Detection of *Leptospira* spp. using polymerase chain reaction technique from kidney of *Rattus norvegicus* from Grenada, West Indies

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Abstract

Aim: This study aimed to find out the prevalence of active infection of *Leptospira* spp. in *Rattus norvegicus* from Grenada, West Indies, through polymerase chain reaction (PCR).

Materials and Methods: One hundred and forty-nine rats were trapped, anesthetized and their kidneys collected aseptically. DNA was extracted from the kidney tissue of each rat. PCR was performed targeting *LipL32* gene. Eighteen PCR-positive amplicons for *LipL32* gene segment were purified and sent for direct sequencing to the sequencing facility of MCLAB (South San Francisco, USA). Results of sequencing were read and interpreted. The prevalence of *Leptospira* spp. in relation to sex and age was also recorded.

Results: All amplified sequences were compared to the sequences present in GenBank using basic local alignment search tool (BLAST) from the online website National Center for Biotechnology Information, the results revealed that six samples had similarity to *Leptospira interrogans strain* 1399/2016 and eight samples had similarity with *Leptospira borgpetersenii* serovar Hardjo-bovis strain L49. Of 149 kidney samples, only 14 were positive for *Leptospira* spp. by PCR giving an incidence of 9.3%. There was no significant difference found in relation to sex and age.

Conclusion: This is the first report confirming active infection of *Leptospira* spp. in *Rattus norvegicus* in Grenada using PCR. The presence of active infection in rats can be considered as high risk for humans. Further research to understand the epidemiology of leptospirosis in Grenada is suggested.

Keywords: Rattus norvegicus, Grenada, kidney, Leptospira spp., polymerase chain reaction.

Introduction

Leptospirosis, a reemerging zoonotic disease of animals and humans, is caused by *Leptospira* spp. of spirochete bacteria. Transmission of *Leptospira* spp. to susceptible hosts occurs by ingestion of water and food contaminated with urine and tissues of infected animals. Another mode of transmission is through cut or abrasion in the skin. After ingestion or skin cut, bacteria circulate in the body and finally localize in proximal convoluted tubules of the kidney where these are protected from antibiotics and other blood defense mechanisms and are excreted chronically in the urine [1].

Of several diagnostic methods, the two commonly used serological tests are the microscopic agglutination test (MAT) and the enzyme-linked immunosorbent assay (ELISA). MAT is considered as the "gold standard" test for leptospirosis, which detects both IgG and IgM. MAT is highly specific and

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generally used in reference laboratories as it requires propagation of live Leptospira strains. MAT can detect infecting serovars, but it has a low sensitivity [2]. The ELISA detects IgG and IgM antibodies separately and is highly sensitive [2]. Other serological tests including MAT and ELISA are insensitive during the early phase of the disease. The need for rapid diagnosis in the early phase of infection led to the development of numerous polymerase chain reaction (PCR) assays. PCR is based on the molecular detection of amplified bacterial genes fragments present in host species. Examples of some of the target genes used for Leptospira PCR are gvrB and rrs (16S rRNA gene) or genes present in pathogenic Leptospira spp. as LipL32, Ifb1, Lig A, and LigB2 [3-5]. Real-time quantitative PCR (qPCR) has replaced conventional PCR, as in later diagnostic value was unclear. Several qPCR methods targeting LipL32 and rss gene for simultaneous detection of pathogenic and non-pathogenic leptospires have been recently developed [4,5].

Rattus norvegicus is considered a major reservoir of leptospires and a source of *Leptospira* infection to humans and animals. In the Caribbean, infection of *Leptospira* spp. has been documented in humans and animals [6]. The first report of *Leptospira* spp. in Grenada was published in 1985 [7], in which MAT-based serological analysis of samples from

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cattle, pigs, sheep, goats, horses, donkeys, and chickens had Leptospira icterohaemorrhagiae as the main serovar along with others. There are few published reports on *Leptospira* spp. exposure of *R*. norvegicus in the Caribbean. Peters et al. [8] while reviewing the serovars of *Leptospira* spp. in the Caribbean reported L. icterohaemorrhagiae serovar Copenhageni and L. icterohaemorrhagiae serovar Icterohaemorrhagiae in rats in Grenada. They also reported serovar Icterohaemorrhagiae in rats in other Caribbean nations (Barbados, Guadeloupe, Jamaica, Trinidad, and Tobago). In Grenada, for the first time, Keenan et al. [9] reported 27% seroprevalence of antibodies to *Leptospira* spp. in *R. norvegicus*, using MAT and ELISA techniques. They found Leptospira icterohaemorrhagiae serogroup with greatest frequency. In another recent survey conducted in R. norvegicus, Sharma et al. [10] found higher seroprevalence (45.5%) in Grenada. Since they used ELISA, serogroups were not identified. Until now, no molecular techniques have been used to identify Leptospira spp. serovars in R. norvegicus in Grenada.

