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Permanent Draft Genome Sequence of *Frankia* sp. Strain ACN1^{ag}, a Nitrogen-Fixing Actinobacterium Isolated from the Root Nodules of *Alnus glutinosa*

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***Frankia* strain ACN1^{ag} is a member of *Frankia* lineage Ia, which are able to re-infect plants of the *Betulaceae* and *Myricaceae* families. Here, we report a 7.5-Mbp draft genome sequence with a G+C content of 72.35% and 5,687 candidate protein-encoding genes.**

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Among the *Actinobacteria*, the genus *Frankia* is well known for its facultative lifestyle as a plant symbiont of dicotyledonous plants, termed actinorhizal plants, and as a free-living soil dweller (1–3). Actinorhizal plants are ecologically important pioneer community plants that are found worldwide in a broad range of ecological and environmental conditions (4). The symbiosis allows actinorhizal plants to colonize harsh environmental terrains. The genus *Frankia* has not yet been described to the species level, but it has become an area of greater interest. Four major *Frankia* lineages have been identified (5–8), and genomes for representatives from each cluster have been sequenced (9–21).

Cluster I contains two subclusters: one subcluster (Cluster Ia) represents *Frankia* strains with the ability to infect a wider range of host plants, including member of the *Betulaceae* and *Myricaceae* families, and the other subcluster (Cluster Ib) contains strains limited to *Casuarina* and *Allocasuarina* host plants. As another member of Cluster Ia, *Frankia* sp. strain ACN1^{ag} was chosen for sequencing to provide more information on this lineage and its interaction with actinorhizal plants. *Frankia* sp. strain ACN1^{ag} is a re-isolate from root nodules of *Alnus glutinosa* inoculated from an isolate of *Alnus viridis crispa* collected from Atikokan, Ontario, Canada (22, 23).

The draft genome of *Frankia* sp. strain ACN1^{ag} was generated at the Hubbard Genome Center (University of New Hampshire, Durham, NH, USA) using Illumina technology (24) techniques. A standard Illumina shotgun library was constructed and sequenced using the Illumina HiSeq2000 platform, which generated 14,474,194 reads (260-bp insert size) totaling 2,127.7 Mbp. The Illumina sequence data were assembled using CLC Genomics Workbench version 8.0.1 and AllPaths-LG version r41043 (25). The final draft assembly contained 108 contigs with an N_{50} of 157.4 kb. The total size of the genome is 7.5 Mbp, and the final assembly is based on 2,127.17 Mb of Illumina draft data and provided an average 220× coverage of the genome.

The high-quality draft genome of *Frankia* sp. strain ACN1^{ag} was resolved to 108 contigs consisting of 7,505,639 bp with a G+C content of 72.35%. The assembled *Frankia* sp. strain ACN1^{ag} genome was annotated via the Integrated Microbial Genomes (IMG) platform developed by the Joint Genome Institute, Walnut Creek, CA, USA (26, 27), and resulted in 5,687 candidate protein-encoding genes, 45 tRNA genes, and 2 rRNA regions.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number LJPA00000000. The version described in this paper is the first version, LJPA01000000.

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