This is a repository copy of *What does a bacterial genome sequence represent? Mis-assignment of MAFF 303099 to the genospecies Mesorhizobium loti.*

White Rose Research Online URL for this paper:
http://eprints.whiterose.ac.uk/292/

Article:
Zhang, X., Li, F., Young, J.P.W. orcid.org/0000-0001-5259-4830 et al. (1 more author) (2002) What does a bacterial genome sequence represent? Mis-assignment of MAFF 303099 to the genospecies Mesorhizobium loti. Microbiology. pp. 3330-3331. ISSN 1350-0872

Reuse
Unless indicated otherwise, fulltext items are protected by copyright with all rights reserved. The copyright exception in section 29 of the Copyright, Designs and Patents Act 1988 allows the making of a single copy solely for the purpose of non-commercial research or private study within the limits of fair dealing. The publisher or other rights-holder may allow further reproduction and re-use of this version - refer to the White Rose Research Online record for this item. Where records identify the publisher as the copyright holder, users can verify any specific terms of use on the publisher’s website.

Takedown
If you consider content in White Rose Research Online to be in breach of UK law, please notify us by emailing eprints@whiterose.ac.uk including the URL of the record and the reason for the withdrawal request.
sMMO genes are expressed in heterologous hosts. We have recently identified a groEL gene located 5' of the mmoX gene cluster in *Methylosinus trichosporium* OB3b which, when mutated, results in a mutant with an sMMO-minus phenotype (Murrell et al., unpublished observations). This groEL, which is not present on the sMMO gene cluster constructs used in experiments by Wood and colleagues (1, 2), may be essential for the correct assembly of the sMMO or sMMO regulatory proteins, which could account for the high level expression of sMMO in the homologous host since this groEL is present both on the chromosome of *Methylosinus trichosporium* OB3b and on the expression plasmid used (3).

**J. Colin Murrell**

Department of Biological Sciences, University of Warwick, Coventry, CV4 7AL, UK

Tel: +44 24 76522553. Fax: +44 24 76523568. E-mail: cmurrell@bio.warwick.ac.uk


---

**What does a bacterial genome sequence represent? Mis-assignment of MAFF 303099 to the genospecies *Mesorhizobium loti***

Doolittle (1) recently discussed the potential and limitations of bacterial genome sequencing, and emphasized the importance of lateral gene transfers in bacterial adaptation, e.g. to become pathogens. The transferable genes, or ‘accessory genome’, should comprise genes that are advantageous intermit-tently and are not uniformly distributed among individuals of a species, though they may be shared between species. The important phenotypes that they encode are often of economic interest to medicine, e.g. pathogenicity islands and antibiotic resistance, and agriculture, e.g. symbiotic nitrogen fixation by rhizobia in association with plant roots. Such traits are sometimes used to identify species. The important phenotype is particularly striking for glutamine synthetase II (glnII), as MAFF 303099 shares a distinctive sequence thought to have been acquired by lateral gene transfer from a *Rhizobium*-like species (5). We found this same glnII signature in four strains representing the dominant (> 96%) chromosomal type (6) among 204 isolates from *Astragalus sinicus*, the typical host of *M. huakuii*. (type A1–4 in Fig. 1).

The affiliation with *M. huakuii* is particularly striking for glutamine synthetase II (glnII), as MAFF 303099 shares a distinctive sequence thought to have been acquired by the ancestor of the *M. huakuii* lineage through lateral gene transfer from a *Rhizobium*-like species (5). We found this same glnII signature in four strains representing the dominant (> 96%) chromosomal type (6) among 204 isolates from *Astragalus sinicus*, the typical host of *M. huakuii*. (type A1–4 in Fig. 1).

In contrast, MAFF 303099 has symbiosis genes (represented here by nodA) that are most similar to those of other *Lotus* symbionts (Fig. 1). Symbiosis genes are mobile, being usually found on plasmids or transmissible genetic islands. All *A. sinicus* symbionts screened to date have identical nodA sequences (7), indicating relatively recent (in evolutionary time) transfer of their symbiosis genes between species. More directly, Sullivan et al. (4) detected transfer of the genes for nodulation of *Lotus* from an inoculant strain into several different chromosomal backgrounds within four years.

Lateral gene transfer thus shapes the bac-
terial genome on two different time scales. The transfer of glnII from Rhizobium to Mesorhizobium was apparently a single, rare event, since other basic ‘housekeeping’ genes generally share a consistent phylogeny (2, 5). By contrast, the accessory genome, here represented by symbiosis genes, undergoes detectable transfers within and between species. Accessory DNA makes up 10–25% of the DNA in the three rhizobial genomes sequenced so far [M. loti (NC_002678), Sinorhizobium meliloti (NC_003047) and Agrobacterium tumefaciens (NC_003305)].

Sequencing an individual bacterial genome will provide a clear picture of the basic genome of the species, but only an arbitrary ‘snapshot’ of that part of the accessory gene pool that happens to be in the chosen isolate. When genome sequences are available from more than one strain of a species, e.g. Escherichia coli, we see clearly that they differ in their complement of accessory genes (3), so that a single strain does not adequately represent the whole species. Characterizing and sequencing more than one member of a species is therefore important, since this will define the common core of genes which defines the species. It will also allow identification of the associated accessory gene pool that provides a species with its adaptations to different niches and determines the variety of key properties such as symbioses or diseases with which the species is associated (1).

Sarah L. Turner,† Xue-Xian Zhang,‡ Fu-Di Li§ and J. Peter W. Young¹
¹Department of Biology, University of York, PO Box 373, York YO10 5YW, UK.
²Department of Microbiology, Huazhong Agricultural University, China.
†Present address: CEH Oxford, Mansfield Road, Oxford OX1 3SR, UK.

Author for correspondence: Sarah L. Turner.
Tel: +44 1865 281 630. Fax: +44 1865 281 696. e-mail: sltu@ceh.ac.uk


**MprF-mediated lysinylation of phospholipids in* Bacillus subtilis* – protection against bacteriocins in terrestrial habitats?**

A common strategy for organisms to inhibit bacteria is the production of antimicrobial peptides that damage bacterial membranes and that usually have cationic properties to enable efficient interactions with the anionic polymers in bacterial cell envelopes. Such cationic antimicrobial peptides (CAMPs) are produced by the innate immune systems of humans, animals and plants (e.g. defensins) (7) and many of the bacterial bacteriocins belong to the same class of molecules (3).

The recently described bacterial mechanisms protecting against a wide range of CAMPs may be beneficial in many kinds of environments. Most of these mechanisms involve modulations of the net charge in the bacterial cell envelope to reduce accumulation of cationic peptides (4). Modification of teichoic acids with positively charged D-