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High-Quality Genome Sequence of the Root-Knot Nematode *Meloidogyne arenaria* Genotype A2-O

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ABSTRACT Root-knot nematodes (*Meloidogyne* spp.) cause serious damage to many crops globally. We report the high-quality genome sequence of *Meloidogyne arenaria* genotype A2-O. The genome assembly of *M. arenaria* A2-O is composed of 2,224 contigs with an N_{50} contig length of 204,551 bp and a total assembly length of 284.05 Mb.

Plant-parasitic nematodes are some of the most agriculturally important pests, causing estimated global losses of $80 billion per year (1). Among plant-parasitic nematodes, mitotic parthenogenetic root-knot nematodes (RKNs) (i.e., *Meloidogyne incognita*, *Meloidogyne arenaria*, and *Meloidogyne javanica*) are obligatory parasites which are remarkably widespread geographically (1, 2). These asexual RKNs have a broader host range and are more devastating than sexual species of RKNs (3). RKNs invade roots and induce redifferentiation of root cells to form "giant cells," which serve as a specialized nutrient source for the parasites. The nematodes develop into adult females which lay eggs in a gelatinous matrix on the root surface.

Several genomes of agriculturally important RKN species have been sequenced using short-read sequencers (4–8). The genomes of asexual *Meloidogyne* species are polyploid and consist of duplicated regions with a high nucleotide divergence (~8%) (4, 7, 8). Moreover, the genomes of asexual *Meloidogyne* species contain more transposable elements (TEs) than the sexual *Meloidogyne hapla* genome. These features might confer genomic plasticity and functional divergence between gene copies in the absence of sex and meiosis. However, these genomic features make it technically difficult to generate contiguous assemblies using short reads. In fact, the reported genome assemblies of the asexual *Meloidogyne* species, such as *M. incognita*, *M. arenaria*, and *M. javanica*, are highly fragmented compared to the *M. hapla* genome assembly (5, 7). To overcome this problem, we applied single-molecule real-time (SMRT) sequencing technology with the PacBio RS II platform (Pacific Biosciences, CA, USA) to sequence the genome of *M. arenaria* genotype A2-O, isolated in Izu Oshima Island in Japan (9). For the preparation of genomic DNA, infective second-stage juveniles of *M. arenaria* A2-O hatched from sterilized eggs were collected by sucrose flotation. Collected nematodes were ground down, and their genomic DNA was extracted using Genomic-tips (Qiagen, Hilden, Germany). The SMRTbell template prep kit 1.0 (Pacific Biosciences) was used to prepare 20-kb insert PacBio libraries. Then, size selection was performed with a 15-kb cutoff using Blue Pippin (Sage Science, MA, USA).

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We generated an approximately 60-fold whole-genome shotgun sequence using P6-C4 chemistry on the PacBio RS II platform. A total of 754,356 reads (9.6 Gb) were assembled with Canu v1.3 (10), and the contigs were polished with Quiver (SMRT Analysis suite v2.3, Pacific Biosciences) (11). The assembled genome contains 2,224 contigs (all of the contigs are greater than 500 bp) with an N_{50} contig length of 204,551 bp and a total length of 284.05 Mb. The assembly was estimated to cover 94.76% of the coding space according to Core Eukaryotic Genes Mapping Approach (CEGMA) analysis (12) and is more contiguous than the previously published *M. arenaria* genome (7), with 14-fold fewer contigs and a 12.9-fold increased N_{50} contig length. This long-read-based high-quality assembly of *M. arenaria* should promote identification of virulence-related genes that often exist in repeat-rich or highly variable regions in the genome (13).

Accession number(s). The sequences obtained by this whole-genome shotgun project have been deposited in DDBJ/ENA/GenBank under the accession number QEUI00000000.

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