Genome sequence of the South American clover-nodulating *Rhizobium leguminosarum* bv. *trifolii* strain WSM597

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*Rhizobium leguminosarum* bv. *trifolii* strain WSM597 is an aerobic, motile, Gram-negative, non-spore-forming rod isolated from a root nodule of the annual clover *Trifolium pallidum* L. growing at Glencoe Research Station near Tacuarembo, Uruguay. This strain is generally ineffective for nitrogen (N\(_2\)) fixation with clovers of Mediterranean, North American and African origin, but is effective on the South American perennial clover *T. polymorphum* Poir. Here we describe the features of *R. leguminosarum* bv. *trifolii* strain WSM597, together with genome sequence information and annotation. The 7,634,384 bp high-quality-draft genome is arranged in 2 scaffolds of 53 contigs, contains 7,394 protein-coding genes and 87 RNA-only encoding genes, and is one of 20 rhizobial genomes sequenced as part of the DOE Joint Genome Institute 2010 Community Sequencing Program.

Introduction

A key factor which limits the productivity of agricultural systems is the availability of soil nitrogen (N). Legumes can overcome soil N limitations by forming symbiotic relationships with root nodule bacteria (rhizobia). Rhizobia, through their interaction with legumes, are able to reduce atmospheric dinitrogen (N\(_2\)) into ammonia, which can supply essential N for growth to the plant. In addition, much of this fixed N is subsequently released into the soil following plant senescence and decay, grazing by livestock or human harvest [1], thereby increasing soil N content and fertility for subsequent crops. Thus, biological N\(_2\) fixation forms a vital component of sustainable agriculture as it provides a means of ameliorating N-deficient soils without the need for industrially synthesized N-based fertilizers, the production and application of which have significant environmental and economic costs [2].

Forage and fodder legumes play an integral role in sustainable farming practice, providing feed for stock while also enriching soil with available N. Worldwide, there are approximately 110 million ha of forage and fodder legumes under production [3], of which *Trifolium* spp. (clover) are of key importance [4]. The bacterial microsymbionts that nodulate clovers are *Rhizobium leguminosarum* bv. *trifolii*. Since *Trifolium* spp. are geographically widely distributed and are also phenologically variable (i.e. they may be either annual [e.g. *T. subterraneum*, *T. pallidum* and *T. scutatum*] or perennial [e.g. *T. pratense*, *T. repens* and *T. polymorphum*]), it is rare that a single strain of *R. leguminosarum* bv. *trifolii* can effectively fix N\(_2\) across a wide diversity of clovers [5].
Rhizobium leguminosarum bv. trifolii strain WSM597 was isolated from the nodules of Trifolium pallidum, which were collected from the INIA Glencoe Research Station, Uruguay in 1999. WSM597 is able to nodulate (Nod+) and fix (Fix+) N₂ effectively on the South American perennial clover Trifolium polymorphum. However, while WSM597 is able to nodulate Trifolium polymorphum and other annual and perennial Trifolium spp. of Mediterranean, African and North American origin, it is not effective for N₂ fixation on any of these hosts (Yates et al., unpublished data). Therefore, WSM597 is highly specific for effectiveness in symbiosis, as is also evident with the recently sequenced South American clover microsymbiont R. leguminosarum bv. trifolii WSM2304 [6]. Thus, both microsymbionts demonstrate that phenological and geographic barriers exist for effective nodulation in clover symbioses. As this phenotype represents a common challenge to managing the legume-rhizobial symbiosis in agriculture, the genome of WSM597 is a valuable comparator for genetic studies of nodulation and N₂ fixation. Here we present a summary classification and a set of general features for R. leguminosarum bv. trifolii strain WSM597 together with a description of the genome sequence and annotation.

### Classification and general features

R. leguminosarum bv. trifolii strain WSM597 is a motile, Gram-negative rod (Figure Left and Center) in the order Rhizobiales of the class Alphaproteobacteria. It is fast growing in laboratory culture, forming colonies within 3-4 days when grown on half Lupin Agar (½LA) [7] at 28°C. Colonies on ½LA are white-opaque, slightly domed, moderately mucoid with smooth margins (Figure 1 Right). Minimum Information about the Genome Sequence (MIGS) is provided in Table 1. Figure 2 shows the phylogenetic neighborhood of R. leguminosarum bv. trifolii strain WSM597 in a 16S rRNA sequence based tree. This strain clusters closest to Rhizobium leguminosarum bv. trifolii T24 and Rhizobium leguminosarum bv. phaseoli RRE6 with 99.9% and 99.8% sequence identity, respectively.

