequencing (mNGS) of bronchial alveolar lavage fluid detected *Leptospira interrogans* and *Aspergillus flavus*. After targeted treatment with penicillin G and voriconazole, the patient's condition improved rapidly, and he was eventually transferred out of the ICU and recovered. Conclusion: Early recognition and diagnosis of leptospirosis is difficult, especially when a patient is co-infected with other pathogens. The use of mNGS to detect pathogens in bronchial alveolar lavage fluid is conducive to early diagnosis and treatment of the disease, and may significantly improve the prognosis in severe cases.

LANGUAGE OF ORIGINAL DOCUMENT: English

Beauté J., Innocenti F., Aristodimou A., Špačková M., Eves C., Kerbo N., Rimhanen-Finne R., Picardeau M., Faber M., Dougas G., Halldórsdóttir A.M., Jackson S., Leitēna V., Vergison A., Borg M.L., Pijnacker R., Sadkowska-Todys M., Martins J.V., Rusu L.C., Grilc E., Estévez-Reboredo R.M., Niskanen T., Westrell T.

Epidemiology of reported cases of leptospirosis in the EU/EEA, 2010 to 2021

(2024) *Eurosurveillance*, 29 (7)

DOI: 10.2807/1560-7917.ES.2024.29.7.2300266

ABSTRACT: Background: Leptospirosis is a zoonotic disease caused by bacteria of the genus *Leptospira*. Humans are infected by exposure to animal urine or urine-contaminated environments. Although disease incidence is lower in Europe compared with tropical regions, there have been reports of an increase in leptospirosis cases since the 2000s in some European countries. Aim: We aimed to describe the epidemiology of reported cases of leptospirosis in the European Union/ European Economic Area (EU/EEA) during 2010–2021 and to identify potential changes in epidemiological patterns. Methods: We ran a descriptive analysis of leptospirosis cases reported by EU/EEA countries to the European Centre for Disease Prevention and Control with disease during 2010–2021. We also analysed trends at EU/EEA and national level. Results: During 2010–2021, 23 countries reported 12,180 confirmed leptospirosis cases corresponding to a mean annual notification rate of 0.24 cases per 100,000 population. Five countries (France, Germany, the Netherlands, Portugal and Romania) accounted for 79% of all reported cases. The highest notification rate was observed in Slovenia with 0.82 cases per 100,000 population. Overall, the notification rate increased by 5.0% per year from 2010 to 2021 (95% CI: 1.2–8.8%), although trends differed across countries. Conclusion: The notification rate of leptospirosis at EU/EEA level increased during 2010–2021 despite including the first 2 years of the COVID-19 pandemic and associated changes in population behaviours. Studies at (sub) national level would help broaden the understanding of differences at country-level and specificities in terms of exposure to *Leptospira*, as well as biases in diagnosis and reporting.

LANGUAGE OF ORIGINAL DOCUMENT: English

Giraud-Gatineau A., Ayachit G., Nieves C., Dagbo K.C., Bourhy K., Pulido F., Huete S.G., Benaroudj N., Picardeau M., Veyrier F.J.

Inter-species Transcriptomic Analysis Reveals a Constitutive Adaptation Against Oxidative Stress for the Highly Virulent Leptospira Species

(2024) *Molecular Biology and Evolution*, 41 (4), art. no. msae066

DOI: 10.1093/molbev/msae066

ABSTRACT: Transcriptomic analyses across large scales of evolutionary distance have great potential to shed light on regulatory evolution but are complicated by difficulties in establishing orthology and limited availability of accessible software. We introduce here a method and a graphical user interface wrapper, called Annotator-RNator, for performing interspecies transcriptomic analysis and studying intragenus evolution. The pipeline uses third-party software to infer homologous genes in various species and highlight differences in the expression of the core-genes. To illustrate the methodology and demonstrate its usefulness, we focus on the emergence of the highly virulent *Leptospira* subclade known as P1+, which includes the causative agents of leptospirosis. Here, we expand on the genomic study through the comparison of transcriptomes between species from P1+ and their related P1- counterparts (low-virulent pathogens). In doing so, we shed light on differentially expressed pathways and focused on describing a specific example of adaptation based on a differential expression of PerRA-controlled genes. We showed that P1+ species exhibit higher expression of the *katE* gene, a well-known virulence determinant in pathogenic *Leptospira* species correlated with greater tolerance to peroxide. Switching PerRA alleles between P1+ and P1- species demonstrated that the lower repression of *katE* and greater tolerance to peroxide in P1+ species was solely controlled by PerRA and partly caused by a PerRA amino-acid permutation. Overall, these results demonstrate the strategic fit of the methodology and its ability to decipher adaptive transcriptomic changes, not observable by comparative genome analysis, that may have been implicated in the emergence of these pathogens.

