Genomic diversity of extremophilic bacilli

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Abstract

It is known that Bacillus-related species can grow in a wide range of environments, at pH 2-12, with temperatures between 5 and 78°C, in salinity from 0 to 30% NaCl, and pressures from 0.1 MPa (atmospheric pressure) to at least 30 MPa (corresponding to the pressure at a depth of 3000 m).

We are now intrigued by the questions of how these adaptive capabilities were acquired, as reflected in their genomes, and what intrinsic genomic structure of Bacillus-related species has allowed them to adapt to such a wide range of environments. On the other hand, phylogenetically related Bacillus-related species share many genes each other although each species has the different capability to adapt to various environments. Thus, it is expected that comparative analysis with Bacillus-related species can be a useful approach for extracting candidate genes associated with the mechanisms of adaptation to the environments.

We initiated the genome sequencing project at the beginning of 1998 and have determined the whole genomic sequences of three extremophilic bacilli, alkaliphilic Bacillus halodurans 1), extremely halotolerant and alkaliphilic Oceanobacillus iheyensis 2), and thermophilic Geobacillus kaustophilus 3) until now. We provide the first comparative analysis of the extremophilic bacillar genome with those of 3 other closely related mesophilic and neutrophilic bacilli, B. subtilis, B. anthracis and B. cereus, in order to highlight commonality and diversity of the bacillar genomes.

References