### Symbiotaxonomy

R. leguminosarum bv. trifolii WSM597 nodulates (Nod+) and fixes N₂ effectively (Fix+) with the South American perennial clover T. polymorphum. However, WSM597 is ineffective on perennial clovers of North American (T. reflexum and T. amabile) and African origin (T. sempisoum). WSM597 is also ineffective on a range of Mediterranean annuals (T. resupinatum, T. clusii, T. michelianum, T. isthmocarpum, T. scutatum, T. incarnatum, T. tomentosum), including its host of origin T. pallidum and the North American annual T. bejariense (Yates, R., pers. comm.).

### Genome sequencing and annotation information

#### Genome project history

This organism was selected for sequencing on the basis of its environmental and agricultural relevance to issues in global carbon cycling, alternative energy production, and biogeochemical importance, and is part of the Community Sequencing Program at the U.S. Department of Energy, Joint Genome Institute (JGI) for projects of relevance to agency missions. The genome project is deposited in the Genomes OnLine Database [25] and an improved-high-quality-draft genome sequence in IMG. Sequencing, finishing and annotation were performed by the JGI. A summary of the project information is shown in Table 2.
**Table 1.** Classification and general features of *Rhizobium leguminosarum* bv. *trifolii* strain WSM597 according to the MIGS recommendations [8].

| MIGS ID | Property                      | Term                      | Evidence code            |
|---------|-------------------------------|---------------------------|--------------------------|
|         | Domain                        | Bacteria                  | TAS [9]                  |
|         | Phylum                        | Proteobacteria            | TAS [10]                 |
| Current classification | Class                        | Alphaproteobacteria       | TAS [11,12]              |
|         | Order                         | Rhizobiales               | TAS [12,13]              |
|         | Family                        | Rhizobiaceae              | TAS [14,15]              |
|         | Genus                         | Rhizobium                 | TAS [14,16-19]           |
|         | Species                       | *Rhizobium leguminosarum* bv. *trifolii* | IDA [14,16,19,20] |
| Gram stain |                               | Negative                  | IDA                      |
| Cell shape |                               | Rod                       | IDA                      |
| Motility |                               | Motile                    | IDA                      |
| Sporulation |                             | Non-sporulating           | NAS                      |
| Temperature range |                         | Mesophile                 | NAS                      |
| Optimum temperature |                       | 28°C                      | NAS                      |
| MIGS-22 | Oxygen requirement            | Aerobic                   | NAS                      |
| Carbon source |                           | Varied                    | IDA                      |
| Energy source |                           | Chemoorganotroph         | NAS                      |
| MIGS-6 | Habitat                       | Soil, root nodule on host | IDA                      |
| MIGS-15 | Biotic relationship          | Free living, symbiotic    | IDA                      |
| MIGS-14 | Pathogenicity                | Non-pathogenic            | NAS                      |
| Biosafety level |                 | 1                         | TAS [21]                 |
| Isolation |                               | Legume root nodule       | IDA                      |
| MIGS-4 | Geographic location           | Tacuarembó, Uruguay       | IDA                      |
| MIGS-5 | Nodule collection date        | 1999                      | IDA                      |
| MIGS-4.1 | Longitude                   | -56                       | IDA                      |
| MIGS-4.2 | Latitude                    | -31.41                    | IDA                      |
| MIGS-4.3 | Depth                       | 5 cm soil depth           | IDA                      |
| MIGS-4.4 | Altitude                    | 130 m                     | IDA                      |

