Complete Genome Sequence of the Type Strain *Corynebacterium mustelae* DSM 45274, Isolated from Various Tissues of a Male Ferret with Lethal Sepsis

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The complete genome of *Corynebacterium mustelae* DSM 45274 comprises 3,474,226 bp and 3,188 genes. Prominent niche and virulence factors are SpaBCA- and SpaDEF-type pili with similarity to pilus proteins of *Corynebacterium resistens* and *Corynebacterium urealyticum* and an immunomodulatory EndoS-like endoglycosidase probably catalyzing the removal of distinct glycans from IgG antibodies.

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REFERENCES


