

**P026** Using Artemis to root around in the genome sequence of *Rhizobium leguminosarum*

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*Rhizobium leguminosarum* is a nitrogen-fixing bacterium capable of nodulating the roots of some leguminous plants. Nitrogen fixation is of immense importance in agriculture and organisms that fix nitrogen can reduce dependence on nitrogenous fertilizers. The genome sequencing project of *R. leguminosarum* biovar *viciae* has been funded by the BBSRC and is being sequenced, finished and annotated at the Sanger Institute.

The genome consists of a circular chromosome of 5.06 Mb with 4742 predicted coding sequences and six plasmids, providing an additional total of 2.3 Mb of genomic DNA. Initial analysis of potentially horizontally acquired regions indicates that these regions encode diverse functions such as polysaccharide biosynthesis, type I secretion and restriction-modification systems. The plasmids encode several of the vital proteins involved in the nitrogen-fixation apparatus.

Further in-depth analysis of the genome sequence will use the Artemis program. Artemis is a genome viewer and annotation tool that acts as a visual aid for the sequence characteristics and analysis within the framework of the sequence and its six-frame translation. Artemis is written in Java and is accessible to various platforms. The Artemis program and all the sequence data is freely available from the Sanger Institute websites ([http://www.sanger.ac.uk/Projects/R\\_leguminosarum](http://www.sanger.ac.uk/Projects/R_leguminosarum) and <http://www.sanger.ac.uk/Software/Artemis/>)