This study aimed to identify the prevalence of pathogenic serovars of *Leptospira* spp. in kidney of *R. norvegicus* from Grenada using PCR technique.

Materials and Methods

Ethical approval

The project (Detection of Zoonotic Pathogens in *Rattus norvegicus* in Grenada) was approved by the Institutional Animal Care and Use Committee (IACUC #16009-R) of St. George's University, Grenada.

Study area

Grenada is the southernmost country in the Caribbean Sea with an area of 348.5 km². The country with low hills, small trees, shrubs, and tropical climate is most suitable for rats. The country is comprised of six parishes: St. Patrick, St. Mark, St. Andrew, St. John, St. George, and St. David. St. David and St. George parishes, which have a higher human population compared to the other four parishes were selected for the study.

Collection of rats

One hundred and forty-nine rats were collected live from May 1 to July 14, 2017, using traps (45 cm 1×15 cm $w \times 15$ cm h) with cheese and various local fruits as bait. Attempts were made to trap the rats from and near the residential buildings. Traps were placed 2 days per week in the evening and visited the morning of the next day. Traps with rats were covered with black cloth and transported to the necropsy laboratory of St. George's University, School of Veterinary Medicine. Rats were anesthetized using 1–2% isoflurane in oxygen through portable vet anesthesia machine isoflurane vaporizer VET CE, manufacturer DRE (Avante Health Solution Company, USA).

Collection of samples and testing

The anesthetized rats were examined for their physical health and weighed. Sex and weight were

recorded. Rats below 100 g were grouped as young and those over 100 g as adult, following the methodology used by Panti-May *et al.* [11]. Blood was collected from the heart through the thoracic wall and rats were exsanguinated this way. The abdominal cavity of each rat was opened using a new surgical blade and forceps. Kidneys were examined for any gross abnormalities and recorded. Kidneys were aseptically removed and stored at -80° C in sterile tubes until tested by PCR.

DNA extraction

One hundred and forty-nine kidney samples from trapped R. norvegicus were processed for DNA extraction. Approximately 25 mg of kidney tissue sample was pulverized using a separate sterile disposable scalpel blade for each rat. Four hundred microliters of phosphate buffer saline were then added to the macerated kidney samples in a microcentrifuge tube and further homogenized using 10-12 silica beads and beating in a bead beater machine for 30 s at pulse. Forty microliters of proteinase-K and 360 µL of tissue lysis buffer (ATL) were added to the samples and incubated at 56°C for overnight digestion. The samples were then processed using the DNeasy blood and tissue kit (QIAGEN, Valencia, CA, USA) according to manufacturer's instruction. The final elution for each sample was 200 µL in buffer AE provided in the DNeasy blood and tissue kit. Each of the DNA sample was quantified spectrophotometrically using Thermo Scientific[™] NanoDrop 2000 (Waltham, MA USA). The extracted DNA was stored at -20°C until PCR was performed.

Polymerase chain reaction

A single-step PCR using the primer pair LipL32-45F (5'-AAG CAT TAC CGC TTG TGG TG-3') and LipL32-286R (5'-GAA CTC CCA TTT CAG CGA TT-3') following Stoddard et al. [12] was performed to amplify a 242 bp fragment of an outer membrane lipoprotein present in the pathogenic Leptospira spp. [12-14]. Nuclease-free water was used as a negative control and genomic DNA from L. interrogans serovar Copenhageni (ATCC® BAA-1198D-5[™]) served as a positive control. Each PCR amplification was carried out using a 25 µl reaction mixture containing a final concentration of $1 \times PCR$ reaction buffer, 1.25 U of Taq DNA polymerase, 1.5 mM MgCl₂, 0.2 mM each of dNTP mixture, with 0.5 μ M of each primer, and 3 μ L (~5 ng-~10 ng) of DNA template. The cycling conditions were as follows: Initial denaturation at 94°C for 5 min followed by 40 cycles of 1 min denaturation at 94°C, 1 min of annealing at 63°C, and 45 s of extension at 72°C, and a final 5 min extension at 72°C after the last cycle.

