



# Draft Genome Sequences of *Enterobacter cloacae* Strains CAPREx E7 and CAPREx E2-2

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**ABSTRACT** *Enterobacter cloacae* strains CAPREx E7 and CAPREx E2-2 were isolated from Ghanaian yams at a London market. The draft genome sequences indicate that the two strains are similar, with genomes of 5,042,838 and 5,039,930 bp and 56.19% and 55.05% G+C content, respectively. Both strains encoded three different  $\beta$ -lactamases, including one of the AmpC family.

*Enterobacter cloacae* is a Gram-negative rod-shaped member of the family *Enterobacteriaceae*. *E. cloacae* strains are often associated with human infections, and many strains of *E. cloacae* carry  $\beta$ -lactamases or carbapenemases that confer antibiotic resistance (1). *E. cloacae* strains have also been isolated from plants, soil, and animals (2–5). Here, we report the genome sequences of two new strains of *E. cloacae*, CAPREx E7 and CAPREx E2-2, isolated from Ghanaian yams purchased from a London produce market. These strains were isolated from slices of yams that were grown on crystal violet pectate agar (6). Both strains were also able to grow at 30°C and 37°C on LB agar.

The draft genomes of both strains were generated by sequencing genomic DNA on Illumina MiSeq and HiSeq platforms using 2 × 250-bp paired-end reads. These reads were trimmed using Trimmomatic (7), assembled using SPAdes (8), and annotated using Prokka (9). The quality of the reads and assembly was also assessed using BWA-mem (10). The final assembly of CAPREx E7 contained 5,042,810 bp, with 56.19% G+C content, 4,712 open reading frames (ORFs), 78 tRNAs, and a mean coverage of 89.9×. The final assembly of CAPREx E2-2 contained 5,039,930 bp, with 55.05% G+C content, 4,720 ORFs, 78 tRNAs, and a mean coverage of 137.07×.

*E. cloacae* strains have been isolated from many sources, and a recent source of interest has been their resistance to antibiotics and presence in persistent bacterial infections. Both CAPREx E2-2 and CAPREx E7 contained a single copy of *ampC*, a gene encoding a clinically important  $\beta$ -lactamase in the cephalosporinase family (1, 11). Two class B metallo- $\beta$ -lactamases (MBLs) were also identified within each genome. The first, E7\_03710 (CAPREx E7) or E2\_03468 (CAPREx E2-2), showed high levels of similarity to a class B MBL in *Brenneria goodwinii*, a bacterium associated with oak trees (12), and *Erwinia toletana*, a bacterium associated with olive tree knots (13). The second class B MBL (E7\_04150 in CAPREx E7 or E2\_00247 in CAPREx E2-2) has previously been identified in many other *E. cloacae* strains but not in other plant-associated organisms.

We were also able to identify putative machinery for several secretion systems, including types I, II, IV, and VI. However, we were unable to identify any type III secretion machinery, although previous work in clinical *E. cloacae* samples found that only 27% contained type III secretion machinery (14). Secondary metabolite production can also be important in virulence. Both sequences contain genetic clusters predicted to encode the production machinery for the siderophore aerobactin (15, 16) and an arylpolyene similar to that produced by *Escherichia coli* (17).

The draft genomes of these two strains contain antibiotic resistance genes characteristic of other *E. cloacae* strains. However, some of their secondary metabolite clusters

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are most similar to those in plant-associated bacterial strains. Our hope is that these genomes will provide further help in elucidating the plant-associated life cycle of some *Enterobacter cloacae* strains.

**Accession number(s).** The draft genomes of these two strains have been deposited in GenBank under accession no. [MWME00000000](https://doi.org/10.2217/fmb.12.61) (CAPREx E2-2) and [MWMD00000000](https://doi.org/10.1128/JB.01790-12) (CAPREx E7).

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