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Saria M. In-Albon

Institute of Veterinary Bacteriology, joachim.frey@vetsuisse.unibe.ch

***Clostridium chauvoei*: an Evolutionary Dead-End Pathogen**

Clostridium chauvoei is a highly pathogenic, histotoxic, anaerobic, endospore forming Gram-positive bacterium causing blackleg, a severe disease of cattle, sheep and other domestic animals. Blackleg is globally spread among ruminants, specified primarily as a myonecrosis with high mortality.

Full genome sequences of 20 strains of *C. chauvoei*, isolated from four different continents over a period of 64 years (1951-2015) were analysed and revealed that the genome of the species *C. chauvoei* is highly homogeneous. Analysis of the CRISPR locus is sufficient to differentiate most *C. chauvoei* strains. It is the most heterogeneous region in the genome, containing in total 187 different spacer elements distributed as 30 – 77 copies in the various strains. The major virulence genes, the highly toxic *Clostridium chauvoei* toxin A (CctA), the sialidase and the two hyaluronidases are fully conserved as the metabolic and structural genes.

These data show that *C. chauvoei*, a strict ruminant pathogen has reached a dead end in its evolution. This knowledge is of basic importance to replace the current guinea pig potency test for batch release of blackleg vaccines by an *in-vitro* procedure to avoid experimental infections of animals.

Keywords

Blackleg, *Clostridium chauvoei*, CRISPR, virulence genes, dead-end evolution