BRAZILIAN JOURNAL OF MICROBIOLOGY

http://www.bjmicrobiol.com.br/

Genome Announcement

Genome sequence of *Prevotella intermedia* SUNY aB G8-9K-3, a biofilm forming strain with drug-resistance

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ARTICLE INFO

Article history:
Received 24 March 2016
Accepted 18 April 2016
Available online 9 June 2016
Associate Editor: John Anthony McCulloch

Keywords:
Prevotella intermedia
Antimicrobial resistant
Biofilm-forming capacity

ABSTRACT

Prevotella intermedia has long been known to be as the principal etiologic agent of periodontal diseases and associated with various systemic diseases. Previous studies showed that the intra-species difference exists in capacity of biofilm formation, antibiotic resistance, and serological reaction among *P. intermedia* strains. Here we report the genome sequence of *P. intermedia* SUNY aB G8-9K-3 (designated ATCC49046) that displays a relatively high antimicrobial resistant and biofilm-forming capacity. Genome sequencing information provides important clues in understanding the genetic bases of phenotypic differences among *P. intermedia* strains.

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Prevotella intermedia is an obligate anaerobic gram-negative rod-shape bacterium that has long been known to be associated with periodontal diseases as well as systemic diseases such as cystic fibrosis and chronic bronchitis.[1] There have been evidences to show that the intra-species difference exists: Takahashi et al.[2] reported that *P. intermedia* SUNY aB G8-9K-3 (designated ATCC 49046) produces 2-fold-larger amount of monospecies biofilm than other strains, including ATCC 25611^T (type strain), and ATCC49046 biofilm exhibited high-level resistance to antibiotics. Furthermore, the bioactivity of ATCC49046 biofilm was even significantly increased after exposure to several antibiotics.[1,2] Nakazawa et al.[3] reported that serogroup A, represented by ATCC 25611^T, accounted for only 5% of the 79 isolates and 6% of the 66 patient plaque samples, while most of the *P. intermedia* isolates (55%) and subjects (52%) were classified as being in the serogroup C, represented by ATCC 49046. The wealth of information on genomic characteristics and virulence traits of ATCC49046 compelled us to define its genetic makeup by sequencing its genome.

The bacterial genomic DNA was extracted and sequencing library was constructed following paired-end sequencing on the Illumina Hi-Seq 2500 platform. In total, 14,668,776

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http://dx.doi.org/10.1016/j.bjm.2016.04.030

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paired-end read pairs (2 × 100 bp) were obtained. After filtering out low quality of the raw reads, A5 assembler (version A5-miseq 20140604)[4] with default parameters was used for the construction of the genome. The genome assembly resulted in 46 scaffolds (>500-bp length). The draft genome size is 2,673,338 bp and G + C content is 43.47%. Gene annotation of the draft genome has been performed using Prokka 1.10[5] and total 2248 protein coding sequences (CDSs), 44 tRNA, 1 tmRNA and 3 repeat regions were annotated. In the annotated genome, Cas1, 2 and 9 genes are located in the same scaffold and 5 clustered regularly interspaced short palindromic repeats (CRISPRs) arrays were identified by PILER-CR.[6] *P. intermedia* ATCC49046 is predicted to encode various resistance determinants toward cobalt, zinc and cadmium, and genes involved in drug resistance: different copies of beta-lactamases, virulence factor BrkB, virulence associated protein E, and multidrug resistance proteins such as MdtN and NorM. Multidrug/efflux transporters, such as ABC-type multidrug transport system, multidrug transporter AcrB, and MATE efflux family proteins were also found.

Global pairwise comparison of the genome sequences between ATCC25611^T and ATCC49046 strains showed that 94% of genome regions were similar with each other. Meanwhile single nucleotide polymorphism (SNP) analysis performed by MUMmer package[7] identified 1643 orthologous genes having at least one SNP, of which 51 genes, including chemotaxis protein CheY, membrane proteins, TonB-dependent receptor, polysaccharide biosynthesis protein, collagen-binding protein, secretion protein and capsid assembly protein, are statistically significantly highly variable. These results provide important clues in understanding the genetic bases of phenotypic differences among *P. intermedia* strains.

This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession LBGT00000000. The version described in this paper is version LBGT00000000.1. The BioProject ID in GenBank is PRJNA281562.

Conflicts of interest

The authors declare no conflicts of interest.

Acknowledgements

This research was supported by a grant of the Korea Health Technology R&D Project through the KHIDI, funded by the Ministry of Health & Welfare, Republic of Korea (HI14C0175) and by a grant from Kyung Hee University in 2014 (KHU-20140679).

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