**Genome Sequence of the Soybean Symbiont *Sinorhizobium fredii* HH103**

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*Sinorhizobium fredii* HH103 is a fast-growing rhizobial strain with a generation time of about 3 to 4 h, which was isolated from Chinese soil from Hubei Province (3). The strain is able to form nodules on agronomically advanced soybean cultivars (3, 7). Competition studies revealed that in an acid soil the slow-growing *Bradyrhizobium japonicum* strain 110 outcompetes HH103, whereas in alkaline soils most of the nodules are colonized by HH103 (2). Besides soybean, which forms determinate nodules, HH103 infects a number of other legumes, including *Glycyrrhiza uralensis*, which develops indeterminate nodules (1, 7). *Sinorhizobium fredii* HH103 is closely related to *Rhizobium* sp. strain NGR234, which develops indeterminate nodules (1, 7). *Sinorhizobium fredii* HH103 is the best-studied fast-growing soybean symbiont. Its genome sequence will expose further details about the genetic basis of growth properties, symbiotic interaction, and host range, which are relevant for agriculture.

For whole-genome sequencing, the GS FLX system (Roche Diagnostics) was used. Shotgun (GS FLX Titanium) and long paired-end (GS FLX standard) sequencing resulted in a 37-fold genome coverage. Reads were assembled with the Newbler software (Roche Diagnostics), which gave rise to 59 scaffolds and 241 contigs. For gap closure, a fosmid library was prepared. By sequencing of 1,114 insert ends, about 90 PCR products, and by using about 350 primer walkings (ABI 3730xl DNA analyzer), five out of six replicons could be finished completely using the Consed (4) software package. Due to a high abundance of repeated sequences, five gaps remain in the symbiotic plasmid pSfHH103d. For an automated annotation of the genome, GenDB was used (8). Replicon sizes (and G+C content) of the chromosome and the plasmids pSfHH103a, pSfHH103b, pSfHH103c, pSfHH103d, and pSfHH103e are 4,305,723 bp (62.61%), 24,036 bp (58.21%), 61,880 bp (58.47%), 144,082 bp (58.68%), ca. 589.4 kb (59.55%), and 2,096,125 bp (62.38%), respectively. The chromosome consists of 3,955 protein-coding sequences as well as 53 tRNA and 3 rRNA loci. The symbiotic plasmid pSfHH103d encodes all of the known nodulation (besides nolR) and nitrogen fixation proteins as well as a type III secretion system. Genes involved in K-antigen capsular polysaccharide, lipopolysaccharide, and exopolysaccharide synthesis are located on the largest plasmid, pSfHH103e, and on the chromosome. Genome comparisons done with the MUMmer package (6) revealed a high degree of synteny of the chromosome and the largest plasmid to the corresponding replicons of *Rhizobium* sp. NGR234. Synteny is much less pronounced with the symbiotic plasmids of both strains. The two smallest plasmids (pSfHH103a and pSfHH103b) encode several transposases and proteins needed for plasmid maintenance. The low G+C content of these plasmids, which is similar to that of pSfHH103c, suggests that they were acquired by horizontal transfer.

**Nucleotide sequence accession numbers.** The nucleotide genome sequence of *S. fredii* HH103 has been deposited in the EMBL Nucleotide Sequence Database (EMBL-Bank) under accession numbers HE616890 to HE616899.

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**REFERENCES**