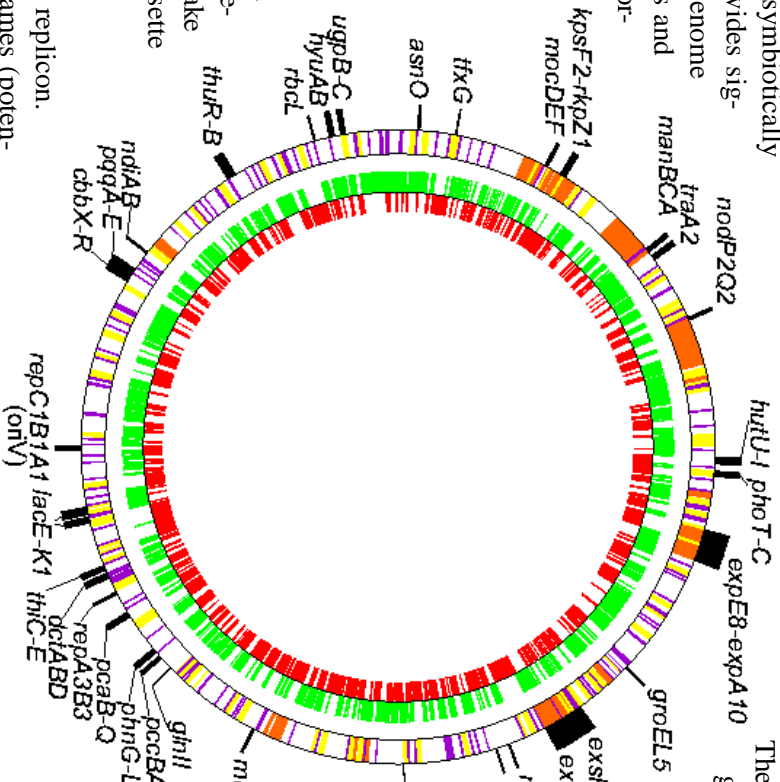


The complete sequence of the 1,683-kb pSymb megaplasmid from the N₂-fixing endosymbiont *Sinorhizobium meliloti*

Sinorhizobium meliloti is a bacteria that symbiotically fixes N₂ in plant root nodules. This provides significant advantages to plant growth. The genome of this bacteria consists of three replicons and we were part of an international consortium to complete the genome this organism. The replicon we sequenced, pSymb, has a total of 1,570 protein-coding regions, with very few insertion elements and few regions duplicated elsewhere in the genome. The replicon appears to be essential to the bacteria since the only copy of an essential arg-tRNA gene and the genes encoding the important cell division minCDE proteins are located on pSymb. Almost 20% of the pSymb sequence carries genes encoding solute uptake systems, most are of the ATP-binding cassette family.

The figure shows a map of the pSymb replicon. The inner circle displays open reading frames (potential genes) on the leading (red) and lagging (green) strands.



The outer circle shows predicted gene regions encoding transcriptional regulators (pink), ABC transport systems (yellow), and genes involved in polysaccharide biosynthesis (orange). The positions of specific genes or sets of genes are also shown on the outer edge of the map.

Arg-tRNA Recognizable gene clusters include many involved in polysaccharide biosynthesis. In total 14% of the pSymb sequence is dedicated to polysaccharide synthesis. The functions of these genes are consistent with the notion that pSymb plays a major role in the ability of this bacteria to survive in the soil environment.

The function of many hundreds of other genes remain unknown.