Genome of the Repetitive-Sequence-Rich
Mycoplasma fermentans Strain M64

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Mycoplasma fermentans is a microorganism commonly found in the genitourinary and respiratory tracts of healthy individuals and AIDS patients. The complete genome of the repetitive-sequence-rich M. fermentans strain M64 is reported here. Comparative genomics analysis revealed dramatic differences in genome size between this strain and the recently completely sequenced JER strain.

Mycoplasma fermentans is a fastidious Gram-negative bacterium commonly isolated from human genitourinary and respiratory tracts. It has been implicated in HIV pathogenesis, sexually transmitted genital tract infections, systemic infections, rheumatic disorders, chronic fatigue syndrome, and other diseases (1, 2, 8, 9, 12, 14, 15, 18, 25, 27, 28). Notwithstanding the clinical significance, the roles it plays and the molecular mechanisms involved in various diseases have yet to be elucidated.

In this study, we have determined the repetitive-sequence-rich genome sequence of M. fermentans strain M64 isolated from a non-AIDS patient (16). Escherichia coli DH5α and pUC18 vector were used in the construction of whole-genome shotgun libraries (2 to 3 kb and 5 to 7 kb) as previously described (7, 30). The whole-genome shotgun sequences (BigDye Terminator 3.1 kit and ABI3730XL DNA analyzer; both from Applied Biosystems, Foster City, CA) were assembled with the Phredphrap software using the “Hide-and-Seek” sequence assembly strategy (4, 13, 22). The assembled genome sequence was validated by restriction mapping and Southern hybridization analyses of BglI, KpnI, MluI, and AhdI fragments resolved by pulsed-field gel electrophoresis (CHEF Southern hybridization) (14, 15). The genome contained nine copies of two families of large repeat sequences (integrative conjugal elements of the M. fermentans genome also bears a high density of transposable elements. The genome contained nine copies of two families of large repeat sequences (integrative conjugal elements of Mycoplasma mycoides subsp. mycoides (29), the M. fermentans M64 genome also bears a high density of transposable elements. After all, unveiling this special reduced genome which is rich in transposable elements may help to elucidate the elusive relationship between this strain and the recently completely sequenced JER strain.
tionships between *M. fermentans* M64 and the implicated diseases.

**Nucleotide sequence accession number.** The genome sequence with annotations of *Mycoplasma fermentans* strain M64 reported in this paper has been deposited in the GenBank database under accession number NC_014921.

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**REFERENCES**


