

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 (*ligA* and *lipL32*) and one for motile-associated flagella (*fliY*). **Results:** All virulent and non-virulent strains studied showed the target genes in DNA. Regarding expression of the virulence-related genes in RNA, the *lipL32* and *ligA* targets obtained positive results in all strains tested in the two moments of this study. For *fliY*, 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 *lipL32* and *ligA* targets studied may not be related to differences in virulence in strains of serogroup Sejroe. The result of the *fliY* 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