Title:

Comparative genomics analysis of a type A Clostridium perfringens strain associated with bovine abomasitis.

Authors

Díaz Carrasco, J. M. [1, 3]
Redondo, L. [1, 3]
Martínez Cáceres, A. [2]
Dailoff, G. [1, 3]
Farber, M. [2, 3]
Fernández Miyakawa, M. [1, 3]

Institutions

[1] Instituto de Patobiología, Centro Nacional de Investigaciones Agropecuarias, Instituto Nacional de Tecnología Agropecuaria, Calle Las Cabañas y Los Reseros s/n, Casilla de Correo 25 (1712), Castelar, Buenos Aires, Argentina.
[2] Instituto de Biotecnología, Centro Nacional de Investigaciones Agropecuarias, Instituto Nacional de Tecnología Agropecuaria, Calle Las Cabañas y Los Reseros s/n, Casilla de Correo 25 (1712), Castelar, Buenos Aires, Argentina.
[3] Consejo Nacional de Investigaciones Científicas y Técnicas, Rivadavia 1917 (1033), Ciudad Autónoma de Buenos Aires, Argentina.

Abstract

Clostridium perfringens is a Gram-positive bacterium that is commonly present in the gastrointestinal tract of many animals, including mammalian and birds. Although generally behaves as a harmless member of the normal microbiota, its ability to multiply quickly and produce multiple toxins can result in diverse enteric diseases. In this study, a type A *C. perfringens* strain isolated from a case of bovine abomasitis was genetically characterized. Complete genome sequencing of strain 68 was performed using the Illumina MiSeq benchtop platform, using total DNA as starting material, and obtaining 798.925 paired-end reads. A draft genome sequence was assembled with SPAdes software and analyzed by means of bioinformatic tools, in search of genetic factors specific to strain 68, which should be absent in reference strains and therefore could be associated with the disease. Complete genome of strain 68 consisted of 151 contigs > 1 kb (3.5 Mb in total) from which 4 contigs (122 kb) corresponded to sequences that were only mapped to plasmidic references. Genome of strain 68 was compared to three complete *C. perfringens* genomes (strain 13, SM101 and ATCC 13124) and one draft genome derived from another case of bovine abomasitis (F262). After annotation in the RAST server, a total of 3159 protein-coding genes were detected, almost the same number as strain F262 (3163 CDS) which is substantially higher than the number of CDS in the remaining strains (max. 3040 CDS in strain ATCC 13124). Average nucleotide identity analysis indicated that strain 68 is closely related to all strains: ATCC 13124 (98.68%), F262 (98.54%), strain 13 (98.33%) and SM101 (97.35%). However, through Pan-seq Novel Region Finder analysis we found that strain 68 contains about 200 genes which were not detected in any of the other four reference genomes. Almost half of these unique genes belonged to hypothetical proteins while the remaining genes code mainly for capsular polysaccharide biosynthesis proteins, phage-related elements and regulatory factors, as well as for adhesion proteins and other putative virulence factors. Our data suggests that strain 68 posses a set of genes that could provide a distinctive adhesion capacity, which may be related to its virulent phenotype. Further bioinformatic and phenotypic characterization of these features will help identify genetic factors associated with this pathology.

Keywords: bovine abomasitis; cattle enteric diseases; clostridial infection; comparative genomics; genome sequencing.

Funding source: Proyecto INTA PNSA 1115056