

## **LBNL-60341 Abs.**

### **Toward a comprehensive overview of the *Bacillus cereus* group genomes.**

Alexei Sorokin<sup>1</sup>, Sandrine Auger<sup>1</sup>, Nathalie Galleron<sup>1</sup>, S.Dusko Ehrlich<sup>1</sup>, Eugene Goltsman<sup>2</sup>, Paul Richardson<sup>2</sup>, Alla Lapidus<sup>2</sup>

<sup>1</sup> Génétique Microbienne, CRJ INRA, Jouy-en-Josas, France

<sup>2</sup> DOE Joint Genome Institute, Walnut Creek, CA, USA

The *Bacillus cereus* group consists of gram-positive, spore-forming bacteria with an impact on human activities due to their pathogenic properties. The most famous pathogens of animals and insects, *B. anthracis* and *B. thuringiensis*, carry their toxins in large plasmids. However, the bacteria of this group are also involved in mild food poisoning, causing rather noxious, although not fatal, vomiting or diarrhea. The emetic group strains appear to represent a very narrow phylogenetic group, and the corresponding toxin is encoded by a plasmid (Ehling-Schulz et al, 2005). Contrary to that, the characterized diarrheic toxins (Nhe, Hbl and CytK) are always present in the chromosome.

To provide the comprehensive genomic characterization of the group, in addition to the genomes already sequenced, we selected three different strains for complete sequencing. The work is being done as a collaboration of INRA (France), Joint Genome Institute (Walnut Creek, USA) and CNS *Génoscope* (Evry, France). One of the strains, NVH398-91, is now completely sequenced. It was isolated from a severe food poisoning case in France (Lund et al, 2000). Surprisingly, the strain contains a gene for only one of known diarrheic toxins – Cyt K, which was shown to be synthesized in elevated amounts and to be particularly effective (Brillard and Lereclus, 2004; Fagerlund et al, 2004). The strain is rather different from other representatives of the *B. cereus* group and has a compact chromosome of 4.1 Mb, compared to 5.2-5.4 Mb genomes of other sequenced strains. This strain can also be regarded as the first bacterium of the group in which a highly effective toxin is chromosome-encoded. Divergence of the strain from other and its phenotypic particularities inspires to consider it as a representative of a new species, for which we propose a name *Bacillus cytotoxis*. However, only one such strain was described for the moment.

The second strain being sequenced, *Bwe* KBAB4, isolated from forest soil, is a typical representative of recently recognized species - *B. weihenstephanensis* (Lechner et al, 1998; Sorokin et al, 2006). 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.

Finally, the third strain, *B. cereus* F0837/76, can be regarded as one of typical strains that can cause a severe diarrheic food poisoning. It synthesizes at least two characteristic toxins, Nhe and Hbl, in elevated amounts and was isolated from a contaminated surgical wound in a hospital (Turnbull et al, 1979; Beecher and MacMillan, 1990; Lund and Granum, 1997). Genomically the strain appeared to be very closely related to *B. anthracis* and this is probably the closest to it *B. cereus* strain known. It does not however contain the relevant pathogenic plasmids.

This work was performed under the auspices of the US Department of Energy's Office of Science, Biological and Environmental Research Program, and by the University of California, Lawrence Livermore National Laboratory under Contract No. W-7405-Eng-48, Lawrence Berkeley National Laboratory under contract No. DE-AC02-05CH11231 and Los Alamos National Laboratory under contract No. DE-AC52-06NA25396.