seguido de análise das membranas pelo programa ImageJ. A expressão do gene OmpL36 foi avaliada durante a formação do biofilme de *L. biflexa*, acessando os dados do transcriptoma (BioProject PRJNA288909). **Resultados:** Por *western blot*, OmpL36 teve maior expressão em biofilme quando comparado ao fenótipo planctônico. A partir da análise do transcriptoma e corroborando este resultado, foi constatado que o gene OmpL36 foi regulado positivamente no fenótipo biofilme em comparação com o planctônico no biofilme tardio de 120h (FDR 7, 00E-3; p < 0,05). No biofilme maduro de 48h, houve regulação positiva, porém essa não foi estatisticamente significativa (FDR 1,60E-2; p < 0,05). **Conclusões:** Os resultados obtidos demonstram que OmpL36 é mais expressa em biofilme que no estado planctônico, o que sugere que essa proteína desempenha um papel em biofilmes de *Leptospira*. **CEUA:** Não aplicável. **Financiamento:** Projeto universal CNPq 425526/2016-0, Fapesb, Capes.

17. EXPRESSION OF THREE VIRULENCE-RELATED GENES IN LEPTOSPIRAL STRAINS OF SEROGROUP SEJROE AFTER WEEKLY SUBCULTURES

Expressão de três genes relacionados à virulência em estirpes leptospirais do sorogrupo Sejroe após subculturas semanais

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Introduction: Bovine leptospirosis is characterized mainly by reproductive problems associated with infections by strains of serogroup Sejroe. Pathogenic strains belonging to same serogroup could present differences in pathogenicity, suggesting existence of unknown molecular mechanisms involved in virulence. Furthermore, it is known that subculture of strains can lead to attenuation of virulence by changes in protein coding genes. **Objective:** Compare the occurrence and expression of three virulence-related genes in leptospiral strains of serogroup Sejroe that were virulent or not in hamster model (*Mesocricetus auratus*) after recovery of strain post infection (first moment) and after twenty weekly subcultures in EMJH media (second moment). **Methods:** Four strains of serogroup Sejroe belonging to *Leptospira santarosai* specie was studied: three of them were virulent. DNA was obtained using Wizard SV Genomic DNA Purification System® (Promega) and RNA using Trizol Reagent (Invitrogen). PCR was performed with GoTaq® DNA Polymerase (Promega) and RT-PCR using OneStep RT-PCR Kit (QIAGEN): for two genes for surface protein (*lig*A and *lip*L32) and one for motile-associated flagella (*fli*Y). **Results:** All virulent and non-virulent strains studied showed the target genes in DNA. Regarding expression of the virulence-related genes in RNA, the *lip*L32 and *lig*A targets obtained positive results in all strains tested in the two moments of this study. For *fli*Y, all strains tested did not express at the first moment. While in the second moment, two virulent strains were positive for the expression of this gene. **Conclusion:** The *lip*L32 and *lig*A targets studied may not be related to differences in virulence in strains of serogroup Sejroe. The result of the *fli*Y gene in strains of the serogroup Sejroe was unexpected and could be related to differences in infection by strains of this serogroup. It is necessary to compare strains of serogroup Sejroe with to other serogroups. **CEUA:** 611/2015. **Funding:** Capes (Finance code 001), Faperj.

18. GENOMIC FEATURES OF *LEPTOSPIRA INTERROGANS* SEROVAR HARDJO STR. NORMA: POTENTIAL RECOMBINATION SITE GENOME DEPICTED BY COMPARATIVE GENOMICS

Características genômicas da *Leptospira interrogans* sorovar Hardjo str. Norma: genoma do local de recombinação potencial representado pela genômica comparativa

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Introduction: Leptospirosis is caused by pathogenic spirochetes of the genus *Leptospira* spp. with

worldwide distribution. In livestock, *Leptospira interrogans* serogroup Sejroe serovar Hardjo remain the major cause of reproductive diseases. The publication of whole genome sequence of the first Brazilian clinical isolate classified as *Leptospira interrogans* serogroup Sejroe serovar Hardjo str. Norma enable now to evaluate genomic features and evolution of this serovar and serogroup. **Objective:** To compare the Brazilian isolate within reference strains classified in *L.interrogans* and *L. borgpetersenii* species and isolated in distinct geographic regions in world. **Methods:** It was selected a total of 10 *Leptospira* spp. strains including reference genomes from distinct serovars classified in *L. interrogans* and *L. borgpetersenii* available in public databases (NCBI). For synteny analysis it was selected reference leptospira strains and historically correlated with whole genome sequences available. It was applied MAUVE and Patric softwares associated with Blast P, Blast N, Clusta W associated with Interpro and Gene ontology analysis. **Results:** The obtained results confirmed the occurrence of potential genomic recombination in *L. interrogans* serovar Hardjo str. Norma encompass 40Kb located upstream of rfb locus. Most of the genes in this region are associated to sugar enzymes associated with carbohydrates and lipids biosynthesis and metabolism. In comparative analysis, the present results also identified identical genomic structure among *L. interrogans* and *L. borgpetersenii* serovars Hardjo, including high amino acid identities and sequence coverages. Furthermore, identification of IS3-family protein in *L. interrogans* serovar Hardjo, str. Norma associated with rfb locus position suggests a mechanism of recombination associated with the acquision of this new region. **Conclusion:** The results suggest a new genetic recombination site in *L. interrogans* serovar Hardjo str. Norma, which may contribute to depict taxonomy classification of *Leptospira* spp. especially to serogroup and serovar classification. **Funding:** CNPq, Fapemig.

19. HIGH FREQUENCY OF GENITAL CARRIERS OF LEPTOSPIRA SP. IN SHEEP SLAUGHTERED IN THE SEMI-ARID REGION OF NORTHEASTERN BRAZIL

Alta frequência de portadores genitais de *Leptospira* sp. em ovelhas abatidas na região semiárida do nordeste brasileiro

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Introduction: Although some leptospirosis investigations performed in sheep have indicated their genital tract colonization, further studies are necessary to clarify the whole role of genital carriers in this species. **Objective:** evaluate the colonization of pathogenic leptospires in the genital and urinary tract of slaughtered sheep. **Methods:** Fifty-seven adult, female woolless sheep destined for slaughter were used. Kidney (n = 57), bladder (n = 57), ovary (n = 34), uterine tube (n = 44), and uterus (n = 33) samples were collected for molecular detection of Leptospira sp. DNA, and blood samples (n = 57) for serological testing. The molecular tests were performed by polymerase chain reaction (PCR), and the serological ones by microscopic agglutination test (MAT). Samples with amplifying DNA were subjected to genetic sequencing. **Results:** Leptospiral DNA was found in the tissues of 44 (77.2%) sheep, whereas only nine animals were positive on both PCR and MAT, there was slight agreement between PCR and MAT techniques ($k = 0.0268$; $p = 0.684$). In 61 (54.9%) genital tract and in five (4.4%) urinary tract samples, the leptospiral DNA was detected, with significant difference ($p < 0.001$). The genes of one sample from the uterine tube and another from the bladder were sequenced and demonstrated 99% similarity