



# Draft Genome Sequence of the Nylon Oligomer-Degrading Bacterium *Arthrobacter* sp. Strain KI72

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**ABSTRACT** We report here the 4.6-Mb genome sequence of a nylon oligomer-degrading bacterium, *Arthrobacter* sp. strain KI72. The draft genome sequence of strain KI72 consists of 4,568,574 bp, with a G+C content of 63.47%, 4,372 coding sequences (CDSs), 54 tRNAs, and six rRNAs.

The genus *Arthrobacter* was first proposed as *Arthrobacter globiformis* by Conn and Dimmick (1). *Arthrobacter* sp. strain KI72 is a Gram-positive aerobic rod bacterium which is able to grow on 6-aminohexanoic acid (Ahx) oligomer (designated nylon oligomer, a by-product of nylon-6 manufacture) as the sole source of carbon and nitrogen. With regard to the enzymatic system responsible for the metabolism of the unnatural amide compounds, we have been studying the degradation of Ahx oligomers by strain KI72 as the model system (2–10). The strain KI72 harbors three kinds of plasmids, pOAD1 (39.7 kbp), pOAD2 (43.6 kbp), and pOAD3 (56.3 kbp). Previous biochemical studies have revealed that three enzymes encoded on pOAD2, NylABC, are responsible for the degradation of Ahx oligomers to monomer form (2–6). The Ahx cyclic dimer hydrolase (NylA; EC 3.5.2.12), a member of the amidase signature hydrolase family, specifically hydrolyzes one of the two amide bonds in the Ahx cyclic dimer, generating an Ahx linear dimer (7). The Ahx dimer hydrolase (NylB; EC 3.5.1.46), a member of the penicillin-recognizing family of serine reactive hydrolases, hydrolyzes Ahx oligomers by an exo-type mode (8, 9). The Ahx oligomer hydrolase (NylC; EC 3.5.-.-) degrades Ahx cyclic and linear oligomers with a degree of polymerization greater than three by an endo-type mode (10). Moreover, we have revealed the three-dimensional structures of NylABC by X-ray crystallographic analyses (7–10). Recently, we found that a thermostable NylC mutant enzyme degrades various aliphatic nylons (11). Here, we present the draft genome sequence of *Arthrobacter* sp. strain KI72 to better understand the metabolism of nylons and their related compounds.

The genome of strain KI72 was sequenced using a shotgun reads obtained on a HiSeq sequencer (Illumina). A total of 78,562,074 reads with an average length of 50.00 nucleotides (~858.3-fold coverage) were used for genome assembly by the Edena assembler version 3 (Genomic Research Laboratory) (12). A total of 105 contigs of >100 bp in length were constructed, with an  $N_{50}$  of 143.01 kb; the largest contig assembled measured 372.75 kbp. The final draft genome sequence consists of 4,568,574 bp, and Microbial Genome Annotation Pipeline (MiGAP) was used for genome annotation (13). The draft genome of strain KI72 contains 4,372 coding sequences (CDSs), 54 tRNAs, and six rRNAs, and the G+C content was 63.47%.

The complete annotated genome sequence shows that strain KI72 contains genes encoding a novel NylC-like amidehydrolase. Also, we find the genes which encode 4-aminobutyrate aminotransferase, succinate semialdehyde dehydrogenase, acyl-coenzyme A (acyl-CoA) dehydrogenase, enoyl-CoA hydratase, 3-hydroxyacyl-CoA de-

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hydrogenase, and acetyl-CoA acyltransferase, which are predicted to be relevant to the subsequent degradation of nylon monomer.

**Accession number(s).** This whole-genome shotgun project has been deposited at DDBJ/EMBL/Genbank under the accession number [BDMH00000000](https://www.ncbi.nlm.nih.gov/nuclseq/BDMH00000000).

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