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Genomic sequence of two strains from the *Bacillus cereus* group, a food poisoner and psychrotrophic, reveals difference in contents of known toxins.

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Food poisoning by *Bacillus cereus* group strains is becoming a notable problem, especially prominent in highly developed countries. An acquired ability of food contaminating strains, some of which can grow at low temperatures, to synthesize highly active toxins, can make them a threat to human health. The three main known toxins in question are hemolysin Hbl, non-hemolytic toxin Nhe and cytotoxin CytK. A gene homologous to CytK is also present in many strains in the form of a paralogue HlyII, but it is still unknown to be the cause of food poisoning. A representative psychrotrophic strain Bwe KBAB4, able to grow at 6°C, and a very distinct and rare strain NVH391-98, isolated from a severe food poisoning case, were chosen for complete genomic sequencing.

Preliminary analysis of genomic data shows that the two strains differ in their genetic makeup. NVH391-98, already known as a severe food poisoner, produces in high amounts only one toxin – CytK (Lund et al, 2000; Brillard and Lereclus, 2004). The strain does not encode any other of the above toxins and its genome represents a small 4 Mb chromosome, instead of 5.2-5.6 Mb usually reported in other strains of the *B. cereus* group. Furthermore, the strain has lost its entire *trp* operon and can only grow at temperatures higher than 20°C. Because the majority of chromosomal genes greatly diverge from those of all other representatives of the group, the strain can be considered as the only known representative of a new species, which we suggest to name *Bacillus cytotoxicus*. The second strain sequenced, Bwe KBAB4, isolated from forest soil, is a typical representative of recently recognized species - *B. weihenstephanensis* (Lechner et al, 1998). It contains a total of 5.6 Mb of genetic material, which includes genes to encode Nhe and Hbl, but lacks genes for CytK and HlyII. Although closely related strains are frequently reported to be food contaminants, they are in almost all cases not poisonous. However, the presence of Nhe and Hbl encoding genes suggests that such strains can also become toxic.

Details of genomic project (sequence, assembly, finishing) and data analysis will be presented.

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