Description of the genome of *Geobacillus thermoleovorans* T80 and comparison with related organisms.

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Thermophilic bacteria belonging to *Bacillus* genetic group 5 have been reclassified as being members of *Geobacillus* gen. nov., with *G. stearothermophilus* as the type strain. *Geobacillus* species, literally meaning earth or soil bacillus, are widely distributed and readily isolated from natural and man-made thermophilic biotopes. At present there is an abundance of genomic information available for this genera with sequencing projects of the isolates *G. stearothermophilus* and *G. kaustophilus* HTA426. Within our own laboratory, and in conjunction with Georgia Institute of Technology (USA) we have been sequencing the genome of *G. thermoleovorans* T80, an isolate obtained from temperate Irish soil. Within this paper we wish to present the pertinent features of the genome and through comparison with genomic information from related species, hope to substantially widen our knowledge and understanding of how these microorganisms are able to adapt and survive in extreme environments. The genome of *G. thermoleovorans* T80 is the smallest at 3.38 Mbp, of all *Bacillus* related species so far sequenced including *G. kaustophilus* (3.54 Mbp). The G+C content was 52.3%, roughly equivalent to that of *G. kaustophilus* (52.1%) and significantly higher than that found in other non-thermophilic Bacilli. The genome of *G. thermoleovorans* had 3830 predicted protein coding sequences (CDS). Given that *G. kaustophilus* had only 3498 CDS despite having a larger total genome size, it is predicted that the average gene length in our isolate is only 771 bp compared with 862 bp in *G. kaustophilus*. Of interest was the finding that as with *G. kaustophilus* and *Bacillus halodurans*, the genome of *G thermoleovorans* contains a large number of transposases, with 84 transposase genes occurring in 14 distinct groups. It is proposed that such genes will have played an important evolutionary role in horizontal gene transfer and also in the internal rearrangement of the genome. It is surprising however to note that none of the transposases identified are related to transposes from hyperthermophilic Archaea, indeed only two of the transposase genes have an Archaeal origin being related to transposons from *Methanosarcina* and *Methanococcoides* respectively. Unlike *Thermatoga maritima* where approximately 30% of the genome is of Archaeal origin and it is suggested that this is indicative of this thermophile sharing the same biotopes as hyperthermophilic Archaea, no such conclusion can be drawn for *G. thermoleovorans*. Given the lack of evidence for lateral gene transfer with hyperthermophilic Archeae, our observation raises questions about the environmental niche to which *G. thermoleovorans* is best suited.