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Changes in gene expression of *Vibrio parahaemolyticus* when shifting from environmental to clinical isolation conditions.

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Abstract: Pathogenic *V. parahaemolyticus* strains are able to adapt from environmental to laboratory isolation conditions that simulate some conditions upon infection in humans. To explore this adaptation, we determined the differential expression by RNAseq when growing in conditions for clinical isolation "I" (LB, NaCl 0.9% and 37 °C plus bile acid) referred to those in their natural environment "E" (LB, NaCl 3% and 12 °C). Analysis or the reads obtained after sequencing the RNA showed that 77% of the annotated genome was expressed in isolation (3841 genes) condition and 84% (4143 genes) in environmental condition.

Our transcriptome analysis revealed that among the 50 genes expressed in higher amount in each conditions, 21 were differentially expressed; 4 were downregulated and 17 upregulated in isolation condition; 14 corresponded to coding sequences (CDS), 5 to small-RNA and 3 to tRNA.

Conflicts of Interest

The authors declare no conflict of interest.