Tipo	Periódico
Título	Selection and validation of reference genes for gene expression studies in *Klebsiella pneumoniae* using Reverse Transcription Quantitative real-time PCR
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Programa/Curso (s)	Programa de Pós-Graduação Stricto Sensu em Ciências da Saúde
DOI	10.1038/s41598-018-27420-2
Assunto (palavras chaves)	Bacterial genes; Gene expression.; Reverse transcription polymerase chain reaction; Transcriptional regulatory elements
Idioma	Inglês
Fonte	Título do periódico: Scientific Reports ISSN: 2045-2322 Volume/Número/Paginação/Ano: v. 8, p. 1, 2018
Data da publicação	13 June 2018
Formato da produção	Digital https://doi.org/10.1038/s41598-018-27420-2
Resumo	For reliable results, Reverse Transcription Quantitative real-time Polymerase Chain Reaction (RT-qPCR) analyses depend on stably expressed reference genes for data normalization purposes. *Klebsiella pneumoniae* is an opportunistic Gram-negative bacterium that has become a serious threat worldwide. Unfortunately, there is no consensus for an ideal reference gene for RT-qPCR data normalization on *K. pneumoniae*. In this study, the expression profile of eleven candidate reference genes was assessed in *K. pneumoniae* cells submitted to various experimental conditions, and the expression stability of these candidate genes was evaluated using statistical algorithms BestKeeper, NormFinder, geNorm, Delta C_T and RefFinder. The statistical analyses ranked *recA*, *rho*, *proC* and *rpoD* as the most suitable reference genes for accurate RT-qPCR data normalization in *K. pneumoniae*. The reliability of the proposed reference genes was validated by normalizing the relative expression of iron-regulated genes in *K. pneumoniae* cells submitted to iron-replete and iron-limited conditions. This work emphasizes that the stable expression of any potential reference candidate gene must be validated in each physiological condition or experimental treatment under study.
Fomento	