Twenty microliters of the PCR products were subjected to electrophoresis with 1.5% agarose gel, stained with ethidium bromide, and photographed under gel documentation system (LabNet International Inc.., Edison, NJ, USA). Amplicons were purified using QIAquick Gel Extract Kit (Qiagen, Valencia, CA, USA) following manufacturer's instructions and sent for sequencing to the sequencing facility provided by MCLAB (South San Francisco, CA, USA).

Statistical analysis

Data were analyzed using a Chi-square analysis and stratified by gender, age, and parish of rats in Microsoft Excel 2017 software (Redmond, Washington, U.S.A.). Statistical significance was set at p=0.05.

Results

Kidney samples of rats under study did not show any gross abnormality. Genomic DNA from 149 rat kidney samples was used to perform PCR to amplify DNA fragments LipL32 gene. An approximately 242 bp PCR product for LipL32 gene was amplified from the kidney samples of 21 rats (14%). Eighteen PCR-positive amplicons for LipL32 gene were purified and sent off for sequencing. Partial sequences for LipL32 gene from 14 samples were submitted to GenBank[®] (Table-1). The LipL32 gene sequences showed 90-100% homology to one another. All the sequences were compared to the sequences present in GenBank[®] using BLAST from the online website, the National Center for Biotechnology Information. The results from LipL32 gene sequences revealed that six samples had highest similarity (between 96.53% and 100%) to L. interrogans strain 1399/2016 (accession number MF663255.1) and eight samples had highest similarity (between 99.01% and 100%) with *L. borgpetersenii* serovar Hardjo-bovis strain L49 (accession number CP033440.1) as recorded in Table-1. The result of PCR in relation to parish, age, and sex of rats is presented in Table-2. The relation between *L.interrogans* serovar Copenhageni and *L. borgpetersenii* serovar Hardjo-bovis strain was not significant (p=0.71). There was no statistical significance in the prevalence of *Leptospira* spp. between St. David and St. George parish (p=0.169). The prevalence of infection in relation to age was not significant (p=0.26).

Discussion

The use of PCR over serological diagnostic tests for leptospirosis is being recommended, due to its ability to distinguish between pathogenic and non-pathogenic *Leptospira* serovars [15]. PCR is also of value in the early phase of the disease where serological tests are not reliable. The previous researchers have used number of gene sequences in their research for conventional PCR and qPCR such as 23S rRNA [15,16]; *GyrB* [17]; *flab* [18]; *16S rRNA* [19]; and *LigA/B* [15]. Xue *et al.* [20] reported the presence of these genes in pathogenic *Leptospira* spp. In the present study, *LipL32* gene was used, which has been used in PCR by the previous researchers [21-24].

Of 149 kidney samples tested from *R. norvegicus*, 14 (9.3%) were positive by PCR for *LipL32* gene.

Sample ID	Accession No.	Sequence length (bp)	Similarity to <i>L. interrogans</i> strain 1399/2016; Accession # MF663255.1 (%)	Similarity to <i>L. borgpetersenii</i> serovar Hardjo-bovis strain L49; Accession # CP033440.1 (%)
RK27	MK895960	202	99.01	
RK69	MK895961	202		99.01
RK147	MK895962	202	96.53	
RK163	MK895963	202		100.00
RK1	MK895964	202	100.00	
RK12	MK895965	202	100.00	
RK85	MK895966	202		100.00
RK139	MK895967	202		100.00
RK158	MK895968	202		100.00
RK162	MK895969	202		100.00
RK165	MK895970	202	100.00	
RK166	MK895971	202	97.03	
RK167	MK895972	202		100.00
RK170	MK895973	202		100.00

Table-1: New sequences submitted to the GenBank® database for LipL32 gene sequence.

L. interrogans=Leptospira interrogans, L. borgpetersenii=Leptospira borgpetersenii

Table-2. Distribution	of Lontochira	corovare targeting	- Linl 32 dono in	R. norvegicus in Grenad	2
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Serovars	Parish		Total	Sex		Age	
	St. George	St. David	positive	м	F	Adults	Juvenile
<i>L. interrogans</i> Copenhageni/ Icterohaemorrhagiae	1	5	6/14 (42.8%)	4	3	4	2
<i>L. interrogans/L. borgpetersenii</i> Hardjo-bovis strain	3	5	8/14 (57.2%)	3	4	5	3
Total	4/149 (2.6%)	10/149 (6%)	. ,	7/14 (50.0%)	7/14 (50.0)	9/14 (64.2%)	5/14 (35.8%)

