

Título: IDENTIFICATION OF VIRULENCE FACTORS IN *YERSINIA ENTEROCOLITICA* STRAINS BY WHOLE-GENOME SEQUENCING

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Resumo:

Yersinia enterocolitica is a zoonotic pathogen with high public health relevance, especially in Europe due to its high levels of occurrence, where it is the third most common bacterial cause of diarrhea. The species is divided into six biotypes, with various levels of pathogenicity: Biotype 1A comprise strains that are mostly nonpathogenic and biotypes 2 to 5 have moderate pathogenicity. However, some biotype 1A isolates have been considered as causative of gastrointestinal disease, yielding symptoms indistinguishable from those produced by pathogenic biotypes. *Y. enterocolitica* is also divided into somatic serotypes and the most widespread worldwide is the biotype 4/ serotype O:3. Regarding clinical aspects, *Y. enterocolitica* O:3 may cause a variety of gastrointestinal problems, such as acute diarrhea, terminal ileitis, and mesenteric lymphadenitis. The usual route of acquisition of this pathogen is through contaminated foods or water. In Brazil, several studies on *Y. enterocolitica* and other *Yersinia* species show its isolation from human, animal, food, and environmental sources and the swine is likely to serve as a main element in *Y. enterocolitica* transmission to humans. The aim of this study was to identify the virulence factors through the whole-genome sequencing (WGS) of two strains of *Y. enterocolitica*: one bioserotype 4/O:3 isolated from swine and other from bioserotype 1A/O:5 isolated from human feces. Genomic DNA was extracted using QIAamp DNA Blood Mini Kit (Qiagen, Germany), whole-genome sequencing (WGS) was obtained by Illumina HiSeq sequencing platform (Illumina Inc., USA). After assembly, genome annotation was performed on the Rapid Annotation using System Technology (RAST) v.2.0 (available at <https://rast.nmpdr.org/>). *Yersinia* contigs were used for Blast searches against GenBank. In both *Yersinia* isolates, we found: Myf/pH6 antigen precursor and/or related genes (such as myfA, psaF, psaE, psaC and psaB) - fibrillar structure that play a role in thermoinducible binding and haemagglutination to the psa locus; Type IV pili related genes (such as pilM, pilN, pilO, pilP, pilQ) – are adhesins; and invasion related genes (inv-like). Those results support the hypothesis that the strains of biotype 1A could play a role in gastrointestinal diseases.

Palavras-chaves: *Yersinia enterocolitica*, whole-genome sequencing, virulence factors, zoonosis.

Agência Fomento: CNPq