Evidence codes – IDA: Inferred from Direct Assay (i.e. first time published); TAS: Traceable Author Statement (i.e., a direct report exists in the literature) NAS: Non-traceable Author Statement (i.e., not directly observed for the living, isolated sample, but based on a generally accepted property for the species, or anecdotal evidence). These evidence codes are from the Gene Ontology project [22].
Figure 2. Phylogenetic tree showing the relationships of *Rhizobium leguminosarum* bv. *trifolii* strain WSM597 (shown in blue print) with some of the root nodule bacteria in the order *Rhizobiales* based on aligned sequences of the 16S rRNA gene (1,307 bp internal region). All sites were informative and there were no gap-containing sites. Phylogenetic analyses were performed using MEGA, version 5.05 [23]. The tree was built using the maximum likelihood method with the General Time Reversible model. Bootstrap analysis [24] with 500 replicates was performed to assess the support of the clusters. Type strains are indicated with a superscript T. Strains with a genome sequencing project registered in GOLD [25] are in bold print and the GOLD ID is mentioned after the accession number. Published genomes are designated with an asterisk.
Table 2. Genome sequencing project information for Rhizobium leguminosarum bv. trifolii strain WSM597.

| MIGS ID | Property                  | Term                                                                 |
|---------|---------------------------|----------------------------------------------------------------------|
| MIGS-31 | Finishing quality         | Improved high-quality draft                                          |
| MIGS-28 | Libraries used            | Illumina GAII shotgun and paired end 454 libraries                   |
| MIGS-29 | Sequencing platforms      | Illumina GAII and 454 GS FLX Titanium technologies                    |
| MIGS-31.2| Sequencing coverage      | 7.8×454 paired end, 764.2×Illumina                                  |
| MIGS-30 | Assemblers                | Velvet 1.0.13, Newbler 2.3, phrap 4.24                               |
| MIGS-32 | Gene calling methods      | Prodigal 1.4, GenePRIMP                                              |
|         | GOLD ID                   | Gi06486                                                              |
|         | NCBI project ID           | 65299                                                                |
|         | Database: IMG             | 2509276021                                                           |
|         | Project relevance         | Symbiotic N₂ fixation, agriculture                                  |

Growth conditions and DNA isolation
Rhizobium leguminosarum bv. trifolii strain WSM597 was grown to mid logarithmic phase in TY rich medium [26] on a gyratory shaker at 28°C. DNA was isolated from 60 mL of cells using a CTAB (Cetyl trimethyl ammonium bromide) bacterial genomic DNA isolation method [27].

Genome sequencing and assembly
The genome of Rhizobium leguminosarum bv. trifolii strain WSM597 was sequenced at the Joint Genome Institute (JGI) using a combination of Illumina [28] and 454 technologies [29]. An Illumina GAII shotgun library which generated 73,610,574 reads totaling 5,594.4 Mb, and a paired end 454 library with an average insert size of 14 Kb which generated 335,966 reads totaling 93.4 Mb of 454 data were generated for this genome. All general aspects of library construction and sequencing performed at the JGI can be found at the JGI website [30]. The initial draft assembly contained 190 contigs in 6 scaffolds. The 454 Titanium standard data and the 454 paired end data were assembled together with Newbler, version 2.3-PreRelease-6/30/2009. The Newbler consensus sequences were computationally shredded into 2 Kb overlapping fake reads (shreds). Illumina sequencing data were assembled with VELVET, version 1.0.13 [31], and the consensus sequences were computationally shredded into 1.5 Kb overlapping fake reads (shreds). The 454 Newbler consensus shreds, the Illumina VELVET consensus shreds and the read pairs in the 454 paired end library were integrated using parallel phrap, version SPS - 4.24 (High Performance Software, LLC). The software Consed (Ewing and Green 1998; Ewing et al. 1998; Gordon et al. 1998) was used in the following finishing process.

Illumina data was used to correct potential base errors and increase consensus quality using the software Polisher developed at JGI (Alla Lapidus, unpublished). Possible mis-assemblies were corrected using gapResolution (Cliff Han, unpublished), Dupfinisher (Han, 2006), or sequencing cloned bridging PCR fragments with subcloning. Gaps between contigs were closed by editing in Consed, by PCR and by Bubble PCR (J-F Cheng unpublished) primer walks. A total of 215 additional reactions were necessary to close gaps and to raise the quality of the finished sequence. The estimated genome size is 7.3 Mb and the final assembly is based on 57.2 Mb of 454 draft data which provides an average 7.8× coverage of the genome and 5,578.3 Mb of Illumina draft data which provides an average 764.2× coverage of the genome.

