GENOME ANNOUNCEMENT

Genome Sequence of the Wolbachia Endosymbiont of Culex quinquefasciatus JHB

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Wolbachia species are endosymbionts of a wide range of invertebrates, including mosquitoes, fruit flies, and nematodes. The wPip strains can cause cytoplasmic incompatibility in some strains of the Culex mosquito. Here we describe the genome sequence of a Wolbachia strain that was discovered in the whole-genome sequencing data for the mosquito Culex quinquefasciatus strain JHB.

The wPip Culex quinquefasciatus strain JHB genome was sequenced as a serendipitous artifact of the Culex sequencing project, just as several previous Wolbachia species were found in Drosophila sequencing data (5). We separated the bacterial data from the mosquito data and assembled a virtually complete genome of the endosymbiont. The final assembly contains 21 contiguous DNA segments containing 1,542,137 nucleotides. Our annotation found 1,378 protein-coding genes, 34 tRNA genes, and one rRNA operon.

We used all the raw sequences (“reads”) from the Culex quinquefasciatus genome (Johannesburg strain; JHB) sequencing project as of September 2007. These comprised 7,379,314 reads, all generated by capillary sequencing. As a reference genome, we used the Wolbachia endosymbiont of Culex quinquefasciatus Pel that was recently sequenced (GenBank accession no. AY072044) (2). We aligned all whole-genome shotgun reads to the reference genome using MUMmer (minimum match of 65 bp at 80% identity) (3) in order to extract reads of bacterial origin. For each bacterial read, we also extracted its match of 65 bp at 80% identity (3) in order to extract reads of bacterial origin. We assembled the reads with the Celera Assembler (4) using default parameters except for the unitig error rate, which was set to 2%. The assembler generated 16 scaffolds containing 21 contigs and 92 additional contigs flagged as low quality by the assembler. We ran further analyses to eliminate nonbacterial contigs and to eliminate near-identical contigs that appeared to represent population variants within the original DNA sample, as were also observed by Klasson et al. (2). The final assembly contains 21 contigs (the largest was 478,325 bp) in a single scaffold, with an average depth of coverage of 14×. Scaffolding utilized both the original mate-pair constraints and the organization of the wPip reference genome.

The JHB strain is very similar to the previously sequenced Pel strain; however, there are several areas of differences. JHB contains four unique regions not found in Pel, with lengths of 524, 565, 640, and 524 bp. One of these regions contains the gene for the DNA repair protein Radc, and another contains a transcripational regulator gene, both with homologs in Wolbachia dMel. The wPip Pel genome contains two regions not found in strain JHB, which are 856 bp and 120 bp in length.

There are 10 large-scale rearrangements distinguishing the genomes, in which large segments of the chromosome have been inverted. Some of these are associated with IS elements from the IS250 family. The greater number of protein-coding genes in wPip JHB—1,378 versus 1,248 in wPip Pel—appears to be due to differences in annotation methods, although both projects used the Glimmer (1) gene finder.

Nucleotide sequence accession number. The genome sequence of the Wolbachia endosymbiont of Culex quinquefasciatus JHB has been deposited at GenBank/EMBL/DDBJ under accession no. ABZA00000000.

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REFERENCES