

Hymenobacter Taeansis Sp. Nov., Radiation Resistant Bacterium Isolated from Coastal Sand Dune

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Research Article

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Abstract

An aerobic, Gram-stain-negative, non-motile, non-spore-forming, rod-shaped, and light pink-colored bacterial strain, designated TS19^T, was isolated from a sand sample obtained from a coastal sand dune after exposure to 3 kGy of gamma radiation. Phylogenetic analysis based on the 16S rRNA gene sequences revealed that the isolate was a member of the genus *Hymenobacter* and was most closely related to *H. wooponensis* WM78T (98.3% similarity). Strain TS19^T and *H. wooponensis* showed resistance to gamma radiation with D₁₀ values (i.e., the dose required to reduce the bacterial population by tenfold) of 7.3 kGy and 3.5 kGy, respectively. The genome of strain TS19^T consists of one contig with 4,879,662 bp and has a G+C content of 56.2%. The genome contains 3,955 protein coding sequences, 44 tRNAs, and 12 rRNAs. The predominant fatty acids of strain TS19^T were iso-C_{15:0}, summed feature 4 (iso-C_{17:1} I and/or anteiso-C_{17:1} B), summed feature 3 (C_{16:1} ω6c and/or C_{16:1} ω7c), and C_{16:1} ω5c. The major polar lipids were phosphatidylethanolamine, and one unknown aminophospholipid. The main respiratory quinone was menaquinone-7. Based on the phylogenetic, physiological, and chemotaxonomic characteristics, strain TS19^T represents a novel species, for which the name *Hymenobacter taeanensis* sp. nov. is proposed. The type strain is TS19^T (=KCTC 72897^T =JCM 34023^T).