LANGUAGE OF ORIGINAL DOCUMENT: English

Lv T., Xie X., Diao L., Jiang S., Ding Y., Yuan X., Gong L., Chen X., Zhang W., Cao Y.

Leptospira-specific immunoglobulin Y (IgY) is protective in infected hamsters

(2024) *Vaccine*

DOI: 10.1016/j.vaccine.2024.04.010

ABSTRACT: Leptospirosis, a globally significant zoonotic disease caused by pathogenic *Leptospira*, continues to threaten the health and public safety of both humans and animals. Current clinical treatment of leptospirosis mainly relies on antibiotics but their efficacy in severe cases is controversial. Passive immunization has a protective effect in the treatment of infectious diseases. In addition, chicken egg yolk antibody (IgY) has gained increasing attention as a safe passive immunization agent. This study aimed to investigate whether hens produce specific IgY after immunization with inactivated *Leptospira* and the protective effect of specific IgY against leptospirosis. First, it was demonstrated that specific IgY could be extracted from the eggs of hens vaccinated with inactivated *Leptospira* and that specific IgY can specifically recognize and bind homotypic *Leptospira* with a high titre, as shown by MAT and ELISA. Next, we tested the therapeutic effects of IgY in early and late leptospirosis using a hamster model. The results showed that early specific IgY treatment increased the survival rate of hamsters to 100%, alleviated pathological damage to the liver, kidney, and lung, reduced leptospiral burden, and restored haematological indices as well as functional indicators of the liver and kidney. The therapeutic effect of early specific IgY was comparable to that of doxycycline. Late IgY

treatment also enhanced the survival rate of hamsters and improved the symptoms of leptospirosis similar to early IgY treatment. However, the therapeutic effect of late IgY treatment was better when combined with doxycycline. Furthermore, no *Leptospira* colonization was observed in the kidneys, livers, or lungs of the surviving hamsters treated with specific IgY. Mechanistically, IgY was found to inhibit the growth and adhesion to cells of *Leptospira*. In conclusion, passive immunotherapy with specific IgY can be considered an effective treatment for leptospirosis, and may replace antibiotics regarding its therapeutic effects.

LANGUAGE OF ORIGINAL DOCUMENT: English

Petakh P., Kamyshnyi O.

AMR mechanisms in *L. interrogans* serovars: a comprehensive study

(2024) *Frontiers in Cellular and Infection Microbiology*, 14, art. no. 1384427

DOI: 10.3389/fcimb.2024.1384427

ABSTRACT: Antimicrobial resistance (AMR) is one of the global health challenges of the 21st century. Data regarding AMR mechanisms in *Leptospira interrogans*, the causative agents of leptospirosis, have been relatively limited. Therefore, our study aimed to identify resistance genes and explore potential resistance mechanisms specific to particular serovars. We conducted a comprehensive analysis of 98 *Leptospira* strains, representing 10 common serovars, using whole-genome sequencing (WGS) FASTA files. Employing the PATRIC tool from the Bacterial and Viral Bioinformatics Resource Center (BV-BRC), we scrutinized the genomes for AMR genes. Our investigation revealed 32 genes associated with AMR, with 20 key genes consistently prevalent across most strains. Notably, we identified unique efflux pump systems in serovar Pomona, indicating distinctive resistance mechanisms in this serovar. In summary, our findings shed light on the genetic landscape of AMR in *Leptospira*, uncovering both common and serovar-specific resistance elements. The presence of unique efflux pump systems in serovar Pomona introduces a novel dimension to our understanding of resistance mechanisms. These insights underscore the importance of tailored intervention strategies and collaborative efforts between human and veterinary healthcare professionals, as well as environmental scientists, to address the complex dynamics of leptospirosis and its implications for antibiotic resistance.

LANGUAGE OF ORIGINAL DOCUMENT: English

Allyn J., Mialhe A.-F., Delmas B., Marti L., Allou N., Jabot J., Reignier J.

Severe leptospirosis in tropical and non-tropical areas: A comparison of two french, multicentre, retrospective cohorts

