

Insights into the Annotated Genome Sequence of *Defluviitoga tunisiensis* L3 Isolated from a Thermophilic Rural Biogas Producing Plant

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Abstract : Within the agricultural sector, the production of biogas from organic substrates represents an economically attractive technology to generate bioenergy. Complex consortia of microorganisms are responsible for biomass decomposition and biogas production. Recently, species belonging to the phylum Thermotogae were detected in thermophilic biogas-production plants utilizing renewable primary products for biomethanation. To analyze adaptive genome features of representative Thermotogae strains, *Defluviitoga tunisiensis* L3 was isolated from a rural thermophilic biogas plant (54°C) and completely sequenced on an Illumina MiSeq system. Sequencing and assembly of the *D. tunisiensis* L3 genome yielded a circular chromosome with a size of 2,053,097 bp and a mean GC content of 31.38%. Functional annotation of the complete genome sequence revealed that the thermophilic strain L3 encodes several genes predicted to facilitate growth of this microorganism on arabinose, galactose, maltose, mannose, fructose, raffinose, ribose, cellobiose, lactose, xylose, xylan, lactate and mannitol. Acetate, hydrogen (H₂) and carbon dioxide (CO₂) are supposed to be end products of the fermentation process. The latter gene products are metabolites for methanogenic archaea, the key players in the final step of the anaerobic digestion process. To determine the degree of relatedness of dominant biogas community members within selected digester systems to *D. tunisiensis* L3, metagenome sequences from corresponding communities were mapped on the L3 genome. These fragment recruitments revealed that metagenome reads originating from a thermophilic biogas plant covered 95% of *D. tunisiensis* L3 genome sequence. In conclusion, availability of the *D. tunisiensis* L3 genome sequence and insights into its metabolic capabilities provide the basis for biotechnological exploitation of genome features involved in thermophilic fermentation processes utilizing renewable primary products.

Keywords : genome sequence, thermophilic biogas plant, Thermotogae, *Defluviitoga tunisiensis*

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