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The results from LipL32 gene sequence revealed 6 samples (42.8%) in similarity with L. interrogans serovar Copenhageni and 8 samples (57.2%) in similarity with L. borgpetersenii serovar Hardjo-bovis strain L42. Our results of serovar distribution in R. norvegicus are similar to Cosson et al. [23], who reported 46% L. borgpetersenii and 36% L. interrogans in rodents in Southeast Asia. In Kaula Lumpur, the ratio of serovars reported by Benacer et al. [25] coincides with our results. They also reported higher prevalence of L. borgpetersenii serovar Javanica, (85%) than 35% L. interrogans serovar Bataviae. Both these Leptospira spp. are known to be pathogenic. The prevalence of Leptospira spp. (7.0%) observed by Cosson et al. [23] in PCR was similar to our results. This indicates a wide prevalence of L. interrogans and L. borgpetersenii species in rodents. Loan et al. [24] used LipL32 gene in RT-PCR and reported 5.8% prevalence of Leptospira spp. in rats in Vietnam, which is slightly lower than our findings. Previous studies found different levels of infection in R. norvegicus using various gene-targets in PCR, for example 11.6% in Cambodia [26]; and 6.7% in Malaysia [25]. However, in Southeast China the infection rate was found to be between 20–40%, depending on the RT-PCR methods used [27]. The variation in the prevalence of Leptospira spp. infection in different locations depends on environmental conditions such as climate and land terrain [26,28].

In the present study, males and females were found to be equally infected. Our findings agree with previous studies [29-31]. However, others [28,32] found that females were more affected than males. A few researchers [25,33] reported higher infection in males than females. An interesting finding on sex has been reported by Adesiyun et al. [34] in humans in the Caribbean nations that infection is higher in males. Our observation on Leptospira spp. infection in *R. norvegicus* in relation to age was not significant (p=0.26) although figures for adult infection were apparently seen higher; adult rats (64.2%) compared to Juvenile (35.8%). In accordance with our results, other researchers found infection more in adults [24,25,30]. Benacer et al. [25] advocated aggressive habits of the adults, to be the reason for higher infection. With aggressive habit, adults are more prone to infection with Leptospira spp. Krøjgaard et al. [30] thought that higher infection in adults was a result of prolonged exposure to Leptospira spp. with age. Suepaul et al. [29] indicated that juveniles were at a higher risk compared to adults. No explanation for this result was given by the authors.

In the Caribbean nations, *Leptospira* spp. antibodies were detected in livestock, rodents, pets, wild species, and humans through ELISA, MAT, and other serological methods. The most common serovars found in animals, in Grenada, were *L. autumnalis*, *L. icterohaemorrhagiae*, and related serogroups [8,9]. In other Caribbean nations, most prevalent serovar in rats were *L. icterohaemorrhagiae*/ Copenhageni (in Barbados and Trinidad), *L. icterohaemorrhagiae*/Icterohaemorrhagiae (in Guadeloupe), and *L. icterohaemorrhagiae*/Copenhageni and *L. icterohaemorrhagiae*/Icterohaemorrhagiae (in Jamaica) [8]. Serovars were not identified that human cases were diagnosed in 14 Caribbean countries including Grenada. The dominant serovar in humans across the Caribbean was *L. interrogans* serovar Copenhageni [34,35]. Based on the prevalence of *Leptospira* spp. serovars in animals and rats, in the Caribbean, transmission of *Leptospira* spp. to humans from animals and rats is indicated.

Conclusion

This is the first report of the prevalence of *Leptospira* serovars in Grenada based on PCR method. Our findings confirm active infection (9.3%) with *Leptospira* spp. in *R. norvegicus* in Grenada. Although the prevalence of active infection with *Leptospira* spp. in kidney of *R. norvegicus* from Grenada was not very high, *R. norvegicus* as reservoir should be considered as a high-risk factor for humans. Control campaign to reduce the population of rats in the country should be implemented. Further research to identify *Leptospira* spp. serovars in humans, rodents, animals, and pets should be taken up to prove the epidemiology of the disease in Grenada.

Authors' Contributions

BS: Developed the concept, conducted PCR and interpreted the sequencing results, and assisted in manuscript writing. KT and NR: Trapping of the rats, anesthesia, collection of kidneys and helping in PCR. RS: Interpretation of results, and writing of the manuscript. All authors read and approved the final manuscript.

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Competing Interests

The authors declare that they have no competing interests.

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