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GENOME ANNOUNCEMENT

# Draft Genome Sequence of *Corynebacterium bovis* DSM 20582, Which Causes Clinical Mastitis in Dairy Cows

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**Bovine mastitis represents the most economically important disease in dairy cows and can be caused by *Corynebacterium bovis*, a commensal in the bovine udder. The draft genome sequence provides insights into the adaptation of this bacterium to the bovine habitat and its lipolytic capabilities to utilize components of cow's milk.**

*Corynebacterium bovis* is frequently isolated from milk samples of infected mammary glands of dairy cows and is associated with reduced milk production (7). It is increasingly recognized as a cause of bovine mastitis in dairy cows, which is an economically important disease of dairy cattle worldwide (4). These bacterial infections are usually spread from cow to cow at milking, particularly if the standard of milking hygiene is low (2). Clinical mastitis therefore continues to be a severe problem in many dairy herds (2). A field study that aimed to describe the occurrence of clinical mastitis in dairy herds in Ontario, Canada, revealed that 19.8% of cows experienced at least one case of mastitis during lactation (4). Up to 30% of lactating cows of dairy farms in New York State showed typical symptoms of clinical mastitis (3). A much higher rate of clinical mastitis was determined in Estonian dairy herds, indicating that 52.7% of cows have inflammations in one or more quarters of the udder (2).

*C. bovis* DSM 20582 (ATCC 7715, NCTC 3224) was originally isolated from the bovine udder (1). Genomic DNA was purified from an overnight culture as described previously (5). The draft genome sequence of *C. bovis* DSM 20582 was generated using the 454 Genome Sequencer FLX System with Titanium technology, resulting in 106,124,403 detected bases and a 42-fold coverage of the genome. The respective 240,862 reads were assembled with the GS Assembler software (version 2.3) to yield 503 contigs. Subsequent bioinformatic analysis of the sequence data followed established protocols for corynebacterial genomes (5). Gaps in the genome sequence of *C. bovis* DSM 20582 are mostly located in DNA regions with very high G+C content, revealing the known limitations of pyrosequencing (6). The mean G+C content of the genome sequence is 72.55% and is thus 5% higher than previously reported (8). The draft genome of *C. bovis* DSM 20582 has a size of 2,522,962 bp and encodes 2,339 predicted proteins.

The reconstruction of metabolic pathways revealed distinct features of *C. bovis* that are associated with the natural habitat in the bovine udder. Relevant genes confer the capability to import and catabolize glucose, fructose, mannose, lactose, galactose, glycerol, and glycerol-3-phosphate and to utilize external caseins by proteolysis. The genome is moreover equipped with a remarkable repertoire of genes contributing to lipolysis, thereby playing an important role in the lipid-requiring lifestyle of *C. bovis*, in fatty acid degradation by β-oxidation, and the conversion of triacylglycerols and phosphoacylglycerols present in cow's milk and the bovine teat canal.

**Nucleotide sequence accession numbers.** The genome sequence has been deposited at GenBank under accession number AENJ00000000 and is available from the RefSeq database with accession number NZ_ AENJ00000000.

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