



# Full Chloroplast Genome Sequence of the Economically Important Dietary Supplement and Spice *Curcuma longa*

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**ABSTRACT** *Curcuma longa* L. is a native species of Asia that is commonly known as turmeric. It is a spice also used in traditional medicine to treat a wide range of illnesses. Here, we present the fully annotated chloroplast genome of *Curcuma longa*.

*Curcuma longa* L., commonly known as turmeric, is a member of the ginger family (Zingiberaceae) native to Asia and widely cultivated in the tropics (1). Frequently used as a spice, *C. longa* also has a long history in Indian Ayurvedic medicine, in which it is used to treat maladies such as inflammation and wound care (2, 3). In the United States, turmeric is a popular dietary supplement, with a 46.7% increase in sales from 2016 to 2017 (4). While curcumin from turmeric is considered to be generally regarded as safe (GRAS) (5, 6), no products have as yet been granted approval as a drug by the FDA.

*Curcuma longa* was identified for inclusion in the U.S. Food and Drug Administration's repository of complete chloroplast genome sequences called GenomeTrakrCP (7) due to its ubiquity and established potential for adulteration (8).

An herbarium voucher specimen (J. Wen 13706) deposited at the United States National Herbarium, U.S. National Museum (USNM), originally collected from a plant cultivated at The Green Farmacy Garden (Fulton, MD, USA), was used. Genomic DNA was extracted from leaf tissue with a DNeasy plant minikit (Qiagen, Inc.). The DNA was sheared with an M220 sonicator (Covaris, Inc.) to obtain ~350-bp DNA fragments. A library was prepared from 100 ng of fragmented DNA with a HyperPrep kit (Kapa Biosystems) and Kapa dual-indexed adapters. Libraries were quantified and qualified on a Qubit 4 fluorometer (Invitrogen) and an Agilent 2100 Bioanalyzer. The library was sequenced with MiSeq technology (Illumina) to produce 2 × 300-bp paired-end reads. Raw reads were trimmed with Trimmomatic 0.36 within the illumiprocessor package (9, 10). A total of 2,311,343 reads with a Q30 of 71.1% were obtained.

A reference-guided assembly using the Bowtie short read mapper 7.2.1 (Biomatters) plugin through Geneious 9.1.8 (Biomatters) mapped 18,175 of 591,022 filtered reads to the reference chloroplast genome of *Curcuma roscoeana* Wall (GenBank accession number [KF601574](https://www.ncbi.nlm.nih.gov/nuccore/KF601574)). This produced a 159,497-bp contig. The genome was annotated against that of *C. roscoeana* using the "annotate from database" tool in Geneious. Inverted repeats were identified with the Geneious repeat finder plugin (Biomatters). Open reading frames (ORFs) were identified for each protein coding sequence using translation and ORF tools within Geneious.

The annotated *C. longa* chloroplast genome contains 159,550 bp with a GC content of 36.3%. The  $N_{50}$  contig length is 17,875 bp. Inverted repeats (IRs) are separated by large single-copy (LSC) and small single-copy (SSC) regions with sizes of 87,058 bp and 18,542 bp, respectively. A total of 125 genes with 86 coding sequences, 38 tRNA genes, and 8 unique rRNA sequences were identified.

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**Data availability.** Raw sequence data and the assembly were deposited in the NCBI Sequence Read Archive (accession number [SRS4339451](#)) and GenBank (accession number [MK919702](#)) as part of the FDA GenomeTrakrCP: chloroplast DNA for botanical product identification (BioProject [PRJNA325670](#)) (7).

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