

Development and application of a core genome-based multilocus sequence typing system for *C. perfringens*

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Whole genome sequencing can provide a comprehensive overview of the genetic information of a pathogen and also represents a powerful molecular epidemiological tool for subtyping and outbreak investigations. In this study, we describe a cgMLST scheme for the Gram-positive anaerobic bacterium *C. perfringens*. A core genome of 1510 genes was initially identified in 38 genomes that represent different phylogroups of *C. perfringens*. We evaluated these genes via performing allele typing in a data set of 80 *C. perfringens* strains. As a result, 60 genes were discarded because no allele number was assigned to them in more than 5% of the genomes. Thus, the final cgMLST scheme comprises 1450 genes which were found typeable in a collection of 160 genomes by an average of 99.5% per each genome. The developed cgMLST scheme has superior discriminatory power compared to classical MLSTs. We applied the developed cgMLST scheme to analyze 87 *C. perfringens* genomes from poultry with regard to the country of isolation, NetB toxin gene presence and clinical disease. Based on the cgMLST results, we discovered a limited diversity among the suspected necrotic enteritis isolates compared to the isolates obtained from healthy birds and meat samples.

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