



[Analysis of complete sequence of cryptic plasmid pTP33 from *Yersinia pestis* isolated in Tuva natural focus of plague].

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Abstract:

This paper studies a full nucleotide sequence of cryptic plasmid pTP33, which was isolated from the typical plague strain of the Tuvian natural focus, *Yersinia pestis* I-2638. Sequencing was carried out using the 454 GS Junior platform (Roche). In analysis using the software package GS De Novo Assembler v. 2.7 (Roche) and the algorithm Newbler v. 2.7, 1855 nucleotide reads, which contained 1101246 nucleotides, were assembled to a contig of 33 978 bp. The GC content of the obtained nucleotide sequence was 50.25%. During annotation, we found 56 open reading frames. Homologs of the predicted reading frames were sought in the BLAST databases. We detected 22 reading frames coding hypothetical proteins, 23 frames coding phage-related proteins, and 11 frames coding proteins with known functions, including toxin-antitoxin system YefM-YoeB, nucleic acids and polysaccharides metabolism proteins (exopolysaccharide production protein ExoZ, exodeoxyribonuclease VIII), and replication proteins (ParA). Some predicted pTP33 proteins were found to be homologs (from 45 to 75%) with sequences of phage-related proteins of certain microorganisms—endosymbionts of insects (*Sodalis glossinidius*) and endosymbionts of entomopathogenic nematodes (*Photorhabdus luminescens*, *P. asymbiotica*, *Xenorhabdus bovienii*).

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