Sinorhizobium meliloti is the symbiotic partner of legumes of the genera Medicago, Melilotus, and Trigonella. The genomes of most of the legume symbionts are organized into several replications and it has been proposed that these multipartite genomes and the genomic plasticity resulting from the presence of repetitive elements may be an ecological advantage, increasing the adaptive potential of these bacteria (1, 2). These repetitive elements include group II introns, a collection of self-splicing catalytic RNAs and retroelements (3, 4) widespread in bacteria (5). The genome sequences of seven S. meliloti strains are publicly available (6–11).

RmInt1 is a mobile group II intron that is widespread in natural populations of Sinorhizobium meliloti and was first described in the GR4 strain (12). This intron is generally associated with and controls (GOLD) (23). GS FLX data processing was performed with Roche 454 GS FLX Titanium platform (Roche Diagnostics) at MACROGEN, Seoul, Korea (18, 19). This RMO17 strain was confirmed to be a strain of S. meliloti by 16S rRNA sequencing and analyses of other taxonomic and phenotypic traits (20). Despite the presence of a large number of copies of the ISrnm11-2 element (12, 17, 21, 22), RMO17 is an RmInt1-less strain (17, 21).

We report the complete genome sequence of the RmInt1 group II intronless Sinorhizobium meliloti strain RMO17 isolated from Medicago orbicularis nodules from Spanish soil. The genome consists of 6.73 Mb distributed between a single chromosome and two megaplasmids (the chromid pSymB and pSymA).

The genome was annotated with the NCBI Prokaryotic Genome Annotation Pipeline. Replicon sizes and G+C contents were 3,649,532 bp (62.7%) for the chromosome, 1,610,737 bp (62.4%) for the chromid (pSymB), and 1,466,845 bp (60.4%) for the megaplasmid (pSymA). The complete genome consists of 6,136 protein-coding sequences. As in other S. meliloti genomes, three complete rrn operons were identified on the chromosome and there are 54 tRNA loci.

The complete sequence of this particular strain provides us with an opportunity to explore the evolutionary history of the presence and acquisition of group II introns and their relationship to the plasticity of complex bacterial genomes.

Nucleotide sequence accession numbers. The nucleotide sequences of the three replicons of the S. meliloti RMO17 genome have been deposited in the GenBank database under accession numbers CP009144 to CP009146.

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RMO17 was isolated by Encarna Velázquez (University of Salamanca).

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