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Figures

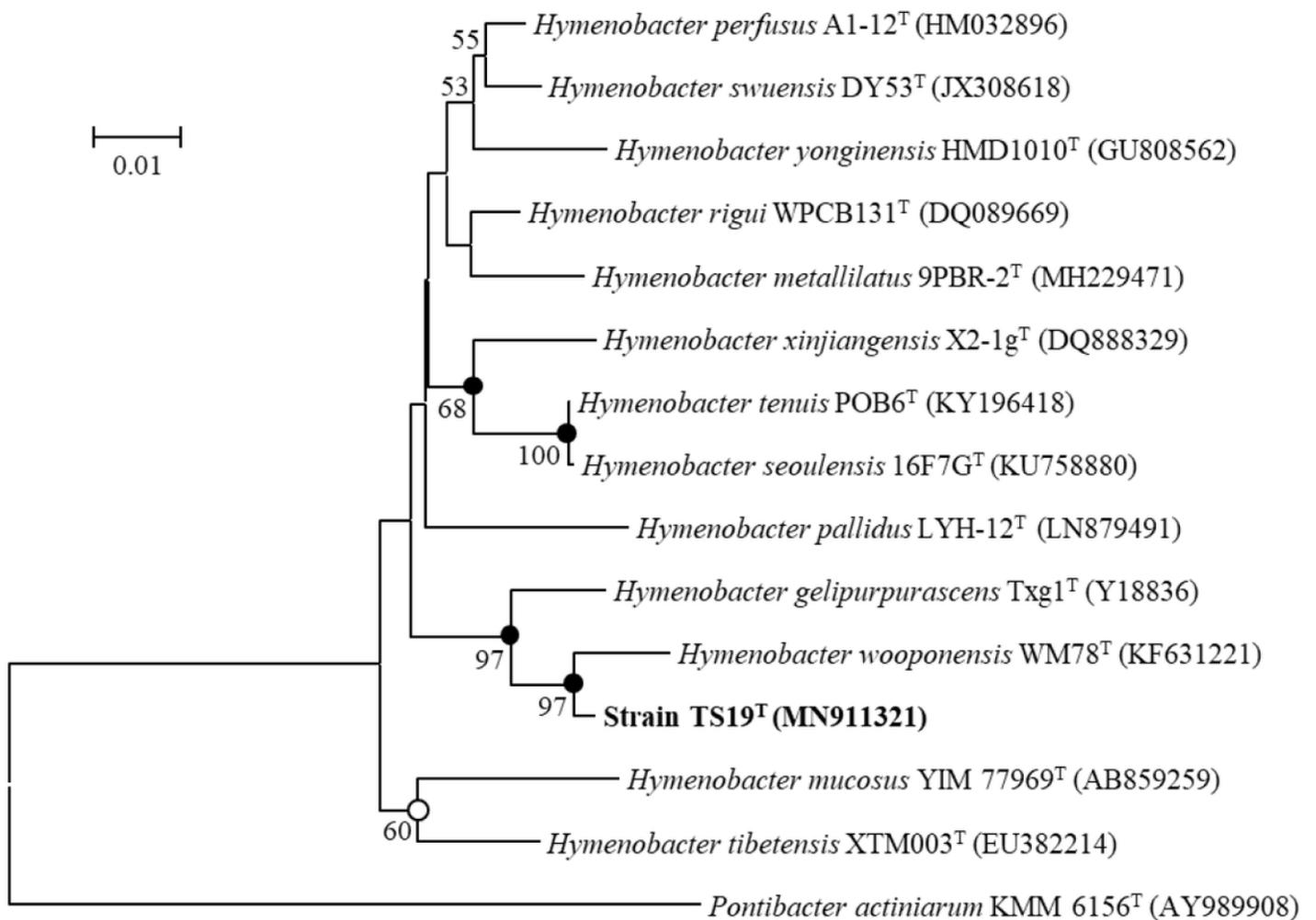


Figure 1

A neighbor-joining tree based on 16S rRNA gene sequences showing the phylogenetic position of strain TS19^T and related strains of the genus *Hymenobacter*. Evolutionary distances, generated using the Kimura two-parameter model, are based on 1,359 unambiguously aligned nucleotides. Bootstrap values greater than 60% (1000 resamplings) for nodes conserved among neighbor-joining analyses are shown. Closed circles indicate that the corresponding nodes were also recovered in trees generated with the maximum-parsimony and maximum-likelihood algorithms. Opened circles indicate branches of the tree that were also recovered using the maximum-parsimony algorithm. *Pontibacter actiniarum* KMM 6156^T (AY989908) was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

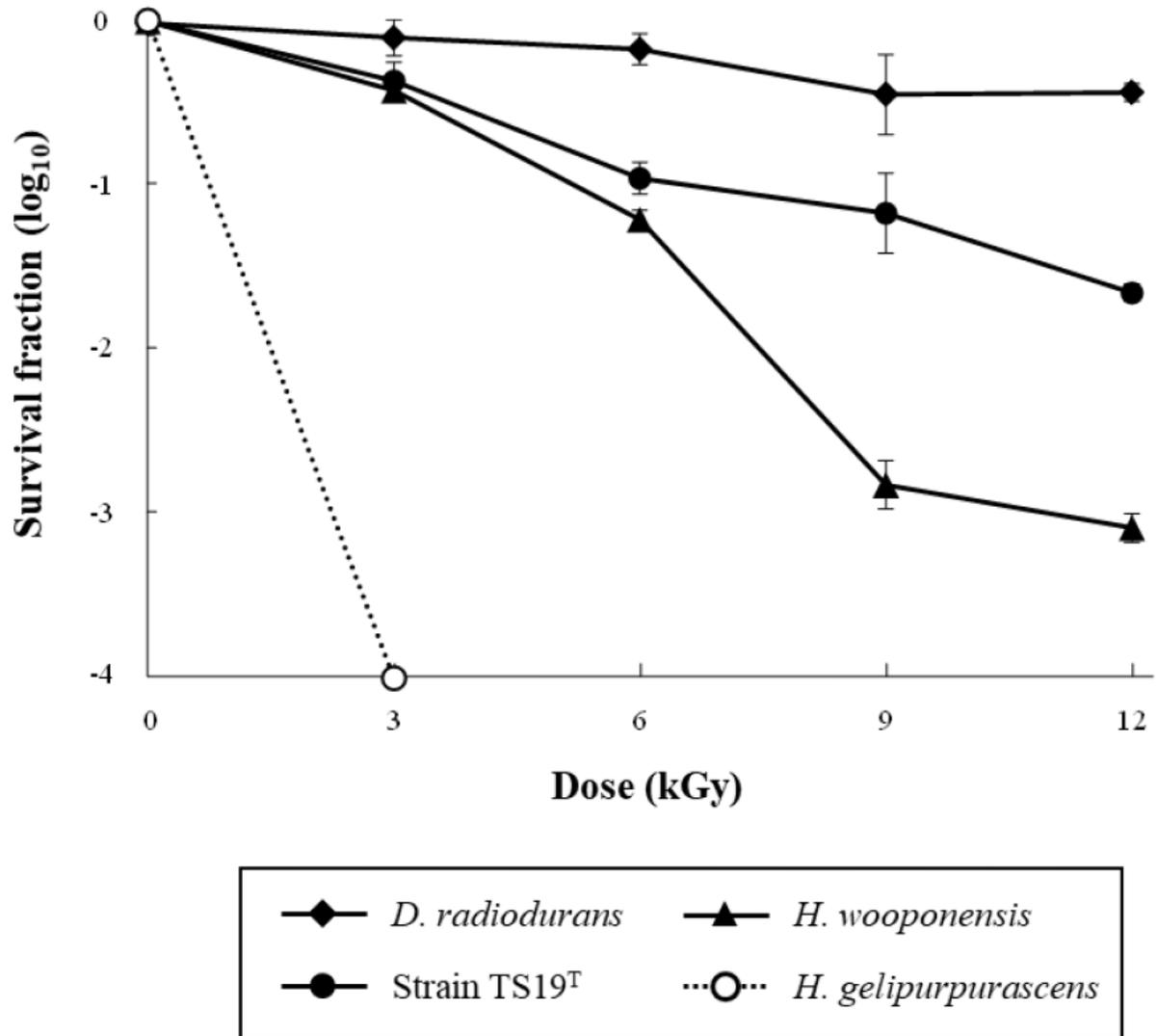


Figure 2

Representative survival curves of strain TS19T and two related species after treatment with various doses of gamma irradiation. *Deinococcus radiodurans* R1T and *Escherichia coli* MG1655T were used as positive and negative controls, respectively.

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