(2024) *PLoS neglected tropical diseases*, 18 (4), pp. e0012084

DOI: 10.1371/journal.pntd.0012084

ABSTRACT: BACKGROUND: Leptospirosis is an anthroozoonosis that occurs worldwide but is more common in tropical regions. Severe forms may require intensive care unit (ICU) admission. Whether the clinical patterns and outcomes differ between tropical and non-tropical regions with similar healthcare systems is unclear. Our objective here was to address this issue by comparing two cohorts of ICU patients with leptospirosis managed in mainland France and in the overseas French department of Réunion, respectively. METHODOLOGY/PRINCIPAL FINDINGS: We compared two retrospective cohorts of patients admitted to intensive care for severe leptospirosis, one from Reunion Island in the Indian Ocean (tropical climate) and the other from metropolitan France (temperate climate). Chi-square and Student's t tests were used for

comparisons. After grouping the two cohorts, we also performed multiple correspondence analysis and hierarchical clustering to search for distinct clinical phenotypes. The Réunion and Metropolitan France cohorts comprised 128 and 160 patients respectively. Compared with the Réunion cohort, the metropolitan cohort had a higher mean age (42.5 ± 14.1 vs. 51.4 ± 16.5 years, $p < 0.001$). Severity scores, length of stay and mortality did not differ between the two cohorts. Three phenotypes were identified: hepato-renal leptospirosis (54.5%) characterized by significant hepatic, renal and coagulation failure, with a mortality of 8.3%; moderately severe leptospirosis (38.5%) with less severe organ failure and the lowest mortality rate (1.8%); and very severe leptospirosis (7%) manifested by neurological, respiratory and cardiovascular failure, with a mortality of 30%. CONCLUSIONS/SIGNIFICANCE: The outcomes of severe leptospirosis requiring ICU admission did not differ between tropical and temperate regions with similar healthcare access, practices, and resources, despite some differences in patient characteristics. The identification of three different clinical phenotypes may assist in the early diagnosis and management of severe leptospirosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Puga R.R., González G.S.G.

Evaluation of the Medical Quality of Care for Hospitalized Patients with Clinical Suspicion of Leptospirosis [Evaluación de la calidad médica asistencial a pacientes hospitalizados con sospecha clínica de leptospirosis]

(2023) Revista Cubana de Salud Publica, 49 (3), art. no. e15887

ABSTRACT: Introduction: The evaluation of the quality of care in the health field has generated important results allowing to improve the services offered. Objective: To evaluate the quality of care for patients with clinical suspicion of leptospirosis. Methods: An investigation was carried out in health services through an observational and analytical design including 166 patients who were admitted with clinical suspicion of leptospirosis at Manuel Ascunce Domenech and Amalia Simoni Provincial Clinical Surgical Hospitals in Camagüey city, during January-December 2022. The studied variables were age groups, sex, skin color, place of origin, structure, process and results indicators. Results: Patients aged between 33-44 years (25.9%), male (84.3%), and from Camagüey municipality (63.9%) predominated. 56.2% were non vaccinated workers under exposure (95.9%). The overall evaluation of the structure indicator was 77.8%, while the process and results obtained 30.4 and 23.1%, respectively. Conclusions: The evaluation of the medical care provided, in terms of process and outcome criteria, was inadequate; in contrast, the structure indicator was adequate.

LANGUAGE OF ORIGINAL DOCUMENT: Spanish

Nguyen-Tran H., Erdem G., Laufer P.M., Patterson L., Ahmed A.A., Bower W.A., Galloway R., Saporta-Keating S.

Use of Advanced Diagnostics for Timely Identification of Travel-associated *Leptospira santarosai* Infection in Four Adolescents Through Plasma Microbial Cell-free DNA Sequencing with the Karius Test

(2024) Pediatric Infectious Disease Journal, 43 (5), pp. E169 - E174

DOI: 10.1097/INF.0000000000004255

ABSTRACT: Background: Leptospirosis is an important zoonotic infection worldwide. Diagnosis of leptospirosis is challenging given its nonspecific clinical symptoms that overlap with other acute febrile illnesses and limitations with conventional diagnostic testing. Alternative advanced diagnostics, such as

microbial cell-free DNA (mcfDNA), are increasingly being used to aid in the diagnosis of infections and can be applied to pathogens with public health importance such as *Leptospira*, a nationally notifiable disease. Methods: The Karius Test uses plasma mcfDNA sequencing to detect and quantify DNA-based pathogens. This test offered through the Karius lab detected 4 cases of *Leptospira santarosai* during a 5-month period across the United States in 2021 and were clinically reviewed. Results: In our case series, 4 adolescents with recent travel to Central America (Costa Rica, n = 3 and Belize, n = 1) from April to August 2021 were diagnosed with leptospirosis. While a large workup was performed in all cases, mcfDNA testing was the first test to detect *L. santarosai* as the microbiological diagnosis in all cases. Conclusions: Results of the Karius Test enabled rapid, noninvasive diagnosis of leptospirosis allowing for targeted therapy. Use of mcfDNA can be utilized for diagnosis of pathogens where conventional testing is challenging or limited. This in turn can enable quick diagnosis for targeted treatment and potentially aid in supporting case definitions of reportable diseases of public health concern.

LANGUAGE OF ORIGINAL DOCUMENT: English