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GENOMIC AND PHENOTYPIC CHARACTERISTICS OF A THERMOPHILIC *Bacillus* sp. 9F ISOLATED FROM DEEP-SEA HYDROTHERMAL VENT PLUME, SOUTHERN OCEAN

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INTRODUCTION

The strain 9F was isolated from deep-sea hydrothermal vent plume in Australian-Antarctic Ridge in the Southern Ocean. Analysis of the 16S rRNA gene sequence of strain 9F showed an affiliation to the type strain of *Bacillus licheniformis* with a high similarity of 99.9%. In the present study, we compared genomic and phenotypic features of strain 9F with those of the type strain of *B. licheniformis* (KCTC 1918^T) to find differences between the strains of different origins; strain 9F is the first strain from deep-sea hydrothermal vent environment, while other strains *B. licheniformis* have been isolated from diverse terrestrial environments including the type strain.

METHODS AND MATERIALS

A genome sequence of strain 9F was determined using an Illumina MiSeq, whereas a complete genome sequence of the type strain of *B. licheniformis* was retrieved from the GenBank under the accession AE017333 (4,222,645 bp with the G+C content of 46.2 mol%). Temperature and salinity ranges for growth were determined for both strains. Enzyme activities, carbon assimilation, acid production from carbohydrates were assayed using the API ZYM, 20NE and 50CH kits.

RESULTS

A draft genome of strain 9F revealed 29 contigs in 4,376,753 bp with the G+C content of 45.6 mol%. Genomic relatedness analyses based on average nucleotide identity and the genome-to-genome distance showed that strain 9F and *B. licheniformis* KCTC 1918^T belonged to single species. A lower limit of temperature for growth was 10°C and 15°C for strain 9F and *B. licheniformis* KCTC 1918^T, respectively, while an upper limit of temperature was 60°C for both strains. Salinity tolerant tests showed an identical result for both strains (0–7.5% NaCl, w/v). No difference between both strains was found in the enzyme profiles with the API ZYM and 20 NE assays. However, an obvious difference in acid production (14 out of 49 carbohydrates in the API 50CH assay) and the assimilation of arabinose were observed between them.

DISCUSSION

Preliminary results of comparative genomics between strain 9F and *B. licheniformis* KCTC 1918^T showed some fragments of DNA were either inserted or deleted in one of the genomes. Interestingly, the different fragments were often attributed to viral DNAs, suggesting that a horizontal gene transfer mediated by phages might serve to shape phenotypic traits of their host bacteria originated from different habitats.

KEYWORDS: GENOME, THERMOPHILE, BACTERIA, VENT, SOUTHERN OCEAN