



Chloroplast Genome Sequence of *Arabidopsis thaliana* Accession Landsberg *erecta*, Assembled from Single-Molecule, Real-Time Sequencing Data

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A publicly available data set from Pacific Biosciences was used to create an assembly of the chloroplast genome sequence of the *Arabidopsis thaliana* genotype Landsberg *erecta*. The assembly is solely based on single-molecule, real-time sequencing data and hence provides high resolution of the two inverted repeat regions typically contained in chloroplast genomes.

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Arabidopsis thaliana is the most used model organism in plant genetics. During the last decades, various genotypes of *A. thaliana* have been sequenced using different sequencing technologies (1, 2). With third-generation sequencing technologies entering the market, novel techniques for DNA sequence generation have become available. The *Ler-0* genotype is currently the second most widely used accession of *A. thaliana* behind Columbia Col-0. The latest published *Ler-0* genome assembly used reads created by third-generation sequencing along with reads from other sources to create a high-quality nuclear genome assembly (3). One of the new technologies is single-molecule, real-time (SMRT) sequencing (4) developed by Pacific Biosciences, which is sometimes referred to as “PacBio sequencing”. This sequencing technology allows long read lengths up to the 20- to 60-kb range, allowing single reads to span long repetitive elements or regions. The typical chloroplast genome contains two of these long (~26 kb) repeat regions, with the additional feature that the two regions are inverted repeats (IR) of each other. These IRs are hard to assemble using only short-read data from next-generation sequencing methods.

Recently, we described an approach to assemble a chloroplast genome based on an SMRT sequencing data set originally dedicated to sequencing a nuclear genome (5). We applied this approach to data from a single SMRT cell obtained from a publically available SMRT sequencing data set for *Arabidopsis thaliana* *Ler-0* provided by Pacific Biosciences (6). Sequence reads from sample number SAMN02724977 created by P5-C3 chemistry were used. We followed our protocol for identification of potential chloroplast reads, assembly, alignment, and polishing as described previously (5) with one exception: instead of using the spinach chloroplast genome sequence (7) as a template for read extraction, we used the chloroplast genome sequence of the *Arabidopsis thaliana* Col-0 genotype (8). We extracted 11,016 sub-reads summing up to 90,383,214 bp. The assembly resulted in a sequence with overlapping ends, and hence we assume that the chloroplast genome sequence is complete. We removed the addi-

tional overlap and aligned the sequence to the standard starting position of chloroplast genome sequences. The resulting assembly, designated *Ler0_cp_smrt*, has a total length of 154,515 bp and differs in 111 positions from the Col-0 chloroplast genome sequence (AP000423.1). We annotated the genome using CpAVAS (9) and identified 123 genes. Of these, 85 genes encode mRNA (i.e., proteins), 8 encode rRNA, and 30 encode tRNA.

Accession number(s). The complete sequence of the *Arabidopsis thaliana* *Ler-0* chloroplast genome was deposited in GenBank under accession number [KX551970](https://www.ncbi.nlm.nih.gov/GenBank/ accession/KX551970).

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