Genome annotation
Genes were identified using Prodigal [32] as part of the DOE-JGI Annotation pipeline [33], followed by a round of manual curation using the JGI GenePRIMP pipeline [34]. The predicted CDSs were translated and used to search the National Center for Biotechnology Information (NCBI) non-redundant database, UniProt, TIGRFam, Pfam, PRIAM, KEGG, COG, and InterPro databases. These data sources were combined to assert a product description for each predicted protein. Non-coding genes and miscellaneous features were predicted using tRNAscan-SE [35], RNAMMer [36], Rfam [37], TMHMM [38], and SignalP [39]. Additional gene prediction analyses and functional annotation were performed within the Integrated Microbial Genomes (IMG-ER) platform [40].
**Genome properties**

The genome is 7,634,384 nucleotides with 61.01% GC content (Table 3) in 2 scaffolds containing 53 contigs. From a total of 7,481 genes, 7,394 were protein encoding and 87 RNA only encoding genes. The majority of genes (79.24%) were assigned a putative function whilst the remaining genes were annotated as hypothetical. The distribution of genes into COGs functional categories is presented in Table 4 and Figure 3.

| Attribute                                | Value    | % of Total |
|------------------------------------------|----------|------------|
| Genome size (bp)                         | 7,634,384| 100.00     |
| DNA coding region (bp)                   | 6,596,806| 86.41      |
| DNA G+C content (bp)                     | 4,657,890| 61.01      |
| Number of scaffolds                      | 2        |            |
| Number of contigs                        | 53       |            |
| Total genes                              | 7,481    | 100.00     |
| RNA genes                                | 87       | 1.16       |
| rRNA operons*                            | 1        |            |
| Protein-coding genes                     | 7,394    | 98.84      |
| Genes with function prediction           | 5,928    | 79.24      |
| Genes assigned to COGs                   | 5,886    | 78.68      |
| Genes assigned Pfam domains              | 6,150    | 82.21      |
| Genes with signal peptides               | 634      | 8.47       |
| Genes with transmembrane helices         | 1,655    | 22.12      |
| CRISPR repeats                           | 0        |            |

*1 extra 5s rRNA and 2 extra 16s rRNA genes

**Figure 3.** Graphical map of the two DNA scaffolds of *Rhizobium leguminosarum* bv. *trifolii* strain WSM597. From outside to the center: Genes on forward strand (color by COG categories as denoted by the IMG platform), Genes on reverse strand (color by COG categories), RNA genes (tRNAs green, sRNAs red, other RNAs black), GC content, GC skew.
Table 4. Number of protein coding genes of *Rhizobium leguminosarum* bv. *trifolii* strain WSM597 associated with the general COG functional categories.

| Code | Value | Value | Description |
|------|-------|-------|-------------|
| J    | 195   | 2.95  | Translation, ribosomal structure and biogenesis |
| A    | 0     | 0.00  | RNA processing and modification |
| K    | 627   | 9.50  | Transcription |
| L    | 233   | 3.53  | Replication, recombination and repair |
| B    | 2     | 0.03  | Chromatin structure and dynamics |
| D    | 44    | 0.67  | Cell cycle control, mitosis and meiosis |
| Y    | 0     | 0.00  | Nuclear structure |
| V    | 73    | 1.11  | Defense mechanisms |
| T    | 375   | 5.68  | Signal transduction mechanisms |
| M    | 333   | 5.05  | Cell wall/membrane biogenesis |
| N    | 108   | 1.64  | Cell motility |
| Z    | 1     | 0.02  | Cytoskeleton |
| W    | 0     | 0.00  | Extracellular structures |
| U    | 107   | 1.62  | Intracellular trafficking and secretion |
| O    | 200   | 3.03  | Posttranslational modification, protein turnover, chaperones |
| C    | 351   | 5.32  | Energy production conversion |
| G    | 674   | 10.21 | Carbohydrate transport and metabolism |
| E    | 748   | 11.33 | Amino acid transport metabolism |
| F    | 109   | 1.65  | Nucleotide transport and metabolism |
| H    | 211   | 3.20  | Coenzyme transport and metabolism |
| I    | 242   | 3.67  | Lipid transport and metabolism |
| P    | 297   | 4.50  | Inorganic ion transport and metabolism |
| Q    | 171   | 2.59  | Secondary metabolite biosynthesis, transport and catabolism |
| R    | 850   | 12.88 | General function prediction only |
| S    | 649   | 9.83  | Function unknown |
| -    | 1,595 | 21.32 | Not in COGS |

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