



# Draft Genome Sequences of *Macrococcus caseolyticus*, *Macrococcus canis*, *Macrococcus bohemicus*, and *Macrococcus goetzii*

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**ABSTRACT** Here, we present the draft genome sequences of 14 strains of 4 species of the genus *Macrococcus*. These strains were isolated from bovine milk and tongue samples obtained during a screening program.

Fourteen strains belonging to four members of the *Macrococcus* genus, namely, 3 *Macrococcus caseolyticus* strains (DPC 6291, DPC 7170, and DPC 7171), 7 *Macrococcus canis* strains (DPC 7158, DPC 7160, DPC 7162, DPC 7163, DPC 7165, DPC 7168, and DPC 7169), 3 *Macrococcus goetzii* strains (DPC 7159, DPC 7164, and DPC 7166), and 1 *Macrococcus bohemicus* strain (DPC 7215), were isolated from bovine milk and tongue by utilizing a *ctaC* PCR, as described previously (1). Recently emerging information regarding multidrug resistance and putative virulence genes present in species belonging to this genus prompted us to perform whole-genome sequencing (WGS) to investigate the presence of such genes in these *Macrococcus* strains (2–4).

The genomic DNA was isolated from overnight cultures grown at 37°C in tryptic soy broth (TSB; Becton, Dickinson and Company, Berkshire, England) using the UltraClean microbial DNA isolation kit (Mo Bio Laboratories, Cambridge, UK) as per the included protocol. Genomic libraries were prepared with a Nextera XT DNA library preparation kit (Illumina, Inc., San Diego, CA, USA). The 2 × 250-bp paired read sequencing was performed on an Illumina HiSeq 2500 platform (MicrobesNG, University of Birmingham, UK). Reads were adapter trimmed using Trimmomatic version 0.30, with a sliding window quality cutoff of Q15 (5). *De novo* assembly was performed on each sample using SPAdes version 3.7 with the program's default parameters (6). Detection of acquired antimicrobial resistance genes in the assembled genomes was analyzed using ResFinder version 3.4 and Resistance Gene Identifier (RGI) version 4.2.2 to search against the Comprehensive Antibiotic Resistance Database (CARD). Virulence genes were identified using VirulenceFinder version 2.0, PathogenFinder version 1.1, and the Virulence Factors Database (VFDB) (7–10). The genome sequences were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (11). The final draft genomes were estimated using CheckM (12) to be ≥96% complete with <2.5% contamination.

All sequenced genomes illustrated the presence of putative virulence factors, namely, hemolysin III (*hlyIII*), aureolysin (*aur*), and capsule (*cap*) genes. An RGI search of the homology models in CARD identified a total of 86 different antibiotic resistance genes, most of which are predicted to confer resistance to fluoroquinolone ( $n = 19$ ), macrolides ( $n = 26$ ), and tetracycline ( $n = 24$ ). The sequencing and assembly statistics of the draft genome sequences of the above-mentioned *Macrococcus* strains are shown

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**TABLE 1** Genome characteristics of the *Macrococcus* strains used in this study

| Organism                        | SRA accession no. | GenBank accession no. | Draft genome size (bp) | G+C content (%) | No. of contigs | Coverage (×) | $N_{50}$ (bp) |
|---------------------------------|-------------------|-----------------------|------------------------|-----------------|----------------|--------------|---------------|
| <i>M. caseolyticus</i> DPC 6291 | SRR8868656        | SDQM00000000          | 2,171,480              | 36.68           | 74             | 70           | 229,924       |
| <i>M. canis</i> DPC 7158        | SRR8868660        | SDQI00000000          | 2,179,466              | 36.75           | 69             | 197          | 578,934       |
| <i>M. goetzii</i> DPC 7159      | SRR8868665        | SDGN00000000          | 2,530,812              | 34.06           | 93             | 184          | 275,573       |
| <i>M. canis</i> DPC 7160        | SRR8868666        | SDQF00000000          | 2,148,516              | 36.58           | 37             | 136          | 413,516       |
| <i>M. canis</i> DPC 7162        | SRR8868667        | SDQG00000000          | 2,139,904              | 36.62           | 44             | 107          | 353,259       |
| <i>M. canis</i> DPC 7163        | SRR8868668        | SDQH00000000          | 2,167,812              | 36.63           | 79             | 147          | 417,178       |
| <i>M. goetzii</i> DPC 7164      | SRR8868659        | SDGO00000000          | 2,563,253              | 34.07           | 61             | 137          | 458,326       |
| <i>M. canis</i> DPC 7165        | SRR8868658        | SDGP00000000          | 2,165,327              | 36.68           | 72             | 158          | 1,280,134     |
| <i>M. goetzii</i> DPC 7166      | SRR8868662        | SDGQ00000000          | 2,591,067              | 34.16           | 95             | 202          | 466,093       |
| <i>M. canis</i> DPC 7168        | SRR8868661        | SDGR00000000          | 2,134,151              | 36.68           | 41             | 95           | 397,880       |
| <i>M. canis</i> DPC 7169        | SRR8868664        | SDGS00000000          | 2,160,199              | 36.56           | 89             | 264          | 1,113,524     |
| <i>M. caseolyticus</i> DPC 7170 | SRR8868655        | SDQK00000000          | 2,106,646              | 36.77           | 67             | 48           | 147,285       |
| <i>M. caseolyticus</i> DPC 7171 | SRR8868657        | SDQJ00000000          | 2,110,528              | 36.77           | 99             | 231          | 108,839       |
| <i>M. bohemicus</i> DPC 7215    | SRR8868663        | SELR00000000          | 2,555,877              | 33.98           | 55             | 160          | 234,144       |

in Table 1. The sequencing data contribute to the pool of available *Macrococcus* genomes and enable further generation of information regarding the presence of antibiotic resistance determinants and other virulence factors present in *Macrococcus* species.

**Data availability.** The draft WGS data were deposited into NCBI GenBank and the Sequence Read Archive (SRA) under the BioProject no. [PRJNA515496](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA515496). The accession numbers are listed in Table 1.

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