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Finished Genome Sequence of *Collimonas arenae* Cal35

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We announce the finished genome sequence of soil forest isolate *Collimonas arenae* Cal35, which comprises a 5.6-Mbp chromosome and 41-kb plasmid. The Cal35 genome is the second one published for the bacterial genus *Collimonas* and represents the first opportunity for high-resolution comparison of genome content and synteny among collimonads.

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Collimonads are oligotrophic, chitinolytic, rhizosphere-competent soil bacteria with antifungal, mycophagous, and mineral-weathering properties (1). To date, three species of *Collimonas* have been described (2, 3), but the only *Collimonas* genome available is that of the Dutch dune soil isolate *C. fungivorans* Ter331 (*CfTer331*, GenBank accession no. CP002745 for the chromosome and EU315244 for plasmid pTer331). The *CfTer331* genome has been instrumental in describing the *Collimonas* chitinolytic system (4), the genes underlying the production of antifungal polyene-like compounds called collimomycins (5), the molecular interactions with model fungus *Aspergillus niger* (6), and the phenotypic variation among other collimonads isolated from the same dune soil as Ter331 (7). However, with only one *Collimonas* genome sequence available to date, intrgeneric comparison at single-nucleotide resolution has not yet been feasible. Here, we report the finished genome sequence of *Collimonas arenae* Cal35 (*CaCal35*), which was recovered from a forest soil in California (8).

Genomic DNA of *CaCal35* was extracted from an overnight culture using a DNeasy Blood and Tissue kit (QIAGEN, Valencia, CA). A 10-kb PacBio RS II-compatible library was constructed by the UC Davis Genome Center and sequenced on 3 single-molecule real-time (SMRT) cells using P4-C2 chemistry. *De novo* assembly was performed with the help of SMRT Analysis software v2.2.0 (Pacific Biosciences) featuring HGAP 2 (9), and subsequent correction with quiver in addition to Gelpard v1.30 (10) to reveal two circular replicons: a 5,603,532-bp chromosome (G+C content 56.15%; 85.54× coverage) and a 41,440-bp plasmid (G+C content 50.54%; 73.21× coverage) which we designated pCal35. Gene prediction by RAST (11) revealed 5,019 coding sequences, 54 tRNA genes, and 3 rRNA operons (5S, 16S, 23S) on the chromosome, in addition to 57 coding sequences on pCal35.

The chromosome of *CaCal35* appears mostly syntenic with that of *CfTer331*, with the exception of one 2.75-Mbp inversion centered on the origin of replication. *CaCal35* shares 69% of its genes with Ter331, of which 80% are >80% identical at the predicted amino acid level. The chitinolytic system of *CaCal35* is very similar to that of *CfTer331*, but *CaCal35* possesses at least two

additional chitinase genes. Clearly missing from the *CaCal35* genome is gene cluster K which is responsible for the production of collimomycins (5–7). Interestingly, in *CfTer331*, this gene cluster is located near one of the chromosome inversion points. Unrelated to pTer331 (12), plasmid pCal35 carries several genes with high coding similarity to plasmids from plant-pathogenic species of *Xanthomonas* (for example, pXAC64, pXCV38, pXcB) and *Ralstonia* (pRSC35). In addition, it harbors a stretch of DNA with high similarity to plasmid 2 from *Polaromonas* JS666 and coding for tRNA 2-selenouridine synthase, alkane 1-monooxygenase, and a LuxR-type regulator.

Nucleotide sequence accession numbers. The Cal35 chromosome and plasmid sequences are available under GenBank accession numbers [CP009962](https://www.ncbi.nlm.nih.gov/nuccore/CP009962) and [CP009963](https://www.ncbi.nlm.nih.gov/nuccore/CP009963), respectively.

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Assembly and annotation of the *CaCal35* genome sequence were performed by V.C.L.d.J. and J.H.J.L. (in the lab of J.H.J.L., visiting from the group of W.-L.D. as part of the ongoing UCD-NCHU collaboration). Interpretation of the annotation data was done by J.H.J.L., who also drafted the manuscript with inputs, edits, and final approval by all other authors. This is NIOO-KNAW publication number 5741.

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