Genomic and transcriptomic differences between a virulent and attenuated *Leptospira interrogans* sv Pomona bovine strain.

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Leptospira interrogans is the main agent of leptospirosis. Pathogenic leptospires are classified in serovars with different seroprevalence according to the host and geographical location. Unlike what happens in other countries, the main serovar in cattle in Argentina is Pomona. Pomona causes a severe infection and frequent mortality in calves. The attenuation of a strain AKRFB Passage 1 (P1) that belong to Pomona was achieved by multiple subcultures in liquid medium obtaining its attenuated counterpart in the Passage 19 (P19). In order to identify genetic changes, we compared *in vitro* genomes and transcriptomes of P1 and P19 using next generation sequencing platforms. Single nucleotide polymorphisms (SNPs) analysis of non-synonymous aminoacid changes in major proteins were identified in P19. The expression analysis (RNAseq) identified 328 differential transcripts between P1 and P19, of which 180 correspond to P1 (54.88%) and 148 to P19 (45.12%). Transcriptional regulators, regulators of two-component systems and membrane transporters were identified among the up-regulated transcripts in P1. Conversely, most of the transcripts up-regulated in P19 correspond to transposases coding genes. Even though the whole attenuation process of P19 cannot be attributed to single point mutations or differentially expressed genes, the set of them identified here, could explained part of the attenuated phenotype and allows the deepen in the regulation of expression in this pathogen.

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