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'Flesh-eater' genome

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Jonathan B Weitzman

Email: jonathanweitzman@hotmail.com

Clostridium perfringens is the most widely distributed pathogen, and is a cause of gas gangrene, necrotic enteritis and diarrhoea. In the January 22 *Proceedings of the National Academy of Sciences*, Shumizu *et al.* report the genome sequence of *C. perfringens* strain 13, the first Gram-positive anaerobic pathogen to be completely sequenced (*Proc Natl Acad Sci USA* 2002, **99**:996-1001). The genome is just over 3 Mb long, with a low G+C content (28.6%). They found 2660 predicted proteins, half of which could be assigned a possible function. Shumizu *et al.* compared the *C. perfringens* genome with that of *C. acetobutylicum* to get clues about gene function. They found genes encoding enzymes for anaerobic fermentation, glycolysis and glycogen metabolism, but none for the tricarboxylic acid cycle; they also found only a partial set of enzymes for amino-acid synthesis. Shumizu *et al.* identified several virulence-associated genes including putative hemolysins, toxins, and adhesins.

References

1. *Clostridium perfringens* toxins (type A, B, C, D, E).
2. *Proceedings of the National Academy of Sciences*, [<http://www.pnas.org>]
3. *Clostridium perfringens* strain 13, [<http://w3.grt.kyushu-u.ac.jp/CPE/>]
4. Genome sequence and comparative analysis of the solvent-producing bacterium *Clostridium acetobutylicum*.