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Data Article

Transcriptome datasets of macrophages infected with different strains of *Leptospira* spp

Erivelto Corrêa de Araújo Junior [a], Leandro Encarnação Garcia [a], Larissa Martins Melo [b], Jaqueline Poleto Bragato [b], Valéria Marçal Félix de Lima [b], Juliana Regina Peiró [b], Flavia Lombardi Lopes [a,*], Márcia Marinho [a]

[a] *Department of Support, Production and Animal Health, São Paulo State University (Unesp), School of Veterinary Medicine, Araçatuba, SP, Brazil*
[b] *Department of Clinic, Surgery and Animal Reproduction, São Paulo State University (Unesp), School of Veterinary Medicine, Araçatuba, SP, Brazil*

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ABSTRACT

The datasets reported herein provide information about microarray experiment of macrophage cell line J774A.1 infected with three different strains of *Leptospira spp*. Transcriptomic profiles were generated using Affymetrix® Mouse Gene 2.1 ST Array Strip. Data was normalized and statically process, p-value < 0.01, FDR < 0.05 and log2 fold change ($\pm$ 2). The microarray raw data are available in Gene Expression Omnibus (GEO) under accession number GSE105141.

Specifications Table

Subject area	Biology
More specific subject area	Gene expression
Type of data	Table and Figures

* Corresponding author.
E-mail address: flavialopes@fmva.unesp.br (F.L. Lopes).

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How data was acquired	Microarray Affymetrix® Mouse Gene 2.1 ST Array Strip
Data format	Raw (CEL.)
Experimental factors	cell lines non-infected x cell lines infected with *Leptospira* spp.
Experimental features	Total RNA, with RIN 10, was extracted from whole macrophage cell line infected and control. Each sample contains three biological replicates and each replicates consists of three culture well.
Data source location	Department of Support, Production and Animal Health, São Paulo State University, School of Veterinary Medicine, Araçatuba, SP, Brazil
Data accessibility	Microarray data are available from Gene Expression Omnibus database with GEO accession number GSE105141

Value of the data

- This is the first comparison of transcriptomic profile of murine macrophages infected with different *Leptospira* spp varying in species and virulence within strain.
- Data reported will help in understanding the pathogenicity and immune response to leptospirosis which is still poorly understood.
- This data can reveal new insight on modulation and function of genes in immune cells following infection by *Leptospira*, with particular focus on differential host immune response to varying bacterial virulence.

1. Data

Total RNA was extracted from murine macrophage cell line J774A.1 infected with virulent, attenuated or saprophyte strains of *Leptospira*, as well as control non-infected cells, 6 h post *in vitro* infection. Affymetrix microarray was performed to obtain transcriptomic profiles of the infected and control groups. Raw data was deposited at NCBI GEO DataSets (GSE105141).

2. Experimental design, materials and methods

2.1. Cell culture

Murine macrophage cell line J774A.1, provided by the Paul Ehrlich cell bank, Rio de Janeiro, Brazil, was maintained in RPMI-1640 media (Sigma, USA) supplemented with 10% heat-inactivated fetal bovine serum (Gibco, USA), 100 ug/mL streptomycin (Sigma Chemical Co St.Louis, MO), 0.03% L-glutamine solution (Sigma) and 100 UI/mL of penicillin. Cells were incubated at 37 °C, 5% CO2 until formation of a confluent monolayer in 6-well cell culture plates (3 cm/well).

2.2. Bacterial culture

Samples of the virulent strain *Leptospira interrogans* sorovar Copenhageni (FIOCRUZ L1-130), attenuated strain *L. interrogans* sorovar Copenhageni M20, and saprophyte strain *L.biflexa* sorovar Patoc (FIOCRUZ -Patoc I) were utilized. Attenuation of sample M20 was performed with successive replications in culture medium. All strains were maintained in Fletcher semi-solid culture medium, and incubated at 30 °C. To restore bacterial virulence (virulent strain), 1 mL of cultured bacteria was inoculated intraperitoneally in Golden Syrian hamsters (*Mesocricetus auratus*) and later recovered from kidneys, whereas the attenuated strain did not undergo intraperitoneal inoculation in hamsters. Virulent leptospires cultures are routinely maintained at the Faculdade de MedicinaVeterinária e